```
                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:          June 16, 2005, 02:42:13 ; Search time 7612.42 Seconds
                                           (without alignments)
                                           10687.319 Million cell updates/sec

Title:           US-10-017-084A-522
Perfect score:   1679
Sequence:        1 gttgtgtccttcagcaaaac..........ataaaaagagcaaaaaaaaa 1679

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:      9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :        GenEmbl:*
                 1:  gb_ba:*
                 2:  gb_htg:*
                 3:  gb_in:*
                 4:  gb_om:*
                 5:  gb_ov:*
                 6:  gb_pat:*
                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
                 12:  gb_sy:*
                 13:  gb_un:*
                 14:  gb_vi:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                     SUMMARIES
                      %
Result              Query
  No.    Score   Match Length DB  ID                          Description
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    1     1679   100.0   1679  6  CQ768055                    CQ768055 Sequence
    2     1679   100.0   1679  6  AR528639                    AR528639 Sequence
    3     1679   100.0   1679  6  AX358872                    AX358872 Sequence
    4     1679   100.0   1679  6  AX362365                    AX362365 Sequence
    5     1679   100.0   1679  6  AX403748                    AX403748 Sequence
    6     1679   100.0   1679  6  AX454470                    AX454470 Sequence
    7     1679   100.0   1679  6  AX464242                    AX464242 Sequence
    8     1679   100.0   1679  6  AX490948                    AX490948 Sequence
    9     1679   100.0   1679  9  AY358331                    AY358331 Homo sapi
   10   1661.4    99.0   1693  6  AR439649                    AR439649 Sequence
   11   1432.8    85.3   1839  6  AX665342                    AX665342 Sequence
   12   1432.8    85.3   1839  9  AF126426                    AF126426 Homo sapi
   13     1032    61.5   1032  6  AR439648                    AR439648 Sequence
   14    996.8    59.4   2040 10   RNU16845                    U16845 Rattus norv
   15    976.4    58.2   1615 10   BC023307                    BC023307 Mus muscu
   16      939    55.9    939  6  AR439650                    AR439650 Sequence
   17    910.6    54.2   1410 10   AF282980                    AF282980 Mus muscu
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   19    874.4    52.1   1104  6  AX665346                    AX665346 Sequence
   20      868    51.7    868  6  CQ729109                    CQ729109 Sequence
   21      856    51.0   1325  9  BC050716                    BC050716 Homo sapi
   22    851.8    50.7   1140  6  AX665348                    AX665348 Sequence
   23    643.8    38.3   1058  5  AF292935                    AF292935 Gallus ga
   24    641.8    38.2   1257  5  GGCEPU1                     Z72497 G.gallus mR
   25    638.2    38.0   1035  5  AB011810                    AB011810 Gallus ga
   26    623.6    37.1   1638 12   AF271233                    AF271233 Synthetic
c  27    609.8    36.3 202505  2  AP000912                    AP000912 Homo sapi
c  28    608.2    36.2 184716  2  AC018368                    AC018368 Homo sapi
   29    608.2    36.2 191071  9  AP004248                    AP004248 Homo sapi
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   31    595.4    35.5 187203  2  AP000832                    AP000832 Homo sapi
   32    571.2    34.0   1533  5  FFNINH55A                   Y08170 Gallus gall
   33    562.6    33.5   6380  9  HSM805672                   BX537377 Homo sapi
   34    560.2    33.4   6005 10   BC076581                    BC076581 Mus muscu
   35    551.8    32.9   1556  5  AF292934                    AF292934 Gallus ga
   36    547.4    32.6   1108  9  BC074742                    BC074742 Homo sapi
   37    545.4    32.5   2593  4  BTOBCAM                     X12672 Bovine mRNA
   38    540.8    32.2   3069 10   RATCALMA                    M88709 Rattus norv
   39    539.2    32.1   1478  9  HUMOBCAM                    L34774 Human (clon
   40    539.2    32.1   3110  6  AX665340                    AX665340 Sequence
   41    537.6    32.0   1111  9  BC074773                    BC074773 Homo sapi
   42      523    31.1   2179 10   RATCALMB                    M88710 Rattus norv
   43      523    31.1   2337 10   RATCALMC                    M88711 Rattus norv
   44    504.6    30.1   1370  5  BC074283                    BC074283 Xenopus l
   45      503    30.0    503  6  CQ768057                    CQ768057 Sequence
   46    491.2    29.3    537  6  AX593044                    AX593044 Sequence
   47    465.2    27.7   2935 12   AF271618                    AF271618 Synthetic
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   51    366.4    21.8   2055  5  BC081685                    BC081685 Danio rer
   52      362    21.6   1107  5  GGLAMPG9                    Z94718 G.gallus mR
   53    359.2    21.4   1158  5  GGLAMPG19                   Z94720 G.gallus mR
   54    357.6    21.3   2050  5  GGB19SPRO                   Y08171 Gallus gall
   55    348.4    20.8   1194  5  GGLAMPG11                   Z94719 G.gallus mR
   56    347.4    20.7   1640  9  BC033803                    BC033803 Homo sapi
   57      343    20.4   1238  6  AR030575                    AR030575 Sequence
   58      343    20.4   1238  6  AR220258                    AR220258 Sequence
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   60    341.6    20.3   1195  6  AR447794                    AR447794 Sequence
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   62    340.6    20.3    977  6  AR030574                    AR030574 Sequence
   63    340.6    20.3    977  6  AR220257                    AR220257 Sequence
   64    340.6    20.3   1014  6  AR030577                    AR030577 Sequence
   65    340.6    20.3   1014  6  AR220260                    AR220260 Sequence
   66    340.6    20.3   1017  9  HSU41901                    U41901 Human limbi
   67    338.6    20.2    861  6  AR030581                    AR030581 Sequence
   68    338.6    20.2    912  6  AR030578                    AR030578 Sequence
   69    337.4    20.1    945  6  AR030580                    AR030580 Sequence
   70    337.4    20.1   1757  6  AX704805                    AX704805 Sequence
   71    333.8    19.9    861  6  AR030582                    AR030582 Sequence
   72    331.8    19.8   1276 10   AY326256                    AY326256 Rattus no
   73    316.2    18.8    333  6  AX907426                    AX907426 Sequence
   74    316.2    18.8    333  6  BD042959                    BD042959 Sequence
   75    313.8    18.7   1410  5  BC074296                    BC074296 Xenopus l
   76    303.6    18.1    756  6  AR030589                    AR030589 Sequence
   77      301    17.9    309  6  AR415672                    AR415672 Sequence
   78      301    17.9    309  6  AX972506                    AX972506 Sequence
   79      301    17.9    309  6  BD111225                    BD111225 EST and e
   80    298.2    17.8    756  6  AR030590                    AR030590 Sequence
   81      282    16.8   1031  6  CQ728011                    CQ728011 Sequence
   82    280.4    16.7   1059  5  GGA132999                   AJ132999 Gallus Ga
   83      279    16.6   1809 10   AB017139                    AB017139 Rattus no
   84    274.4    16.3   1179 10   MMU487032                   AJ487032 Mus muscu
c  85    273.4    16.3 110000  2  AC110642_2                  Continuation (3 of
   86    273.2    16.3   1941  5  AF241638                    AF241638 Danio rer
   87    272.6    16.2   1165  6  AX662343                    AX662343 Sequence
   88    272.6    16.2   1196  6  AX662341                    AX662341 Sequence
   89    272.6    16.2   1327  6  AX704747                    AX704747 Sequence
   90    272.6    16.2   4834  6  AX358748                    AX358748 Sequence
   91    272.6    16.2   4834  6  AX362241                    AX362241 Sequence
   92    272.6    16.2   4834  6  AX403774                    AX403774 Sequence
   93   272.6   16.2   5582  9  HSM806161          BX538014 Homo sapi
   94     271   16.1   1119  6  AX675563           AX675563 Sequence
   95     271   16.1   2383  6  AX747470           AX747470 Sequence
   96     271   16.1   2383  9  AK092307           AK092307 Homo sapi
   97   269.4   16.0   2840  9  AY358132           AY358132 Homo sapi
   98   260.4   15.5   1017  6  AX644995           AX644995 Sequence
   99   258.8   15.4   1018  6  AX644993           AX644993 Sequence
  100   257.2   15.3   1136  6  AX644997           AX644997 Sequence
c 101     256   15.2    257  11  G07361             G07361 human STS W
  102   254.2   15.1   5605  9  BC036771           BC036771 Homo sapi
  103   248.2   14.8 186110  2  AC102204           AC102204 Mus muscu
  104     246   14.7   1169  6  AX644999           AX644999 Sequence
  105   238.4   14.2  20731  9  AP004721           AP004721 Homo sapi
  106   238.4   14.2  43087  9  AP005155           AP005155 Homo sapi
c 107   235.6   14.0 203572  9  AC016769           AC016769 Homo sapi
c 108   229.2   13.7    251  11  BV199013           BV199013 sqnm19956
  109   223.2   13.3   2070  5  BC080221           BC080221 Danio rer
  110   223.2   13.3   2455  5  AF241637           AF241637 Danio rer
  111   221.8   13.2   4323  10  AK122576           AK122576 Mus muscu
c 112   220.4   13.1 197553  2  AC146103           AC146103 Pan trogl
  113   217.4   12.9  36000  9  AP003166           AP003166 Homo sapi
c 114   209.4   12.5 152686  2  AC018913           AC018913 Homo sapi
  115   207.6   12.4    786  5  GGA132998          AJ132998 Gallus Ga
  116   207.2   12.3 168745  2  AC119552           AC119552 Rattus no
  117   207.2   12.3 248329  2  AC109989           AC109989 Rattus no
c 118   205.6   12.2 110000  2  AC102028_1         Continuation (2 of
  119   203.8   12.1 189323  2  AC150620           AC150620 Callithri
  120   203.8   12.1 191545  2  AC151029           AC151029 Callithri
  121   197.4   11.8 189037  2  AC150026           AC150026 Papio anu
  122   193.6   11.5    352  6  AX886912           AX886912 Sequence
  123   193.6   11.5    352  6  BD026522           BD026522 Sequence
  124   180.4   10.7   5666  6  AX740565           AX740565 Sequence
c 125   177.6   10.6 215743  2  AC148958           AC148958 Otolemur
  126   176.6   10.5    540  6  AX665354           AX665354 Sequence
  127   176.6   10.5 116069  2  AP000784           AP000784 Homo sapi
c 128   176.6   10.5 123320  9  AP000863           AP000863 Homo sapi
  129   176.6   10.5 176676  2  AC012234           AC012234 Homo sapi
  130   176.6   10.5 177102  2  AP002808           AP002808 Homo sapi
  131     175   10.4    642  6  CQ732119           CQ732119 Sequence
  132   174.4   10.4    182  6  AR413330           AR413330 Sequence
  133   174.4   10.4    182  6  AX970164           AX970164 Sequence
  134   174.4   10.4    182  6  BD108883           BD108883 EST and e
c 135   173.2   10.3 242565  2  AC094728           AC094728 Rattus no
  136   173.2   10.3 251570  2  AC094463           AC094463 Rattus no
  137   172.2   10.3 133989  2  AC149777           AC149777 Bos tauru
c 138   172.2   10.3 205738  4  AC150499           AC150499 Bos tauru
  139   171.2   10.2 184012  10  AC116523           AC116523 Mus muscu
  140   166.8    9.9    504  6  CQ715694           CQ715694 Sequence
  141   164.8    9.8    531  6  CQ719449           CQ719449 Sequence
  142   163.2    9.7    585  6  AX079674           AX079674 Sequence
c 143     160    9.5    408  6  AX684132           AX684132 Sequence
  144     156    9.3    371  6  CQ731074           CQ731074 Sequence
  145   152.4    9.1    793  5  BX932289           BX932289 Gallus ga
c 146   152.2    9.1 168191  2  AC151813           AC151813 Dasypus n
  147   147.6    8.8 259743  2  AC113965           AC113965 Mus muscu
  148     146    8.7    200  6  AX898567           AX898567 Sequence
  149     146    8.7    200  6  BD034100           BD034100 Sequence
c 150     145    8.6 150308  10  AC098294           AC098294 Rattus no
  151     145    8.6 225433  2  AC106484           AC106484 Rattus no
  152     145    8.6 237199  10  AC094830           AC094830 Rattus no
  153   140.6    8.4 152686  2  AC018913           AC018913 Homo sapi
  154   135.2    8.1    268  4  AF271984           AF271984 Bos tauru
c 155   135.2    8.1 110000  2  AC102028_0         AC102028 Mus muscu
c 156   135.2    8.1 186110  2  AC102204           AC102204 Mus muscu
  157     128    7.6 184716  2  AC018368           AC018368 Homo sapi
  158   113.6    6.8 195993  2  AC134953           AC134953 Pan trogl
  159   113.6    6.8 212752  9  AC063977           AC063977 Homo sapi
c 160   112.8    6.7 157263  2  BX957285           BX957285 Danio rer
  161   110.6    6.6    292  6  CQ716587           CQ716587 Sequence
c 162   110.4    6.6 213331  2  AC125960           AC125960 Rattus no
  163   109.6    6.5 175963  2  AC148913           AC148913 Sus scrof
  164   109.4    6.5 134184  2  AC150028           AC150028 Canis fam
  165     108    6.4 168861  2  AC130786           AC130786 Papio anu
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  166     108    6.4 172146  2  AC130272           AC130272 Papio anu
c 167   107.8    6.4 169206  10  AC123550           AC123550 Mus muscu
c 168   107.8    6.4 277603  2  AC079543           AC079543 Mus muscu
  169   106.2    6.3 229330  2  AC137057           AC137057 Rattus no
  170   106.2    6.3 238070  2  AC134313           AC134313 Rattus no
c 171   106.2    6.3 242260  2  AC094567           AC094567 Rattus no
c 172   106.2    6.3 255120  2  AC127219           AC127219 Rattus no
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  174   105.6    6.3    913  6  AR542162           AR542162 Sequence
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c 176   104.4    6.2 277228  2  AC106911           AC106911 Rattus no
  177   102.2    6.1 131490  10  AC122207           AC122207 Mus muscu
  178   102.2    6.1 177251  10  AC124565           AC124565 Mus muscu
  179     100    6.0    219  6  AR030583           AR030583 Sequence
  180      99    5.9 219713  2  AC112456           AC112456 Rattus no
  181      99    5.9 234283  2  AC114113           AC114113 Rattus no
c 182      99    5.9 250355  2  AC127766           AC127766 Rattus no
  183      99    5.9 263661  2  AC106603           AC106603 Rattus no
c 184      99    5.9 319104  2  AC106602           AC106602 Rattus no
  185    98.4    5.9    411  6  CQ731080           CQ731080 Sequence
  186    96.8    5.8 187746  2  AC087123           AC087123 Mus muscu
  187    95.2    5.7    219  6  AR030584           AR030584 Sequence
c 188    92.6    5.5 214942  10  AC125214           AC125214 Mus muscu
  189    89.8    5.3 114269  2  AP002341           AP002341 Homo sapi
  190    89.8    5.3 152797  2  AC012134           AC012134 Homo sapi
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  192    89.8    5.3 172128  2  AP000762           AP000762 Homo sapi
  193    89.8    5.3 190104  2  AP002831           AP002831 Homo sapi
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c 195      89    5.3    987  6  CQ734933           CQ734933 Sequence
c 196      89    5.3 170006  9  AP005122           AP005122 Homo sapi
  197      88    5.2    882  6  CQ732721           CQ732721 Sequence
c 198    87.2    5.2 163120  5  BX296535           BX296535 Zebrafish
c 199    87.2    5.2 180842  2  CR536619           CR536619 Danio rer
  200      87    5.2    438  6  AR416888           AR416888 Sequence
  201      87    5.2    438  6  AX977582           AX977582 Sequence
  202      87    5.2    438  6  BD112441           BD112441 EST and e
c 203    86.6    5.2 169582  2  AC102190           AC102190 Mus muscu
c 204    86.2    5.1  74368  9  AL391239           AL391239 Human DNA
c 205    86.2    5.1 131457  9  AL356600           AL356600 Human DNA
c 206    86.2    5.1 153852  2  AC009694           AC009694 Homo sapi
  207    86.2    5.1 315761  2  AL158079           AL158079 Homo sapi
  208    85.8    5.1 162247  2  AC102328           AC102328 Mus muscu
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c 211    83.4    5.0 162717  10  AC127259           AC127259 Mus muscu
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  215    78.6    4.7    420  6  AX665356           AX665356 Sequence
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  219    77.8    4.6    177  6  AR030585           AR030585 Sequence
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  221    76.8    4.6    479  6  AX665358           AX665358 Sequence
  222    71.4    4.3    480  6  AX665357           AX665357 Sequence
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  224      69    4.1 146352  2  CR548641           CR548641 Danio rer
  225      69    4.1 186279  5  BX950870           BX950870 Zebrafish
c 226      69    4.1 191779  2  CR376789           CR376789 Danio rer
  227      67    4.0 176744  2  AC027631           AC027631 Homo sapi
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c 230      65    3.9 249701  2  AC106525           AC106525 Rattus no
  231    63.4    3.8    198  6  AR030588           AR030588 Sequence
  232    61.6    3.7    270  6  AX665353           AX665353 Sequence
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  236    58.6    3.5   2000  6  AX655393           AX655393 Sequence
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c 238      58    3.5 143672  2  AP001806           AP001806 Homo sapi
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    239    57.6    3.4     420  6  AX665355              AX665355 Sequence
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    242    55.6    3.3     247  6  CQ524931              CQ524931 Sequence
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c   246      55    3.3    6359  6  AX348331              AX348331 Sequence
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    249    53.8    3.2    3294  10  BC053924              BC053924 Mus muscu
    250    53.8    3.2  134609  2  AC021416              AC021416 Homo sapi
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    257      53    3.2    3000  9  BC041174              BC041174 Homo sapi
    258    52.8    3.1     514  10  BC061178              BC061178 Mus muscu
    259    52.8    3.1     601  5  BC082926              BC082926 Xenopus l
    260    52.8    3.1     645  3  AY168768              AY168768 Branchios
    261    52.8    3.1    3351  3  AF031517              AF031517 Drosophil
c   262    52.8    3.1    5567  6  AX346491              AX346491 Sequence
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c   272    52.2    3.1     666  6  CQ418830              CQ418830 Sequence
    273    52.2    3.1     766  8  AF531371              AF531371 Gossypium
    274    52.2    3.1     828  10  BC049756              BC049756 Mus muscu
    275    52.2    3.1    2010  6  CQ586755              CQ586755 Sequence
    276    52.2    3.1    3063  6  AX817158              AX817158 Sequence
    277    52.2    3.1    3927  3  DMU78177              U78177 Drosophila
    278    52.2    3.1    4052  3  AY060363              AY060363 Drosophil
    279    52.2    3.1    5154  9  HSM805947             BX537505 Homo sapi
c   280    52.2    3.1   18218  6  AX346850              AX346850 Sequence
c   281    52.2    3.1  153869  10  AF532114              AF532114 Mus muscu
    282    52.2    3.1  177617  2  AC123634              AC123634 Mus muscu
c   283    52.2    3.1  189627  10  AC122934              AC122934 Mus muscu
    284    52.2    3.1  199909  2  AC114668              AC114668 Mus muscu
    285      52    3.1     484  6  CQ526860              CQ526860 Sequence
    286      52    3.1    1732  9  HSM806991             BX640874 Homo sapi
    287      52    3.1    1788  9  HSM806673             BX640627 Homo sapi
    288      52    3.1    1877  5  BC077826              BC077826 Xenopus l
    289      52    3.1    3720  9  BC028048              BC028048 Homo sapi
    290      52    3.1    4807  9  HSM808173             BX648027 Homo sapi
c   291      52    3.1    5739  6  AX345621              AX345621 Sequence
    292      52    3.1  180842  2  CR536619              CR536619 Danio rer
    293    51.8    3.1    1590  9  HSM803698             AL832390 Homo sapi
    294    51.8    3.1    1657  10  BC057688              BC057688 Mus muscu
    295    51.8    3.1    1885  10  BC051143              BC051143 Mus muscu
    296    51.8    3.1    2910  9  BC042070              BC042070 Homo sapi
    297    51.6    3.1     681  5  BC071507              BC071507 Danio rer
    298    51.6    3.1     935  3  AK174210              AK174210 Ciona int
    299    51.6    3.1    1604  9  BC044260              BC044260 Homo sapi
    300    51.6    3.1    1620  10  BC046622              BC046622 Mus muscu
    301    51.6    3.1    3508  6  BD227241              BD227241 Secreted
c   302    51.6    3.1    5759  6  CQ807289              CQ807289 Sequence
c   303    51.6    3.1    8759  6  CQ807079              CQ807079 Sequence
c   304    51.6    3.1    8759  6  AX598909              AX598909 Sequence
c   305    51.6    3.1    8759  6  AX599037              AX599037 Sequence
c   306    51.6    3.1    8759  6  AX767495              AX767495 Sequence
c   307    51.6    3.1    8759  6  AX795857              AX795857 Sequence
c   308    51.6    3.1    8759  6  AX822377              AX822377 Sequence
c   309    51.6    3.1    8759  6  AX826017              AX826017 Sequence
c   310    51.6    3.1    8979  6  AX251876              AX251876 Sequence
c   311    51.6    3.1    8979  6  AX344266              AX344266 Sequence
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c   312    51.6    3.1    8979  6  AX345686              AX345686 Sequence
c   313    51.6    3.1    8979  6  AX348663              AX348663 Sequence
c   314    51.6    3.1   68009  2  AC136304              AC136304 Homo sapi
c   315    51.4    3.1     921  8  NTPSAHPHI             X61665 N.tabacum p
    316    51.4    3.1    1933  9  HSM806048             BX537929 Homo sapi
    317    51.4    3.1   77139  2  AC008466              AC008466 Homo sapi
c   318    51.4    3.1   86789  10  AL928642              AL928642 Mouse DNA
c   319    51.4    3.1  179187  9  AC091549              AC091549 Homo sapi
    320    51.2    3.0     392  6  CQ516508              CQ516508 Sequence
    321    51.2    3.0     504  6  CQ526778              CQ526778 Sequence
    322    51.2    3.0    1719  3  AK116650              AK116650 Ciona int
    323    51.2    3.0    2099  9  BC043572              BC043572 Homo sapi
    324    51.2    3.0    2207  10  BC066857              BC066857 Mus muscu
    325    51.2    3.0    2217  9  BC073932              BC073932 Homo sapi
    326    51.2    3.0    2286  9  BC020211              BC020211 Homo sapi
    327    51.2    3.0    2419  9  BC043583              BC043583 Homo sapi
    328    51.2    3.0    2704  3  AB073429              AB073429 Ciona sav
    329    51.2    3.0    3305  10  BC040407              BC040407 Mus muscu
    330    51.2    3.0    3383  9  HSM803701             AL832393 Homo sapi
    331    51.2    3.0    3626  9  BC012147              BC012147 Homo sapi
    332    51.2    3.0    5123  10  BC064466              BC064466 Mus muscu
    333    51.2    3.0  202533  2  AC146464              AC146464 Saimiri s
    334      51    3.0    1637  5  BC064270              BC064270 Xenopus t
    335      51    3.0    1950  9  BC042196              BC042196 Homo sapi
    336      51    3.0    2730  9  BC053349              BC053349 Homo sapi
    337      51    3.0  179371  10  AC140335              AC140335 Mus muscu
    338    50.8    3.0     897  10  BC049625              BC049625 Mus muscu
    339    50.8    3.0    1026  6  CQ708603              CQ708603 Sequence
    340    50.8    3.0    1383  5  BC074687              BC074687 Xenopus t
    341    50.8    3.0    1429  9  BC043584              BC043584 Homo sapi
    342    50.8    3.0    1447  9  BC044232              BC044232 Homo sapi
    343    50.8    3.0    1763  10  BC061098              BC061098 Mus muscu
    344    50.8    3.0    1882  5  BC068036              BC068036 Xenopus t
    345    50.8    3.0    1959  10  BC060504              BC060504 Mus muscu
    346    50.8    3.0    2313  10  BC021410              BC021410 Mus muscu
    347    50.8    3.0    2643  9  BC032495              BC032495 Homo sapi
    348    50.8    3.0    5966  9  HSM808164             BX648018 Homo sapi
    349    50.8    3.0  163311  2  AC102506              AC102506 Mus muscu
c   350    50.8    3.0  171550  2  AC117731              AC117731 Mus muscu
    351    50.8    3.0  195601  2  AL807787              AL807787 Mus muscu
    352    50.8    3.0  201821  10  AL671901              AL671901 Mouse DNA
c   353    50.6    3.0     393  6  CQ408183              CQ408183 Sequence
    354    50.6    3.0     909  10  BC035323              BC035323 Mus muscu
    355    50.6    3.0    1930  5  BC066725              BC066725 Danio rer
    356    50.6    3.0    2356  10  BC061208              BC061208 Mus muscu
    357    50.6    3.0    2924  6  AX683129              AX683129 Sequence
    358    50.6    3.0    2924  10  S68736                S68736 Rattus sp.
    359    50.6    3.0    3758  9  HSM801755             AL136787 Homo sapi
c   360    50.6    3.0    4990  6  CQ493127              CQ493127 Sequence
c   361    50.6    3.0    4990  6  CQ493522              CQ493522 Sequence
c   362    50.6    3.0    6029  6  AX279994              AX279994 Sequence
c   363    50.6    3.0    6029  6  AX356432              AX356432 Sequence
c   364    50.6    3.0  170788  2  AC139387              AC139387 Rattus no
c   365    50.6    3.0  186488  10  AC102668              AC102668 Mus muscu
    366    50.6    3.0  221903  10  AC125223              AC125223 Mus muscu
    367    50.6    3.0  224635  2  AC094848              AC094848 Rattus no
c   368    50.6    3.0  263637  2  AC094254              AC094254 Rattus no
c   369    50.6    3.0  349980  6  AX344556              AX344556 Sequence
c   370    50.4    3.0     310  6  AX187085              AX187085 Sequence
    371    50.4    3.0     319  6  CQ670102              CQ670102 Sequence
    372    50.4    3.0     655  3  AK174309              AK174309 Ciona int
    373    50.4    3.0     669  9  HSM800251             AL049466 Homo sapi
    374    50.4    3.0     931  10  BC049725              BC049725 Mus muscu
    375    50.4    3.0    1027  9  BC035292              BC035292 Homo sapi
    376    50.4    3.0    1044  10  BC049565              BC049565 Mus muscu
    377    50.4    3.0    1245  10  BC049747              BC049747 Mus muscu
    378    50.4    3.0    2677  9  BC050385              BC050385 Homo sapi
    379    50.4    3.0    2815  9  BC038597              BC038597 Homo sapi
    380    50.4    3.0    3183  9  BC044242              BC044242 Homo sapi
c   381    50.4    3.0    6668  6  AX346598              AX346598 Sequence
c   382    50.4    3.0  230193  10  AL929570              AL929570 Mouse DNA
    383    50.2    3.0     201  6  CQ487162              CQ487162 Sequence
    384    50.2    3.0     240  6  I48979                I48979 Sequence 6
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c 385    50.2    3.0     383  6  CQ502211          CQ502211 Sequence
c 386    50.2    3.0     383  6  CQ511079          CQ511079 Sequence
c 387    50.2    3.0     384  6  CQ395463          CQ395463 Sequence
c 388    50.2    3.0     384  6  CQ401799          CQ401799 Sequence
  389    50.2    3.0     384  6  CQ487104          CQ487104 Sequence
  390    50.2    3.0     448  6  CQ516969          CQ516969 Sequence
  391    50.2    3.0     861  9  AK026600          AK026600 Homo sapi
  392    50.2    3.0    1090  10  BC049543          BC049543 Mus muscu
  393    50.2    3.0    1448  10  BC052344          BC052344 Mus muscu
  394    50.2    3.0    1619  9  BC032001          BC032001 Homo sapi
  395    50.2    3.0    2078  9  BC042098          BC042098 Homo sapi
  396    50.2    3.0    2104  9  BC032371          BC032371 Homo sapi
  397    50.2    3.0    2641  10  BC044860          BC044860 Mus muscu
  398    50.2    3.0    4064  10  BC072632          BC072632 Mus muscu
c 399    50.2    3.0    6476  6  AX345442          AX345442 Sequence
c 400    50.2    3.0 150751  9  AC092609          AC092609 Homo sapi
c 401    50.2    3.0 168136  2  AC138388          AC138388 Mus muscu
  402    50.2    3.0 182871  3  AC117176          AC117176 Dictyoste
c 403    50.2    3.0 189631  2  AC009920          AC009920 Homo sapi
  404    50.2    3.0 203114  2  AC011818          AC011818 Homo sapi
c 405    50.2    3.0 349980  6  AX344553          AX344553 Sequence
  406    50      3.0     325  6  CQ527169          CQ527169 Sequence
  407    50      3.0     464  6  CQ519083          CQ519083 Sequence
  408    50      3.0     471  6  CQ522475          CQ522475 Sequence
  409    50      3.0     646  5  BC083988          BC083988 Xenopus l
  410    50      3.0     653  10  BC039566          BC039566 Mus muscu
  411    50      3.0     842  9  BC051899          BC051899 Homo sapi
  412    50      3.0     870  6  BD231669          BD231669 31 human
  413    50      3.0    2240  9  BC062587          BC062587 Homo sapi
  414    50      3.0    2556  9  HSM805953         BX537854 Homo sapi
  415    50      3.0    2936  5  BC077828          BC077828 Xenopus l
  416    50      3.0    3203  9  BC040941          BC040941 Homo sapi
  417    50      3.0    3645  10  BC062916          BC062916 Mus muscu
  418    50      3.0    3806  5  AJ720876          AJ720876 Gallus ga
  419    50      3.0    4942  9  HSM808887         BX648736 Homo sapi
c 420    50      3.0    5387  6  AX344633          AX344633 Sequence
  421    50      3.0    9747  9  HSM806689         BX640641 Homo sapi
c 422    50      3.0   21537  6  AX346901          AX346901 Sequence
c 423    50      3.0 110000  2  PFMAL13_07        Continuation (8 of
  424    50      3.0 137697  2  AC126419          AC126419 Mus muscu
c 425    50      3.0 160706  2  AC137910          AC137910 Canis fam
c 426    50      3.0 173053  10  AL844145          AL844145 Mouse DNA
c 427    50      3.0 184057  10  AL928579          AL928579 Mouse DNA
  428    50      3.0 184163  2  AC120245          AC120245 Rattus no
c 429    50      3.0 189649  2  AC139641          AC139641 Rattus no
  430    50      3.0 212996  2  CR548633          CR548633 Danio rer
c 431    50      3.0 245677  10  AC129162          AC129162 Rattus no
  432    50      3.0 249734  2  AC097362          AC097362 Rattus no
  433    49.8    3.0     263  6  CQ663258          CQ663258 Sequence
  434    49.8    3.0     270  6  CQ655781          CQ655781 Sequence
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  436    49.8    3.0     376  6  CQ526056          CQ526056 Sequence
  437    49.8    3.0     381  6  CQ522618          CQ522618 Sequence
  438    49.8    3.0     543  6  CQ524637          CQ524637 Sequence
c 439    49.8    3.0     545  6  AX185705          AX185705 Sequence
  440    49.8    3.0     573  11  BV060605          BV060605 S209P6332
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  442    49.8    3.0     815  9  BC070265          BC070265 Homo sapi
  443    49.8    3.0     854  3  AK174348          AK174348 Ciona int
  444    49.8    3.0     894  9  BC044257          BC044257 Homo sapi
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  447    49.8    3.0    1073  6  BD190930          BD190930 Secreted
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  450    49.8    3.0    2005  9  BC013372          BC013372 Homo sapi
  451    49.8    3.0    2012  9  AY125488          AY125488 Homo sapi
  452    49.8    3.0    2266  9  BC047898          BC047898 Homo sapi
  453    49.8    3.0    2496  6  BD191411          BD191411 Secreted
  454    49.8    3.0    2539  9  BC041100          BC041100 Homo sapi
  455    49.8    3.0    2630  9  BC038222          BC038222 Homo sapi
  456    49.8    3.0    3230  9  BC063118          BC063118 Homo sapi
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c 458    49.8    3.0    8712  6  AX344694          AX344694 Sequence
c 459    49.8    3.0   13758  3  SST558163         AJ558163 Strongylo
c 460    49.8    3.0   84299  5  BX469900          BX469900 Zebrafish
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c 464    49.8    3.0 193796  2  AC123600          AC123600 Mus muscu
c 465    49.8    3.0 198615  10  AC123678          AC123678 Mus muscu
  466    49.8    3.0 212604  5  AL805945          AL805945 Zebrafish
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  468    49.8    3.0 251721  2  AC136566          AC136566 Rattus no
c 469    49.8    3.0 263341  2  AC094581          AC094581 Rattus no
c 470    49.8    3.0 266869  2  AC123456          AC123456 Rattus no
  471    49.8    3.0 289973  2  AC135678          AC135678 Rattus no
  472    49.6    3.0     762  9  BC070287          BC070287 Homo sapi
  473    49.6    3.0     793  9  BC018189          BC018189 Homo sapi
  474    49.6    3.0    1003  5  BC067645          BC067645 Danio rer
  475    49.6    3.0    1044  9  AB019565          AB019565 Homo sapi
  476    49.6    3.0    1218  9  BC065742          BC065742 Homo sapi
  477    49.6    3.0    1250  9  BC051908          BC051908 Homo sapi
  478    49.6    3.0    1271  9  AF090934          AF090934 Homo sapi
  479    49.6    3.0    1340  9  BC073835          BC073835 Homo sapi
  480    49.6    3.0    1458  9  BC041443          BC041443 Homo sapi
  481    49.6    3.0    1530  9  BC036925          BC036925 Homo sapi
  482    49.6    3.0    1606  10  BC051176          BC051176 Mus muscu
  483    49.6    3.0    1657  8  NTACCS            X98492 Nicotiana t
  484    49.6    3.0    1787  9  BC046645          BC046645 Homo sapi
  485    49.6    3.0    1993  3  AK112520          AK112520 Ciona int
  486    49.6    3.0    2027  9  BC063512          BC063512 Homo sapi
  487    49.6    3.0    2081  9  HSM806272         BX537592 Homo sapi
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c 489    49.6    3.0    2161  6  CQ414527          CQ414527 Sequence
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  493    49.6    3.0    3141  10  BC017634          BC017634 Mus muscu
  494    49.6    3.0    3232  9  AF090901          AF090901 Homo sapi
  495    49.6    3.0    3914  9  HSM803724         AL832416 Homo sapi
  496    49.6    3.0    4385  9  HSM806219         BX538049 Homo sapi
  497    49.6    3.0    5134  9  BC032404          BC032404 Homo sapi
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c 499    49.6    3.0    5520  6  AX346420          AX346420 Sequence
c 500    49.6    3.0    6015  6  AX345579          AX345579 Sequence
  501    49.6    3.0 110000  2  AC102349_0        AC102349 Mus muscu
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c 503    49.6    3.0 151802  3  AC114263          AC114263 Dictyoste
  504    49.6    3.0 173854  2  AC073047          AC073047 Homo sapi
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  516    49.4    2.9    1081  9  BC043527          BC043527 Homo sapi
  517    49.4    2.9    1310  9  HSM807559         BX647414 Homo sapi
  518    49.4    2.9    1589  9  BC043543          BC043543 Homo sapi
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  524    49.4    2.9    2002  9  BC068030          BC068030 Homo sapi
  525    49.4    2.9    2395  9  AF090903          AF090903 Homo sapi
  526    49.4    2.9    3475  9  HSM808741         BX648590 Homo sapi
  527    49.4    2.9    4066  10  BC048824          BC048824 Mus muscu
  528    49.4    2.9    4744  5  BC066770          BC066770 Xenopus l
  529    49.4    2.9    4782  14  AY744492          AY744492 Tomato sp
c 530    49.4    2.9   71532  2  AC023655          AC023655 Homo sapi
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  532    49.4    2.9 110000  3   AC116305_0        AC116305 Dictyoste
c 533    49.4    2.9 138604  2   CR847865          CR847865 Danio rer
c 534    49.4    2.9 169736  2   AC126225          AC126225 Papio anu
c 535    49.4    2.9 187024  2   CR759947          CR759947 Gorilla g
c 536    49.4    2.9 227273  2   AC141526          AC141526 Rattus no
c 537    49.4    2.9 335050  3   PFA929356         AL929356 Plasmodiu
c 538    49.4    2.9 349980  6   AX344559          AX344559 Sequence
c 539    49.4    2.9 349980  6   AX344566          AX344566 Sequence
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  542    49.2    2.9    544  6   CQ524776          CQ524776 Sequence
  543    49.2    2.9    554  6   CQ526772          CQ526772 Sequence
  544    49.2    2.9    575  6   CQ526566          CQ526566 Sequence
c 545    49.2    2.9    621  6   AX187131          AX187131 Sequence
  546    49.2    2.9    650  9   BC034814          BC034814 Homo sapi
  547    49.2    2.9    758  9   BC062750          BC062750 Homo sapi
  548    49.2    2.9   1191  9   BC014547          BC014547 Homo sapi
  549    49.2    2.9   1381  5   BC063358          BC063358 Xenopus t
  550    49.2    2.9   1537  9   HSM803079         AL713709 Homo sapi
  551    49.2    2.9   1629  10  BC033451           BC033451 Mus muscu
  552    49.2    2.9   1702  9   BC052993          BC052993 Homo sapi
  553    49.2    2.9   2270  9   HSM806047         BX537526 Homo sapi
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  556    49.2    2.9   2628  9   BC032691          BC032691 Homo sapi
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  558    49.2    2.9   3030  3   AK116919          AK116919 Ciona int
  559    49.2    2.9   3300  9   BC011656          BC011656 Homo sapi
  560    49.2    2.9   3341  9   BC032308          BC032308 Homo sapi
  561    49.2    2.9   3392  3   AF300334          AF300334 Dictyoste
  562    49.2    2.9   3686  10  BC023773           BC023773 Mus muscu
  563    49.2    2.9   3836  9   BC063854          BC063854 Homo sapi
  564    49.2    2.9   4265  9   HSM807603         BX647458 Homo sapi
  565    49.2    2.9   6644  6   E23356            E23356 Virus vecto
c 566    49.2    2.9   7058  6   AX348438          AX348438 Sequence
  567    49.2    2.9   7372  6   E23357            E23357 Virus vecto
  568    49.2    2.9   7797  6   E23355            E23355 Virus vecto
  569    49.2    2.9   7996  6   E23359            E23359 Virus vecto
c 570    49.2    2.9  11394  6   AX323608          AX323608 Sequence
c 571    49.2    2.9  35962  6   AX598904          AX598904 Sequence
  572    49.2    2.9 153064  9   AC011492          AC011492 Homo sapi
c 573    49.2    2.9 162473  9   AC005803          AC005803 Homo sapi
  574    49.2    2.9 226142  2   AC126422          AC126422 Mus muscu
  575    49.2    2.9 245117  2   AC111284          AC111284 Rattus no
  576    49.2    2.9 302156  3   AC116977          AC116977 Dictyoste
c 577    49.2    2.9 349980  6   AX344573          AX344573 Sequence
c 578      49    2.9    256  6   AX182154          AX182154 Sequence
  579      49    2.9    347  6   CQ526680          CQ526680 Sequence
  580      49    2.9    429  6   CQ525532          CQ525532 Sequence
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  584      49    2.9    608  10  BC061544           BC061544 Rattus no
  585      49    2.9    757  9   BC051791          BC051791 Homo sapi
  586      49    2.9    967  9   HSM802777         AL390167 Homo sapi
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  588      49    2.9   1414  3   AK112149          AK112149 Ciona int
  589      49    2.9   1755  9   BC031825          BC031825 Homo sapi
  590      49    2.9   1763  5   AY079192          AY079192 Xenopus t
  591      49    2.9   1850  9   BC040123          BC040123 Homo sapi
  592      49    2.9   1853  10  BC052346           BC052346 Mus muscu
  593      49    2.9   1869  5   BC076804          BC076804 Xenopus l
  594      49    2.9   1891  9   HSM807589         BX647444 Homo sapi
  595      49    2.9   1912  10  BC027060           BC027060 Mus muscu
  596      49    2.9   1935  5   BC065678          BC065678 Danio rer
  597      49    2.9   1954  6   BD270057          BD270057 Secreted
  598      49    2.9   1960  9   BC038806          BC038806 Homo sapi
  599      49    2.9   2045  9   BC047761          BC047761 Homo sapi
  600      49    2.9   2116  9   BC034379          BC034379 Homo sapi
  601      49    2.9   2197  9   BC045177          BC045177 Homo sapi
  602      49    2.9   2347  9   BC027875          BC027875 Homo sapi
  603      49    2.9   2553  10  BC061558           BC061558 Rattus no
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  604      49    2.9   2700  9   BC064849          BC064849 Homo sapi
  605      49    2.9   2728  9   BC022218          BC022218 Homo sapi
  606      49    2.9   3020  10  BC055068           BC055068 Mus muscu
  607      49    2.9   3482  9   HSM800550         AL050393 Homo sapi
  608      49    2.9   3499  10  BC007476           BC007476 Mus muscu
  609      49    2.9   3856  9   HSM805531         AL834437 Homo sapi
  610      49    2.9   3870  9   HSM806049         BX537527 Homo sapi
  611      49    2.9   3916  10  BC018439           BC018439 Mus muscu
  612      49    2.9   5703  10  BC054080           BC054080 Mus muscu
c 613      49    2.9   5845  6   AX346564          AX346564 Sequence
  614      49    2.9   5930  6   CQ412529          CQ412529 Sequence
c 615      49    2.9   6012  6   AX346960          AX346960 Sequence
c 616      49    2.9   6161  6   AX345313          AX345313 Sequence
c 617      49    2.9   6211  6   AX345708          AX345708 Sequence
c 618      49    2.9   6522  6   AX345952          AX345952 Sequence
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c 621      49    2.9  11416  6   AX345020          AX345020 Sequence
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c 623      49    2.9  40862  6   AX346974          AX346974 Sequence
c 624      49    2.9 125020  9   AF429315          AF429315 Homo sapi
c 625      49    2.9 135050  2   AC118536          AC118536 Canis fam
  626      49    2.9 160230  10  BX072552           BX072552 Mouse DNA
  627      49    2.9 180352  2   AC120550          AC120550 Mus muscu
  628      49    2.9 198792  2   AC117825          AC117825 Mus muscu
c 629      49    2.9 203422  2   AC107857          AC107857 Mus muscu
  630      49    2.9 248353  2   AC106139          AC106139 Rattus no
c 631      49    2.9 349980  6   AX344561          AX344561 Sequence
c 632      49    2.9 349980  6   AX344565          AX344565 Sequence
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  642    48.8    2.9    836  6   AX704815          AX704815 Sequence
  643    48.8    2.9    844  9   BC009571          BC009571 Homo sapi
  644    48.8    2.9   1007  10  BC049682           BC049682 Mus muscu
  645    48.8    2.9   1345  10  BC048718           BC048718 Mus muscu
  646    48.8    2.9   1362  9   BC065292          BC065292 Homo sapi
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  651    48.8    2.9   1990  10  BC042668           BC042668 Mus muscu
  652    48.8    2.9   2064  10  BC053424           BC053424 Mus muscu
  653    48.8    2.9   2394  5   BC063911          BC063911 Xenopus t
  654    48.8    2.9   2500  9   BC065207          BC065207 Homo sapi
  655    48.8    2.9   2735  9   BC046366          BC046366 Homo sapi
  656    48.8    2.9   2823  9   BC018694          BC018694 Homo sapi
  657    48.8    2.9   2968  9   BC060758          BC060758 Homo sapi
  658    48.8    2.9   3134  9   HSM805794         BX537718 Homo sapi
  659    48.8    2.9   3380  9   HSM807223         BX647079 Homo sapi
  660    48.8    2.9   4436  10  BC058961           BC058961 Mus muscu
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c 666    48.8    2.9 141914  2   AC108177          AC108177 Felis cat
c 667    48.8    2.9 174495  2   AC101795          AC101795 Mus muscu
  668    48.8    2.9 175202  9   AC134684          AC134684 Homo sapi
c 669    48.8    2.9 188884  9   AC130367          AC130367 Homo sapi
c 670    48.8    2.9 214132  2   AC124975          AC124975 Mus muscu
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  673    48.8    2.9 274097  2   AC111767          AC111767 Rattus no
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   687    48.6    2.9   1642  5  BC064224          BC064224 Xenopus t
   688    48.6    2.9   1781  9  BC043529          BC043529 Homo sapi
   689    48.6    2.9   1808  6  AX535019          AX535019 Sequence
   690    48.6    2.9   1959  9  BC043548          BC043548 Homo sapi
   691    48.6    2.9   1994  3  AK116078          AK116078 Ciona int
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   695    48.6    2.9   2390  9  AF090900          AF090900 Homo sapi
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c  704    48.6    2.9 157311  10  AC132236          AC132236 Mus muscu
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   706    48.6    2.9 167728  2  AC115889          AC115889 Mus muscu
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   713    48.6    2.9 210233  2  AC128584          AC128584 Rattus no
   714    48.6    2.9 210269  2  BX927280          BX927280 Danio rer
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c  716    48.6    2.9 212908  2  CR847533          CR847533 Danio rer
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   738    48.4    2.9   2184  9  AB060903          AB060903 Macaca fa
   739    48.4    2.9   2238  5  BC063964          BC063964 Danio rer
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   742    48.4    2.9   2652  3  AK174388          AK174388 Ciona int
   743    48.4    2.9   2679  10  BC006021          BC006021 Mus muscu
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c  759    48.4    2.9   4316  6  AX826028          AX826028 Sequence
c  760    48.4    2.9   5195  6  AX345823          AX345823 Sequence
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c  762    48.4    2.9   6070  6  AX346581          AX346581 Sequence
c  763    48.4    2.9   6070  6  AX348804          AX348804 Sequence
c  764    48.4    2.9   6070  6  AX458614          AX458614 Sequence
c  765    48.4    2.9   6577  6  AX251920          AX251920 Sequence
c  766    48.4    2.9   6577  6  AX346258          AX346258 Sequence
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c  772    48.4    2.9   6944  6  AX657867          AX657867 Sequence
c  773    48.4    2.9   6944  6  AX659141          AX659141 Sequence
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   775    48.4    2.9   8546  6  AX828406          AX828406 Sequence
   776    48.4    2.9   8546  9  HSA306906         AJ306906 Homo sapi
c  777    48.4    2.9   9117  6  AX345970          AX345970 Sequence
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c  784    48.4    2.9  73778  6  AX344575          AX344575 Sequence
c  785    48.4    2.9 145275  9  AF189745          AF189745 Homo sapi
c  786    48.4    2.9 149813  2  BX942840          BX942840 Danio rer
   787    48.4    2.9 165146  2  AP002415          AP002415 Homo sapi
c  788    48.4    2.9 167671  2  AC142166          AC142166 Mus muscu
   789    48.4    2.9 176929  9  AC004887          AC004887 Homo sapi
c  790    48.4    2.9 182871  3  AC117176          AC117176 Dictyoste
c  791    48.4    2.9 183648  3  AC117081          AC117081 Dictyoste
c  792    48.4    2.9 188555  10  AC122417          AC122417 Mus muscu
   793    48.4    2.9 198377  2  CR792437          CR792437 Danio rer
   794    48.4    2.9 199472  9  AC022267          AC022267 Homo sapi
c  795    48.4    2.9 204278  10  AC124507          AC124507 Mus muscu
c  796    48.4    2.9 208921  2  AP001911          AP001911 Homo sapi
c  797    48.4    2.9 215676  2  AC131299          AC131299 Mus muscu
   798    48.4    2.9 221944  2  AC119914          AC119914 Mus muscu
   799    48.4    2.9 228178  2  AC101866          AC101866 Mus muscu
c  800    48.4    2.9 232304  2  AC103201          AC103201 Rattus no
c  801    48.4    2.9 258658  3  AE014832          AE014832 Plasmodiu
c  802    48.4    2.9 349980  6  AX344558          AX344558 Sequence
c  803    48.4    2.9 349980  6  AX344570          AX344570 Sequence
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c  805    48.2    2.9    268  6  AX185659          AX185659 Sequence
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c  808    48.2    2.9    385  6  CQ398297          CQ398297 Sequence
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   813    48.2    2.9    527  10  BC049658          BC049658 Mus muscu
   814    48.2    2.9    633  10  BC059147          BC059147 Rattus no
   815    48.2    2.9    724  10  BC049721          BC049721 Mus muscu
   816    48.2    2.9    745  10  BC049606          BC049606 Mus muscu
   817    48.2    2.9   1119  10  BC021629          BC021629 Mus muscu
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   821    48.2    2.9   1770  10  BC060519          BC060519 Rattus no
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   823    48.2    2.9   2038  6  AX573129                    AX573129 Sequence
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   825    48.2    2.9   2137  9  AB062938                    AB062938 Macaca fa
   826    48.2    2.9   2406  9  BC017107                    BC017107 Homo sapi
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c  829    48.2    2.9   7238  6  AX345350                    AX345350 Sequence
c  830    48.2    2.9   8895  6  AX345234                    AX345234 Sequence
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   834    48.2    2.9 161297  10  AC139135                    AC139135 Mus muscu
   835    48.2    2.9 167418  10  AC133944                    AC133944 Mus muscu
c  836    48.2    2.9 171298  10  AC123735                    AC123735 Mus muscu
   837    48.2    2.9 179206  2  AC113199                    AC113199 Mus muscu
c  838    48.2    2.9 185634  2  AC119930                    AC119930 Mus muscu
c  839    48.2    2.9 195888  10  AC114604                    AC114604 Mus muscu
c  840    48.2    2.9 218297  2  AC126035                    AC126035 Mus muscu
   841    48.2    2.9 219106  10  AC123640                    AC123640 Mus muscu
   842    48.2    2.9 222725  2  AC110732                    AC110732 Mus muscu
c  843    48.2    2.9 257700  2  AC147391                    AC147391 Pan trogl
   844      48    2.9    312  6  CQ699683                    CQ699683 Sequence
   845      48    2.9    323  6  CQ524910                    CQ524910 Sequence
   846      48    2.9    452  6  CQ527434                    CQ527434 Sequence
   847      48    2.9    515  6  CQ526571                    CQ526571 Sequence
   848      48    2.9    533  6  CQ525634                    CQ525634 Sequence
   849      48    2.9    540  6  CQ526524                    CQ526524 Sequence
   850      48    2.9    580  10  BC006049                    BC006049 Mus muscu
   851      48    2.9    583  11  HUMUT5097                   L17690 Human STS U
   852      48    2.9    585  6  CQ526237                    CQ526237 Sequence
   853      48    2.9    602  9  BC008488                    BC008488 Homo sapi
c  854      48    2.9    606  6  CQ503221                    CQ503221 Sequence
c  855      48    2.9    606  6  CQ512068                    CQ512068 Sequence
   856      48    2.9    721  9  AK026526                    AK026526 Homo sapi
   857      48    2.9    760  9  BC032326                    BC032326 Homo sapi
   858      48    2.9    836  10  BC049716                    BC049716 Mus muscu
   859      48    2.9    869  10  BC054421                    BC054421 Mus muscu
   860      48    2.9    927  10  BC047927                    BC047927 Mus muscu
   861      48    2.9    988  5  BC055636                    BC055636 Danio rer
   862      48    2.9   1248  5  BC071085                    BC071085 Xenopus l
   863      48    2.9   1277  5  BC084489                    BC084489 Xenopus t
   864      48    2.9   1352  3  AK115954                    AK115954 Ciona int
   865      48    2.9   1391  5  BC074604                    BC074604 Xenopus t
   866      48    2.9   1409  5  BC064261                    BC064261 Xenopus t
   867      48    2.9   1409  10  BC040771                    BC040771 Mus muscu
   868      48    2.9   1415  10  BC020016                    BC020016 Mus muscu
   869      48    2.9   1426  5  BC054250                    BC054250 Xenopus l
   870      48    2.9   1483  9  AK026528                    AK026528 Homo sapi
   871      48    2.9   1526  5  BC084459                    BC084459 Xenopus t
   872      48    2.9   1608  9  AY358187                    AY358187 Homo sapi
   873      48    2.9   1622  9  BC043524                    BC043524 Homo sapi
   874      48    2.9   1632  5  BC068370                    BC068370 Danio rer
   875      48    2.9   1637  6  AX460089                    AX460089 Sequence
   876      48    2.9   1643  10  BC024405                    BC024405 Mus muscu
   877      48    2.9   1646  9  BC051812                    BC051812 Homo sapi
   878      48    2.9   1690  6  E32442                      E32442 Mammal-deri
   879      48    2.9   1720  10  BC046603                    BC046603 Mus muscu
   880      48    2.9   1727  5  BC071446                    BC071446 Danio rer
   881      48    2.9   1860  9  BC058897                    BC058897 Homo sapi
   882      48    2.9   1985  6  BD172402                    BD172402 Secreted
   883      48    2.9   1985  6  BD172721                    BD172721 Secreted
   884      48    2.9   1985  6  BD173040                    BD173040 Secreted
   885      48    2.9   1985  6  BD173359                    BD173359 Secreted
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   894      48    2.9   1985  6  AX697621                    AX697621 Sequence
   895      48    2.9   1985  6  BD075542                    BD075542 Secretory

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   897      48    2.9   2003  9  BC051760                    BC051760 Homo sapi
   898      48    2.9   2081  10  BC043712                    BC043712 Mus muscu
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   900      48    2.9   2202  10  BC052362                    BC052362 Mus muscu
   901      48    2.9   2209  9  BC063878                    BC063878 Homo sapi
   902      48    2.9   2248  5  BC068963                    BC068963 Xenopus l
   903      48    2.9   2590  9  BC064421                    BC064421 Homo sapi
   904      48    2.9   2632  9  BC030698                    BC030698 Homo sapi
   905      48    2.9   2777  5  BC063344                    BC063344 Xenopus t
   906      48    2.9   2905  3  AK174395                    AK174395 Ciona int
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   914      48    2.9   4306  10  BC059824                    BC059824 Mus muscu
   915      48    2.9   4389  10  BC058345                    BC058345 Mus muscu
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c  919      48    2.9   6145  6  AX345875                    AX345875 Sequence
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c  924      48    2.9  18281  6  AX345864                    AX345864 Sequence
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   927      48    2.9 184039  10  AC139376                    AC139376 Mus muscu
   928      48    2.9 184365  2  AC079639                    AC079639 Mus muscu
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c  930      48    2.9 194180  2  AC069140                    AC069140 Homo sapi
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c  934      48    2.9 232080  2  AC145374                    AC145374 Mus muscu
   935      48    2.9 232234  2  AC108634                    AC108634 Rattus no
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   937      48    2.9 247650  2  AC094213                    AC094213 Rattus no
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   939      48    2.9 309805  2  AC026340                    AC026340 Homo sapi
   940      48    2.9 321708  2  AC087142                    AC087142 Mus muscu
c  941      48    2.9 349980  6  AX344554                    AX344554 Sequence
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   945    47.8    2.8    233  6  CQ516563                    CQ516563 Sequence
   946    47.8    2.8    309  6  CQ513146                    CQ513146 Sequence
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   951    47.8    2.8    497  6  CQ526425                    CQ526425 Sequence
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   955    47.8    2.8    515  6  CQ522671                    CQ522671 Sequence
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   957    47.8    2.8    543  11  BV064080                    BV064080 S208P6631
   958    47.8    2.8    548  6  CQ516864                    CQ516864 Sequence
   959    47.8    2.8    574  6  CQ525654                    CQ525654 Sequence
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   964    47.8    2.8    791  9  BC038970                    BC038970 Homo sapi
   965    47.8    2.8    798  10  BC005501                    BC005501 Mus muscu
   966    47.8    2.8    872  6  AX068322                    AX068322 Sequence
   967    47.8    2.8    885  3  AK174656                    AK174656 Ciona int
   968    47.8    2.8    980  10  BC063173                    BC063173 Rattus no
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  972    47.8    2.8    1035  10  BC055104                 BC055104 Mus muscu
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  979    47.8    2.8    1345  9  BC073861                 BC073861 Homo sapi
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  984    47.8    2.8    1580  5  BC067146                 BC067146 Danio rer
  985    47.8    2.8    1728  9  AB070110                 AB070110 Macaca fa
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  988    47.8    2.8    1788  5  BC084147                 BC084147 Xenopus t
  989    47.8    2.8    1819  9  BC073865                 BC073865 Homo sapi
  990    47.8    2.8    1963  10  BC083817                 BC083817 Rattus no
  991    47.8    2.8    2076  5  BC053185                 BC053185 Danio rer
  992    47.8    2.8    2158  9  AB070046                 AB070046 Macaca fa
  993    47.8    2.8    2172  9  AB096991                 AB096991 Macaca fa
  994    47.8    2.8    2173  10  BC048927                 BC048927 Mus muscu
  995    47.8    2.8    2208  10  BC052921                 BC052921 Mus muscu
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  997    47.8    2.8    2556  9  AF125948                 AF125948 Homo sapi
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 1002    47.8    2.8    3430  9  BC065220                 BC065220 Homo sapi
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c1017    47.8    2.8    9021  6  AX347134                 AX347134 Sequence
c1018    47.8    2.8    9021  6  AX347426                 AX347426 Sequence
c1019    47.8    2.8    9021  6  AX348462                 AX348462 Sequence
c1020    47.8    2.8    9021  6  AX349147                 AX349147 Sequence
c1021    47.8    2.8    9021  6  AX657808                 AX657808 Sequence
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c1027    47.8    2.8   11913  6  AX826025                 AX826025 Sequence
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  1117    47.6    2.8    2447  9  BC027927             BC027927 Homo sapi
 c1118    47.6    2.8    2501  6  AX598878             AX598878 Sequence
  1119    47.6    2.8    2607  5  BC054610             BC054610 Danio rer
  1120    47.6    2.8    2610  10  BC063267             BC063267 Mus muscu
  1121    47.6    2.8    2621  10  MUSBRED              L31396 Mus musculu
  1122    47.6    2.8    2674  6  AR183261             AR183261 Sequence
  1123    47.6    2.8    2674  6  AR456323             AR456323 Sequence
  1124    47.6    2.8    2752  9  HSM806735            BX641046 Homo sapi
  1125    47.6    2.8    2770  9  HSM807752            BX647606 Homo sapi
  1126    47.6    2.8    2782  9  HSM803706            AL832398 Homo sapi
  1127    47.6    2.8    2804  9  HSM807489            BX647345 Homo sapi
  1128    47.6    2.8    2840  10  BC052769             BC052769 Mus muscu
  1129    47.6    2.8    3448  10  BC034679             BC034679 Mus muscu
  1130    47.6    2.8    3582  10  BC053927             BC053927 Mus muscu
  1131    47.6    2.8    3924  10  MUSBREDA             L31397 Mus musculu
 c1132    47.6    2.8    4001  6  AX347363             AX347363 Sequence
 c1133    47.6    2.8    4001  6  AX349084             AX349084 Sequence
 c1134    47.6    2.8    4001  6  AX657851             AX657851 Sequence
 c1135    47.6    2.8    4001  6  AX659125             AX659125 Sequence
  1136    47.6    2.8    4004  9  BC041086             BC041086 Homo sapi
  1137    47.6    2.8    4418  9  BC006195             BC006195 Homo sapi
  1138    47.6    2.8    4421  10  BC042512             BC042512 Mus muscu
  1139    47.6    2.8    4447  9  HSM808517            BX648369 Homo sapi
  1140    47.6    2.8    4675  9  HSM803445            AL832138 Homo sapi
 c1141    47.6    2.8    5306  6  AX345413             AX345413 Sequence
 c1142    47.6    2.8    6134  6  AX458624             AX458624 Sequence
 c1143    47.6    2.8    6436  6  AX345583             AX345583 Sequence
  1144    47.6    2.8    6458  9  HSM806837            BX641067 Homo sapi
 c1145    47.6    2.8    6775  6  AX458643             AX458643 Sequence
 c1146    47.6    2.8    6802  6  AX346133             AX346133 Sequence
  1147    47.6    2.8    7416  6  CQ574115             CQ574115 Sequence
 c1148    47.6    2.8    7967  3  AF222717             AF222717 Plasmodiu
 c1149    47.6    2.8    8900  6  CQ806977             CQ806977 Sequence
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 c1152    47.6    2.8    9483  6  AX251786             AX251786 Sequence
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 c1155    47.6    2.8    9666  6  AX281420             AX281420 Sequence
 c1156    47.6    2.8    9666  6  AX345987             AX345987 Sequence
 c1157    47.6    2.8    9666  6  AX348688             AX348688 Sequence
  1158    47.6    2.8   11700  2  AC013911             AC013911 Drosophil
 c1159    47.6    2.8   17848  6  AX277865             AX277865 Sequence
 c1160    47.6    2.8   17848  6  AX323550             AX323550 Sequence
 c1161    47.6    2.8   17848  6  AX348363             AX348363 Sequence
 c1162    47.6    2.8   35962  6  AX598758             AX598758 Sequence
  1163    47.6    2.8   63585  2  AC026983             AC026983 Homo sapi
 c1164    47.6    2.8   77322  2  AC021334             AC021334 Homo sapi
 c1165    47.6    2.8   84492  2  AC021676             AC021676 Homo sapi
 c1166    47.6    2.8   95026  3  AC125292             AC125292 Drosophil
  1167    47.6    2.8 110000  2  AC110244_0           AC110244 Mus muscu
 c1168    47.6    2.8 110000  2  PFMAL13_I1           Continuation (12 o
 c1169    47.6    2.8 110000  2  PFMAL13P2_2          Continuation (3 of
  1170    47.6    2.8 110000  3  PFMAL1P2_0           AL031745 Plasmodiu
  1171    47.6    2.8 113027  9  AC090669             AC090669 Homo sapi
 c1172    47.6    2.8 120211  10  AL773515             AL773515 Mouse DNA
 c1173    47.6    2.8 127580  9  HSDJ74J1             AL049692 Human DNA
  1174    47.6    2.8 151501  9  BS000215             BS000215 Pan trogl
  1175    47.6    2.8 155320  2  AC135762             AC135762 Rattus no
  1176    47.6    2.8 155646  9  AC146044             AC146044 Pan trogl
  1177    47.6    2.8 156459  10  AC147155             AC147155 Mus muscu
 c1178    47.6    2.8 158803  2  AC117771             AC117771 Mus muscu
 c1179    47.6    2.8 166025  10  AL844493             AL844493 Mouse DNA
  1180    47.6    2.8 166292  10  AC123049             AC123049 Mus muscu
 c1181    47.6    2.8 168439  10  AC131803             AC131803 Mus muscu
  1182    47.6    2.8 173585  2  AC021113             AC021113 Homo sapi
 c1183    47.6    2.8 174893  5  BX004876             BX004876 Zebrafish
  1184    47.6    2.8 175106  2  AC148984             AC148984 Mus muscu
  1185    47.6    2.8 176261  5  BX927252             BX927252 Zebrafish
 c1186    47.6    2.8 179312  3  AC023745             AC023745 Drosophil
 c1187    47.6    2.8 185195  10  AC134565             AC134565 Mus muscu

 c1188    47.6    2.8 187545  10  AC127550             AC127550 Mus muscu
 c1189    47.6    2.8 188823  2  AC016990             AC016990 Homo sapi
 c1190    47.6    2.8 194760  9  CNS01RG7             AL157792 Human chr
  1191    47.6    2.8 199537  10  AL837510             AL837510 Mouse DNA
 c1192    47.6    2.8 202640  2  AC113851             AC113851 Rattus no
  1193    47.6    2.8 211371  2  CR450764             CR450764 Danio rer
 c1194    47.6    2.8 213397  2  AC125027             AC125027 Mus muscu
 c1195    47.6    2.8 213558  2  AC149587             AC149587 Mus muscu
  1196    47.6    2.8 217740  2  AC139949             AC139949 Rattus no
 c1197    47.6    2.8 226256  2  AC130087             AC130087 Rattus no
  1198    47.6    2.8 226734  2  AC103431             AC103431 Rattus no
  1199    47.6    2.8 233219  2  AC113253             AC113253 Rattus no
 c1200    47.6    2.8 235660  2  AC128377             AC128377 Rattus no
 c1201    47.6    2.8 241394  2  AC131549             AC131549 Rattus no
 c1202    47.6    2.8 248214  2  AL138811             AL138811 Homo sapi
  1203    47.6    2.8 257700  2  AC147391             AC147391 Pan trogl
  1204    47.6    2.8 258818  2  AC135265             AC135265 Rattus no
 c1205    47.6    2.8 264350  2  AC127094             AC127094 Rattus no
 c1206    47.6    2.8 301536  2  AC134158             AC134158 Rattus no
 c1207    47.6    2.8 315790  3  AE003484             AE003484 Drosophil
 c1208    47.6    2.8 334028  2  AC116537             AC116537 Drosophil
 c1209    47.6    2.8 349980  6  AX344552             AX344552 Sequence
 c1210    47.6    2.8 349980  6  AX344572             AX344572 Sequence
  1211    47.4    2.8     267  6  CQ525163             CQ525163 Sequence
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  1215    47.4    2.8     301  6  CQ516510             CQ516510 Sequence
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  1217    47.4    2.8     406  6  CQ517355             CQ517355 Sequence
  1218    47.4    2.8     407  6  CQ522526             CQ522526 Sequence
  1219    47.4    2.8     439  6  CQ518358             CQ518358 Sequence
 c1220    47.4    2.8     453  6  CQ477688             CQ477688 Sequence
  1221    47.4    2.8     467  3  AF156168             AF156168 Buthus ma
  1222    47.4    2.8     472  6  CQ518059             CQ518059 Sequence
  1223    47.4    2.8     484  6  CQ526160             CQ526160 Sequence
  1224    47.4    2.8     506  6  CQ518031             CQ518031 Sequence
  1225    47.4    2.8     516  6  CQ524041             CQ524041 Sequence
  1226    47.4    2.8     546  6  AX186746             AX186746 Sequence
  1227    47.4    2.8     589  10  BC049706             BC049706 Mus muscu
  1228    47.4    2.8     631  10  BC049570             BC049570 Mus muscu
 c1229    47.4    2.8     643  6  CQ423476             CQ423476 Sequence
  1230    47.4    2.8     671  5  BC082915             BC082915 Xenopus l
  1231    47.4    2.8     682  10  BC049545             BC049545 Mus muscu
  1232    47.4    2.8     685  10  BC049720             BC049720 Mus muscu
  1233    47.4    2.8     685  11  CNS06EJ4             AL395174 T3 end of
  1234    47.4    2.8     686  10  BC060302             BC060302 Mus muscu
 c1235    47.4    2.8     688  6  CQ422987             CQ422987 Sequence
  1236    47.4    2.8     690  9  BC040927             BC040927 Homo sapi
  1237    47.4    2.8     705  9  HSM800237            AL049452 Homo sapi
  1238    47.4    2.8     805  10  BC063183             BC063183 Rattus no
  1239    47.4    2.8     811  11  BV073335             BV073335 S212P6813
  1240    47.4    2.8     824  9  BC070291             BC070291 Homo sapi
  1241    47.4    2.8     843  10  BC038641             BC038641 Mus muscu
  1242    47.4    2.8     883  10  BC049726             BC049726 Mus muscu
  1243    47.4    2.8     887  9  AB125184             AB125184 Macaca fa
  1244    47.4    2.8     902  10  BC048724             BC048724 Mus muscu
  1245    47.4    2.8     935  10  BC049693             BC049693 Mus muscu
  1246    47.4    2.8     942  5  BC049498             BC049498 Danio rer
  1247    47.4    2.8     971  10  BC030946             BC030946 Mus muscu
  1248    47.4    2.8     989  10  BC051033             BC051033 Mus muscu
  1249    47.4    2.8     997  9  BC047943             BC047943 Homo sapi
  1250    47.4    2.8    1068  9  BC071641             BC071641 Homo sapi
  1251    47.4    2.8    1071  9  BC073941             BC073941 Homo sapi
  1252    47.4    2.8    1107  3  AK173973             AK173973 Ciona int
  1253    47.4    2.8    1113  9  BC030277             BC030277 Homo sapi
  1254    47.4    2.8    1222  9  BC035237             BC035237 Homo sapi
  1255    47.4    2.8    1240  9  BC055418             BC055418 Homo sapi
  1256    47.4    2.8    1281  5  BC083538             BC083538 Danio rer
  1257    47.4    2.8    1299  10  BC021404             BC021404 Mus muscu
  1258    47.4    2.8    1332  10  BC060992             BC060992 Mus muscu
  1259    47.4    2.8    1348  9  BC070154             BC070154 Homo sapi
  1260    47.4    2.8    1425  9  BC036851             BC036851 Homo sapi
 1261    47.4    2.8    1433   5  BC082836              BC082836 Xenopus l
 1262    47.4    2.8    1445  10   BC071177              BC071177 Rattus no
 1263    47.4    2.8    1463   6  CQ491467              CQ491467 Sequence
 1264    47.4    2.8    1463   6  CQ497350              CQ497350 Sequence
 1265    47.4    2.8    1493   9  HSM805897             BX538346 Homo sapi
 1266    47.4    2.8    1500   3  AK174058              AK174058 Ciona int
 1267    47.4    2.8    1591   9  HSM807298             BX647154 Homo sapi
 1268    47.4    2.8    1653  10   BC083548              BC083548 Rattus no
 1269    47.4    2.8    1661   9  BC025753              BC025753 Homo sapi
 1270    47.4    2.8    1696   6  AR256293              AR256293 Sequence
 1271    47.4    2.8    1719  10   BC045148              BC045148 Mus muscu
 1272    47.4    2.8    1738   6  AR560934              AR560934 Sequence
 1273    47.4    2.8    1738   8  BT009079              BT009079 Triticum
 1274    47.4    2.8    1744   9  BC019265              BC019265 Homo sapi
 1275    47.4    2.8    1750   9  BC048294              BC048294 Homo sapi
 1276    47.4    2.8    1925   9  BC050524              BC050524 Homo sapi
 1277    47.4    2.8    1939   5  BC079974              BC079974 Xenopus l
 1278    47.4    2.8    1980  10   BC027199              BC027199 Mus muscu
 1279    47.4    2.8    1999   9  BC020684              BC020684 Homo sapi
 1280    47.4    2.8    2161   9  AB063084              AB063084 Macaca fa
 1281    47.4    2.8    2224   6  BD189940              BD189940 Tumor ant
 1282    47.4    2.8    2224   9  AB062292              AB062292 Homo sapi
 1283    47.4    2.8    2237   3  AK112710              AK112710 Ciona int
 1284    47.4    2.8    2245   9  BC037547              BC037547 Homo sapi
 1285    47.4    2.8    2307   5  BC081197              BC081197 Xenopus l
 1286    47.4    2.8    2320  10   BC046962              BC046962 Mus muscu
 1287    47.4    2.8    2335   5  BC068409              BC068409 Danio rer
 1288    47.4    2.8    2372   9  BC042652              BC042652 Homo sapi
 1289    47.4    2.8    2403   9  HSM808752             BX648601 Homo sapi
 1290    47.4    2.8    2477   9  BC034692              BC034692 Homo sapi
 1291    47.4    2.8    2539  10   BC046284              BC046284 Mus muscu
 1292    47.4    2.8    2593   9  HSM807470             BX647326 Homo sapi
 1293    47.4    2.8    2601   5  BC072034              BC072034 Xenopus l
 1294    47.4    2.8    2765   3  AK115430              AK115430 Ciona int
 1295    47.4    2.8    2783  10   BC058527              BC058527 Mus muscu
 1296    47.4    2.8    2789   3  AK114441              AK114441 Ciona int
 1297    47.4    2.8    2824   9  BC042665              BC042665 Homo sapi
 1298    47.4    2.8    2980   6  BD270060              BD270060 Secreted
 1299    47.4    2.8    3149  10   BC040763              BC040763 Mus muscu
 1300    47.4    2.8    3186   5  BC068331              BC068331 Danio rer
 1301    47.4    2.8    3446   9  HSM802955             AL713742 Homo sapi
 1302    47.4    2.8    3492   5  BC078645              BC078645 Danio rer
 1303    47.4    2.8    3502   9  HSM807726             BX647580 Homo sapi
c1304    47.4    2.8    3664   6  AX598782              AX598782 Sequence
c1305    47.4    2.8    3664   6  AX598928              AX598928 Sequence
c1306    47.4    2.8    3664   6  AX705378              AX705378 Sequence
c1307    47.4    2.8    3664   6  AX705400              AX705400 Sequence
 1308    47.4    2.8    3930   9  BC027963              BC027963 Homo sapi
 1309    47.4    2.8    3964   5  BC077739              BC077739 Xenopus l
 1310    47.4    2.8    3997   6  AX086658              AX086658 Sequence
 1311    47.4    2.8    4154   9  HSM803629             AL832322 Homo sapi
 1312    47.4    2.8    4180  10   BC042645              BC042645 Mus muscu
 1313    47.4    2.8    4237   6  BD057918              BD057918 Secreted
 1314    47.4    2.8    4550  10   AB015672              AB015672 Mus muscu
 1315    47.4    2.8    4679   9  HSM808418             BX648270 Homo sapi
c1316    47.4    2.8    5182   6  AX252007              AX252007 Sequence
c1317    47.4    2.8    5182   6  AX348780              AX348780 Sequence
c1318    47.4    2.8    5349   6  AX345242              AX345242 Sequence
c1319    47.4    2.8    5437   6  AX346644              AX346644 Sequence
c1320    47.4    2.8    5893   6  AX345761              AX345761 Sequence
c1321    47.4    2.8    6664   6  AX252071              AX252071 Sequence
c1322    47.4    2.8    6664   6  AX822358              AX822358 Sequence
c1323    47.4    2.8    6664   6  AX822486              AX822486 Sequence
c1324    47.4    2.8    6664   6  AX825998              AX825998 Sequence
c1325    47.4    2.8    6664   6  AX826126              AX826126 Sequence
c1326    47.4    2.8    6898   6  AX344814              AX344814 Sequence
 1327    47.4    2.8    8059   5  BC076779              BC076779 Xenopus l
c1328    47.4    2.8    8305   6  AX346470              AX346470 Sequence
c1329    47.4    2.8    8607   6  AR453095              AR453095 Sequence
c1330    47.4    2.8    8607   6  AX281207              AX281207 Sequence
c1331    47.4    2.8    8607   6  AX356478              AX356478 Sequence
c1332    47.4    2.8   12138   6  AX346530              AX346530 Sequence
c1333    47.4    2.8   12138   6  AX348420              AX348420 Sequence

c1334    47.4    2.8  14006   6  AX346860               AX346860 Sequence
c1335    47.4    2.8  14798   6  AX345934               AX345934 Sequence
c1336    47.4    2.8  17721   6  AX346631               AX346631 Sequence
c1337    47.4    2.8  19289   2  AC090926               AC090926 Homo sapi
c1338    47.4    2.8  40324   6  AX458633               AX458633 Sequence
 1339    47.4    2.8  57538   3  AC115682               AC115682 Dictyoste
c1340    47.4    2.8  67374   2  AC118933               AC118933 Mus muscu
c1341    47.4    2.8  72981  10   BX511117                BX511117 Mouse DNA
c1342    47.4    2.8  73778   6  AX344562               AX344562 Sequence
c1343    47.4    2.8  82771   2  AC011953               AC011953 Homo sapi
 1344    47.4    2.8  85916   3  AC117080               AC117080 Dictyoste
c1345    47.4    2.8 110000   2  AC113129_2             Continuation (3 of
c1346    47.4    2.8 110000   2  AC114623_1             Continuation (2 of
c1347    47.4    2.8 110000  10   AE014180_1             Continuation (2 of
 1348    47.4    2.8 120653   5  BX649590               BX649590 Zebrafish
 1349    47.4    2.8 121554   2  AC142244               AC142244 Mus muscu
c1350    47.4    2.8 142324   5  BX005420               BX005420 Zebrafish
c1351    47.4    2.8 148053   2  CR352222               CR352222 Danio rer
c1352    47.4    2.8 152506  10   AC145589                AC145589 Mus muscu
 1353    47.4    2.8 156060   2  AC004153               AC004153 Plasmodiu
c1354    47.4    2.8 162646   2  AC112977               AC112977 Mus muscu
 1355    47.4    2.8 163035   2  AC142822               AC142822 Macaca mu
 1356    47.4    2.8 164520   2  AC020738               AC020738 Homo sapi
c1357    47.4    2.8 166529  10   AC147621                AC147621 Mus muscu
 1358    47.4    2.8 179253   5  AL928870               AL928870 Zebrafish
 1359    47.4    2.8 181571  10   AC108949                AC108949 Mus muscu
c1360    47.4    2.8 191119   2  CR749163               CR749163 Danio rer
c1361    47.4    2.8 194362  10   AC124716                AC124716 Mus muscu
 1362    47.4    2.8 195972  10   AC117567                AC117567 Mus muscu
 1363    47.4    2.8 198590  10   AC113983                AC113983 Mus muscu
 1364    47.4    2.8 199274   2  AC123626               AC123626 Mus muscu
 1365    47.4    2.8 200934  10   AC123850                AC123850 Mus muscu
c1366    47.4    2.8 205878   2  CR392366               CR392366 Danio rer
 1367    47.4    2.8 212144   2  AC140356               AC140356 Mus muscu
 1368    47.4    2.8 215427   2  AC130980               AC130980 Rattus no
 1369    47.4    2.8 219491   2  AC092256               AC092256 Mus muscu
 1370    47.4    2.8 221068   2  AC102378               AC102378 Mus muscu
c1371    47.4    2.8 222932   2  AC137869               AC137869 Mus muscu
c1372    47.4    2.8 223869   2  AC119834               AC119834 Mus muscu
 1373    47.4    2.8 227395  10   AL512346                AL512346 Mouse DNA
 1374    47.4    2.8 230184  10   AC138679                AC138679 Mus muscu
 1375    47.4    2.8 235664   2  AC126522               AC126522 Rattus no
 1376    47.4    2.8 238781  10   AC127351                AC127351 Mus muscu
c1377    47.4    2.8 240185   2  AC115132               AC115132 Rattus no
 1378    47.4    2.8 240931   2  AC107097               AC107097 Rattus no
c1379    47.4    2.8 240931   2  AC107097               AC107097 Rattus no
c1380    47.4    2.8 244656  10   AC091278                AC091278 Mus muscu
c1381    47.4    2.8 245859   2  AC099418               AC099418 Rattus no
c1382    47.4    2.8 252632   3  AE014818               AE014818 Plasmodiu
c1383    47.4    2.8 253441   2  AC135668               AC135668 Mus muscu
c1384    47.4    2.8 255189   2  AC106391               AC106391 Rattus no
 1385    47.4    2.8 258938   2  AC099416               AC099416 Mus muscu
c1386    47.4    2.8 262640   2  AC139057               AC139057 Mus muscu
c1387    47.4    2.8 267140   2  AC097568               AC097568 Rattus no
 1388    47.4    2.8 275156   2  AC105868               AC105868 Rattus no
c1389    47.4    2.8 302489   2  AC100742               AC100742 Mus muscu
 1390    47.2    2.8     203   6  CQ524826              CQ524826 Sequence
 1391    47.2    2.8     240   6  CQ663206              CQ663206 Sequence
c1392    47.2    2.8     281   6  CQ410312              CQ410312 Sequence
 1393    47.2    2.8     348   6  CQ524785              CQ524785 Sequence
 1394    47.2    2.8     396   6  CQ525748              CQ525748 Sequence
 1395    47.2    2.8     504   6  CQ526419              CQ526419 Sequence
 1396    47.2    2.8     539  10   BC031454               BC031454 Mus muscu
 1397    47.2    2.8     623   9  BC043516              BC043516 Homo sapi
 1398    47.2    2.8     625  10   BC059134               BC059134 Rattus no
 1399    47.2    2.8     656   6  CQ487057              CQ487057 Sequence
 1400    47.2    2.8     675  10   BC059112               BC059112 Rattus no
 1401    47.2    2.8     720   3  AK174023              AK174023 Ciona int
 1402    47.2    2.8     749   9  BC008417              BC008417 Homo sapi
c1403    47.2    2.8     756   6  CQ399155              CQ399155 Sequence
c1404    47.2    2.8     756   6  CQ405433              CQ405433 Sequence
 1405    47.2    2.8     760   9  BC040885              BC040885 Homo sapi
c1406    47.2    2.8     780   8  CNS019TW              AL112092 Botrytis
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 1407    47.2    2.8     859   9  AK026608            AK026608 Homo sapi
 1408    47.2    2.8     891  14  TMO308687            AJ308687 Tobacco m
 1409    47.2    2.8    1087   5  BC083541            BC083541 Danio rer
 1410    47.2    2.8    1097   6  AX082180            AX082180 Sequence
 1411    47.2    2.8    1117   8  AF243375            AF243375 Glycine m
 1412    47.2    2.8    1155   9  BC036792            BC036792 Homo sapi
 1413    47.2    2.8    1285   9  HSM801947           AL137283 Homo sapi
 1414    47.2    2.8    1316   9  BC073942            BC073942 Homo sapi
 1415    47.2    2.8    1352   9  BC043573            BC043573 Homo sapi
 1416    47.2    2.8    1368   5  BC064278            BC064278 Xenopus t
 1417    47.2    2.8    1464   9  IR2005397           AL389978 Homo sapi
 1418    47.2    2.8    1490   5  BC074522            BC074522 Xenopus t
 1419    47.2    2.8    1556   5  BC063349            BC063349 Xenopus t
 1420    47.2    2.8    1563   9  BC071790            BC071790 Homo sapi
 1421    47.2    2.8    1568   5  BC050177            BC050177 Danio rer
 1422    47.2    2.8    1738   3  AK112524            AK112524 Ciona int
 1423    47.2    2.8    1742   9  HSM806670           BX640624 Homo sapi
 1424    47.2    2.8    1756   9  BC069223            BC069223 Homo sapi
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 1428    47.2    2.8    1877   5  BC066464            BC066464 Danio rer
 1429    47.2    2.8    1885   9  HSM807866           BX647720 Homo sapi
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 1434    47.2    2.8    2000   9  BC063423            BC063423 Homo sapi
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 1438    47.2    2.8    2196   9  HSM805743           BX537439 Homo sapi
 1439    47.2    2.8    2244   9  HSM807352           BX647208 Homo sapi
 1440    47.2    2.8    2287   9  BC044220            BC044220 Homo sapi
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 1442    47.2    2.8    2499   9  HSM801350           AL133016 Homo sapi
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 1444    47.2    2.8    2660  10   BC046318            BC046318 Mus muscu
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 1450    47.2    2.8    3307   9  BC025714            BC025714 Homo sapi
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 1454    47.2    2.8    3739   5  BC076951            BC076951 Xenopus t
 1455    47.2    2.8    3899   6  BD191414            BD191414 Secreted
 1456    47.2    2.8    3937   5  BC068837            BC068837 Xenopus l
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 1458    47.2    2.8    4124   3  AK112284            AK112284 Ciona int
 1459    47.2    2.8    4345   9  HSM808518           BX648370 Homo sapi
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 1462    47.2    2.8    7216   9  HSM805762           BX537480 Homo sapi
c1463    47.2    2.8   15782   6  AX323521            AX323521 Sequence
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c1466    47.2    2.8   61940   2  AC109312            AC109312 Homo sapi
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c1469    47.2    2.8  121141  10   AC125314            AC125314 Mus muscu
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c1474    47.2    2.8  167088  10   AC122556            AC122556 Mus muscu
 1475    47.2    2.8  167403   2  AC015686            AC015686 Homo sapi
 1476    47.2    2.8  168766   2  BX936450            BX936450 Danio rer
c1477    47.2    2.8  173173   2  BX005170            BX005170 Mus muscu
 1478    47.2    2.8  174545   2  AC140200            AC140200 Mus muscu
 1479    47.2    2.8  180645  10   AL732468            AL732468 Mouse DNA
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c1480    47.2    2.8 182870  2  AC016563            AC016563 Homo sapi
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 1483    47.2    2.8 194851  9  AC079264            AC079264 Homo sapi
 1484    47.2    2.8 195580 10   AC148982            AC148982 Mus muscu
 1485    47.2    2.8 198318  2  BX957253            BX957253 Danio rer
 1486    47.2    2.8 198582  9  AC005291            AC005291 Homo sapi
c1487    47.2    2.8 199632  2  AC116728            AC116728 Mus muscu
c1488    47.2    2.8 203657  2  BX927302            BX927302 Danio rer
 1489    47.2    2.8 204210  2  AC015583            AC015583 Mus muscu
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 1491    47.2    2.8 207197  2  AC133054            AC133054 Rattus no
 1492    47.2    2.8 210676  2  AC108768            AC108768 Mus muscu
 1493    47.2    2.8 214170  2  AC118037            AC118037 Mus muscu
 1494    47.2    2.8 226457  2  AC114452            AC114452 Rattus no
c1495    47.2    2.8 227489  2  AC117015            AC117015 Rattus no
 1496    47.2    2.8 228651 10   AL845373            AL845373 Mouse DNA
c1497    47.2    2.8 232814  2  AC120129            AC120129 Mus muscu
 1498    47.2    2.8 238079  2  AC096000            AC096000 Rattus no
 1499    47.2    2.8 242663  2  AC099067            AC099067 Rattus no
c1500    47.2    2.8 244538  2  AC105696            AC105696 Rattus no
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ALIGNMENTS

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RESULT 1
CQ768055
LOCUS       CQ768055                1679 bp    DNA     linear   PAT 04-MAR-2004
DEFINITION  Sequence 522 from Patent EP1386931.
ACCESSION   CQ768055
VERSION     CQ768055.1  GI:45108887
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wood,W.I., Goddard,A., Gurney,A., Yuan,J., Baker,K.P. and Chen,J.
  TITLE     Human neurotrimin homologue
  JOURNAL   Patent: EP 1386931-A 522 04-FEB-2004;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1679
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ORIGIN

  Query Match            100.0%;  Score 1679;  DB 6;  Length 1679;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

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Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 2
AR528639
LOCUS       AR528639                1679 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 375 from patent US 6725730.
ACCESSION   AR528639
VERSION     AR528639.1  GI:53916717
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Bollinger,C.L. Jr.
  TITLE     Crane test weight assembly and method
  JOURNAL   Patent: US 6725730-A 375 27-APR-2004;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy         721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
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Db         721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy         781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db         781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy         841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy         901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db         901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy         961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy        1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy        1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Db        1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy        1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy        1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy        1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy        1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGAAGAACACAGCACACCCGGCTTGGA 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy        1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGCAAGGGCTCAGCCTC 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Db        1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy        1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
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Db        1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy        1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 3
AX358872
LOCUS       AX358872                1679 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 125 from Patent WO0193983.
ACCESSION   AX358872
VERSION     AX358872.1  GI:18675337
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0193983-A 125 13-DEC-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1679;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy          61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy         121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db         121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy         181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy         241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy         301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db         301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy         361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy         421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
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Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
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Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
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Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
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Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 4
AX362365
LOCUS       AX362365                1679 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 125 from Patent WO0208288.
ACCESSION   AX362365
VERSION     AX362365.1  GI:18694640
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0208288-A 125 31-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1679;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
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Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
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Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
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Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 5
AX403748
LOCUS       AX403748                1679 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 103 from Patent WO0077037.
ACCESSION   AX403748
VERSION     AX403748.1  GI:21437184
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A., Baker,K., Botstein,D., Desnoyers,L., Eaton,D.L.,
            Ferrara,N., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
            Goddard,A., Godowski,P., Gurney,A., Kljavin,I.J., Mather,J.,
            Napier,M., Pan,J., Paoni,N., Roy,M., Tumas,D., Watanabe,C.,
            Williams,P.M., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0077037-A 103 21-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1679;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Db        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
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Db        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780

Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 6
AX454470
LOCUS       AX454470                1679 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 55 from Patent WO0208284.
ACCESSION   AX454470
VERSION     AX454470.1  GI:21713859
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0208284-A 55 31-JAN-2002;
            Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
            (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
            Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
            Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
            ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
            Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
            I. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1679;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Db          1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60

Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Qy        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Db        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Db        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540

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Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660
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Db        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC 660

Qy        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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Db        661 GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
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Qy        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840
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Db        781 GGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGG 840

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Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
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Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
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Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
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Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

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Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
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Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGAAGAACACAGCACACCCGGCTTGGA 1440
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Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
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Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 7
AX464242
LOCUS       AX464242                1679 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 375 from Patent WO0140466.
ACCESSION   AX464242
VERSION     AX464242.1  GI:21899137
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
            Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Wood,W.L. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            same
  JOURNAL   Patent: WO 0140466-A 375 07-JUN-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
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ORIGIN

  Query Match             100.0%;  Score 1679;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
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Db         61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120

Qy        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Db        121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180

Qy        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Db        181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240

Qy        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Db        241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Qy         1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
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RESULT 8
AX490948
LOCUS       AX490948                1679 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 55 from Patent WO0200690.
ACCESSION   AX490948
VERSION     AX490948.1  GI:22323811
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0200690-A 55 03-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 1679;  DB 6;  Length 1679;
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Qy            1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Qy          121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
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Qy          181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Qy          241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Qy          301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Qy        721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAA 780
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RESULT 9
AY358331
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DEFINITION  Homo sapiens clone DNA43316 HNT (UNQ297) mRNA, complete cds.
ACCESSION   AY358331
VERSION     AY358331.1  GI:37181786
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1679)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
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Qy        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900
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Db        841 ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTA 900

Qy        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT 960

Qy        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT 1020

Qy       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080
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Db       1021 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT 1080

Qy       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140
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Db       1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1140

Qy       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200
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Db       1141 GGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT 1200

Qy       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260

Qy       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320

Qy       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATA 1380

Qy       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGA 1440

Qy       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560
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Db       1501 TCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCA 1560

Qy       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG 1620

Qy       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db       1621 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679


RESULT 10
AR439649
LOCUS       AR439649                1693 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 2 from patent US 6664383.
ACCESSION   AR439649
VERSION     AR439649.1  GI:42665573
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1693)
  AUTHORS   Fukushima,D., Shibayama,S. and Tada,H.
  TITLE     Polypeptides, cDNA encoding the same and utilization thereof
  JOURNAL   Patent: US 6664383-A 2 16-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .1693
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.0%;  Score 1661.4;  DB 6;  Length 1693;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1673;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          6 GTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAATCT 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAATCT 60

Qy         66 ATCAGGAAAGAAAGAAAG-AAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGA 124
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db         61 ATCAGGAAAGAAAGAAAGAAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGA 120

Qy        125 AAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC 180

Qy        185 ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACC 240

Qy        245 TTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGC 304
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Db        241 TTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGC 300
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Qy         305 ACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCT 364
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Db         301 ACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCT 360

Qy         365 GGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAG 424
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAG 420

Qy         425 TACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTG 484
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Db         421 TACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTG 480

Qy         485 CAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAA 544
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAA 540

Qy         545 ATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGC 604
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 ATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGC 600

Qy         605 ATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTT 664
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Db         601 ATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTT 660

Qy         665 GGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGG 724
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 GGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGG 720

Qy         725 GACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTC 784
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Db         721 GACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTC 780

Qy         785 ACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAA 844
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Db         781 ACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAA 840

Qy         845 AAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAG 904
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAG 900

Qy         905 GATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTC 964
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTC 960

Qy         965 TCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCC 1024
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 TCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCC 1020

Qy        1025 TCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGC 1084
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 TCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGC 1080

Qy        1085 GAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTC 1144
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 GAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTC 1140

Qy        1145 TTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCG 1204
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Db        1141 TTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCG 1200

Qy        1205 CCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATATATA 1264
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Db        1201 CCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATATATA 1260

Qy        1265 CAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAAG 1324
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Db        1261 CAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAAG 1320

Qy        1325 AATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTA 1384
               |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        1321 AATACTTTGGGGGGAAAAAAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTA 1380

Qy        1385 GGTACAATGGAGTTTTCTTTTCCCAAACGGAAGAACACAGCACACCCGGCTTGGACCCA 1444
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Db        1381 GGTACAATGGAGTTTTCTTTTCCCAAACGGAAGAACACAGCACACCCGGCTTGGACCCA 1440

Qy        1445 CTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTG 1504
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 CTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTG 1500

Qy        1505 CCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCC 1564
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 CCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCC 1560

Qy        1565 ATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAG 1624
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 ATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAG 1620

Qy        1625 ACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 ACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1675


RESULT 11
AX665342
LOCUS       AX665342                1839 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 100 from Patent WO03002765.
ACCESSION   AX665342
VERSION     AX665342.1  GI:29290464
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sellar,G.C. and Gabra,H.
  TITLE     Cancer
  JOURNAL   Patent: WO 03002765-A 100 09-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .1839
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             85.3%;  Score 1432.8;  DB 6;  Length 1839;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1464;  Conservative    0;  Mismatches    2;  Indels   20;  Gaps    1;

Qy         214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         345 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 404

Qy         274 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 333
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         405 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 464

Qy         334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         465 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 524

Qy         394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
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Db         525 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 584

Qy         454 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 513
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Db         585 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 644

Qy         514 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 573
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Db         645 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 704

Qy         574 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 633
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Db          705 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 764

Qy          634 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 693
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Db          765 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 824

Qy          694 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 753
                ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          825 AATTCAGGGCATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 884

Qy          754 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 813
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          885 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 944

Qy          814 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 873
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Db          945 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 1004

Qy          874 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 933
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Db         1005 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 1064

Qy          934 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 993
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Db         1065 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 1124

Qy          994 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 1053
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Db         1125 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 1184

Qy         1054 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 1113
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Db         1185 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 1244

Qy         1114 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGA 1173
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Db         1245 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGA 1304

Qy         1174 GTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATG 1233
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Db         1305 GTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATG 1364

Qy         1234 GCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCA 1293
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Db         1365 GCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCA 1424

Qy         1294 TGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAA 1353
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1425 TGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAA 1484

Qy         1354 AAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACG 1413
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Db         1485 AAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACG 1544

Qy         1414 GGAAGAACACAGCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGG 1473
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Db         1545 GGAAGAACACAGCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGG 1604

Qy         1474 TGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTC 1533
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Db         1605 TGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCACAGACTGCCCCCACGTGGAACATTC 1664

Qy         1534 TGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGAC------- 1586
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Db         1665 TGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGG 1724

Qy         1587 -------------CTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCA 1633
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Db         1725 CCCAAGCGTGGCGCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCA 1784

Qy         1634 CCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
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Db         1785 CCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1830


RESULT 12
AF126426
LOCUS       AF126426                1839 bp    mRNA    linear   PRI 10-JUN-2002
DEFINITION  Homo sapiens neurotrimin (HNT) mRNA, complete cds.
ACCESSION   AF126426
VERSION     AF126426.1  GI:7158997
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1839)
  AUTHORS   Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
  TITLE     Cloning and identification of human neurotrimin full length cDNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1839)
  AUTHORS   Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical
            Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
FEATURES             Location/Qualifiers
     source          1. .1839
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     gene            1. .1839
                     /gene="HNT"
     CDS             265. .1299
                     /gene="HNT"
                     /note="similar to Rattus norvegicus neurotrimin"
                     /codon_start=1
                     /product="neurotrimin"
                     /protein_id="AAF37591.1"
                     /db_xref="GI:7158998"
                     /translation="MGVCGYLFLPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDN
                     VTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEI
                     QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIAT
                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVT
                     VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPF
                     LSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLP
                     LLVLHLLLKF"
ORIGIN

  Query Match             85.3%;  Score 1432.8;  DB 9;  Length 1839;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1464;  Conservative    0;  Mismatches    2;  Indels   20;  Gaps    1;

Qy          214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          345 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 404

Qy          274 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 333
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          405 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 464

Qy          334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          465 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 524

Qy          394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          525 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 584

Qy          454 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 513
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          585 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 644

Qy          514 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 573
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          645 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 704
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Qy          574 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 633
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          705 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 764

Qy          634 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 693
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          765 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 824

Qy          694 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 753
                ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          825 AATTCAGGGCATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 884

Qy          754 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 813
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          885 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 944

Qy          814 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 873
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          945 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 1004

Qy          874 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 933
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1005 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 1064

Qy          934 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 993
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1065 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 1124

Qy          994 ACATGACTATGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 1053
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1125 ACATGACTATGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 1184

Qy         1054 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 1113
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1185 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 1244

Qy         1114 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGA 1173
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1245 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGA 1304

Qy         1174 GTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATG 1233
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1305 GTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATG 1364

Qy         1234 GCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCA 1293
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1365 GCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCA 1424

Qy         1294 TGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAA 1353
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1425 TGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAA 1484

Qy         1354 AAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACG 1413
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1485 AAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACG 1544

Qy         1414 GGAAGAACACAGCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGG 1473
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1545 GGAAGAACACAGCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGG 1604

Qy         1474 TGCCAGTGTGGGCAAGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTC 1533
                |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db         1605 TGCCAGTGTGGGCAAGGCTCAGCCTCTCTGCCCACAGACTGCCCCCACGTGGAACATTC 1664

Qy         1534 TGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGAC------- 1586
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1665 TGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGG 1724

Qy         1587 -------------CTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCA 1633
                             |||||||||||||||||||||||||||||||||||||||||||||||
Db         1725 CCCAAGCGTGGCGCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCA 1784
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Qy         1634 CCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1679
                ||||||||||||||||||||||||||||||||||||||||||||||
Db         1785 CCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAAA 1830


RESULT 13
AR439648
LOCUS       AR439648                1032 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 1 from patent US 6664383.
ACCESSION   AR439648
VERSION     AR439648.1  GI:42665572
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1032)
  AUTHORS   Fukushima,D., Shibayama,S. and Tada,H.
  TITLE     Polypeptides, cDNA encoding the same and utilization thereof
  JOURNAL   Patent: US 6664383-A 1 16-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .1032
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             61.5%;  Score 1032;  DB 6;  Length 1032;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-262;
  Matches 1032;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60

Qy          194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120

Qy          254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180

Qy          314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 240

Qy          374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 300

Qy          434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360

Qy          494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420

Qy          554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480

Qy          614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 540

Qy          674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600

Qy          734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
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Qy         794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720

Qy         854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780

Qy         914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840

Qy         974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900

Qy        1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960

Qy        1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020

Qy        1154 CTTCTCAAATTT 1165
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Db        1021 CTTCTCAAATTT 1032
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RESULT 14
RNU16845
LOCUS       RNU16845                2040 bp    mRNA    linear   ROD 26-MAY-1995
DEFINITION  Rattus norvegicus neurotrimin mRNA, complete cds.
ACCESSION   U16845
VERSION     U16845.1  GI:755184
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 2040)
  AUTHORS   Struyk,A.F., Canoll,P.D., Wolfgang,M.J., Rosen,C.L., D'Eustachio,P.
            and Salzer,J.L.
  TITLE     Cloning of neurotrimin defines a new subfamily of differentially
            expressed neural cell adhesion molecules
  JOURNAL   J. Neurosci. 15 (3 Pt 2), 2141-2156 (1995)
  MEDLINE   95198094
   PUBMED   7891157
REFERENCE   2  (bases 1 to 2040)
  AUTHORS   Salzer,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical
            Center, 550 First Avenue, New York, NY 10016, USA
FEATURES             Location/Qualifiers
     source          1. .2040
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
     CDS             484. .1518
                     /note="neural cell adhesion molecule"
                     /codon_start=1
                     /product="neurotrimin"
                     /protein_id="AAA67445.1"
                     /db_xref="GI:755185"
                     /translation="MGVCGYLFLPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDN
                     VTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEI
                     QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIAT
                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGEYECSASNDVAAPVVRRVNVT
                     VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWFKDDKRLVEGKKGVKVENRPF
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                     LLVLHLLLKF"
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ORIGIN

  Query Match             59.4%;  Score 996.8;  DB 10;  Length 2040;
  Best Local Similarity   84.3%;  Pred. No. 4.2e-253;
  Matches 1249;  Conservative    0;  Mismatches  202;  Indels   31;  Gaps   10;

Qy         214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
               ||||||||| ||||| ||||||||||||||||| ||||||||||||||||||||||||||
Db         564 AGGAGTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAACGTGACGGT 623

Qy         274 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 333
               | ||||||||||||||||||||||||||||||||| |||||||||||| ||||||||||||||
Db         624 CAGGCAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCGGGTGGC 683

Qy         334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
               ||||||||||||||| ||||||||||||||||||| |||||||||||||||||| ||||||||
Db         684 CTGGCTAAACCGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGATCCTCG 743

Qy         394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
                ||||| || ||||| ||||||||| || ||||||||||||| ||||||||||| ||||||||
Db         744 TGTGGTTCTCCTGAGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGTGGATGT 803

Qy         454 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 513
               |||||| ||||||||||| ||||||||||||||||||||||||||||| |||||||| ||
Db         804 GTATGATGAGGGCCCTTATACCTGCTCGGTGCAGACAGACAACCACCCTAAGACCTCCAG 863

Qy         514 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 573
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         864 GGTCCACCTCATTGTACAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 923

Qy         574 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 633
               ||||||||||||||| || |||||||||| |||||||||| || |||||||| ||||||| ||
Db         924 TAATGAAGGGAACAACATCAGCCTCACTTGCATAGCCACAGGTAGACCGGAGCCTACAGT 983

Qy         634 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 693
                || |||||||| || |||||||||| || |||||||||||||||| || || ||| ||||
Db         984 AACCTGGAGACATATTTCTCCCAAAGCTGTCGGCTTTGTGAGTGAGGATGAGTACCTGGA 1043

Qy         694 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 753
                || |||||||||||| |||||||||||||||| || || |||||||| |||||||| |||||
Db        1044 GATCCAGGGCATCACTCGGGAGCAGTCAGGCGAGTATGAGTGCAGCGCCTCCAACGACGT 1103

Qy         754 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 813
               ||| || || || ||||| ||||| || ||||||||||||||||||||||||| |||||
Db        1104 GGCAGCACCAGTCGTACGAAGAGTGAACGTCACCGTGAACTATCCACCATACATCTCAGA 1163

Qy         814 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 873
               ||| ||||||||||||||||||||||| || |||||||| ||||||||||||||||| ||
Db        1164 AGCTAAGGGTACAGGTGTCCCCGTGGGGCAGAAGGGGACTCTGCAGTGTGAAGCCTCGGC 1223

Qy         874 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 933
               |||||| ||||||||||| |||||||||| |||||||||||||||||||||| ||||||| |||||
Db        1224 AGTCCCTTCAGCAGAATTTCAGTGGTTCAAGGATGACAAAAGACTGGTTGAAGGGAAGAA 1283

Qy         934 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 993
                || || ||||||||||||||||||||||||| |||| ||||| ||| ||||| ||||||||
Db        1284 GGGAGTCAAAGTGGAAAACAGACCTTTCCTTTCAAGACTCACCTTTTTCAACGTCTCTGA 1343

Qy         994 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 1053
               ||| ||||||||||||||||| || ||||| ||||||||| ||||||||||||||||||||
Db        1344 ACACGACTATGGGAACTACACATGTGTGGCATCCAACAAGTTGGGCCACACCAATGCCAG 1403

Qy        1054 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 1113
               ||||||||||||||| ||||| || ||||||||||| | ||| || ||||| ||||||||
Db        1404 CATCATGCTATTTGGCCCAGGTGCTGTCAGCGAGGTCAACAATGGGACGTCAAGGAGGGC 1463

Qy        1114 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGA 1173
               ||||||| | ||||| || ||||||||||||||| |||||||| ||||||||||||||||||
Db        1464 AGGCTGCATTTGGCTCCTCCCTCTTCTGGTCTTACACCTGCTCCTCAAATTTTGATGTGA 1523

Qy        1174 GTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATG 1233
               ||||| ||||||  || |||| | ||||| |||||| |  |   |||  |||||||| ||
Db        1524 GTGCCCCTTCCCTGCCGGGGAGA-GCTGCTGCCACCGCATC--TCAATTCAACAGCACTG 1580
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Qy          1234 GCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCA 1293
                        | |||  || |||  ||  | |  |||||||||||   |||| |||||||  |
Db          1581 -------CAACATGAAGCAACAAGTCAGAATCAAATGAAATTCCGAGAATCACAGCC-AA 1632

Qy          1294 TGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGG---------GGAAAAGA 1344
                 || |||||||||| ||||||||||||||||| ||||| |||             |||||
Db          1633 TGAGACAGAAATTCGAGGGAGGGGAACAAAGCATACTGTGGTAAAGGGGAAAAAAAAAGT 1692

Qy          1345 GTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGT----TTT 1400
                  |   ||||   || ||||||||||||||||||| |||| ||||| |  ||||    |||
Db          1693 CTAAAAAAAGGAAATTTGAAAATTGCCTTGCAGACATTTCGGTACCACTGAGTTTTCTTT 1752

Qy          1401 CTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCA-CTGCAAGCTGCATCG 1459
                 ||||||||||| ||||||||    || ||||  ||||||||||| |  |||||||||  |
Db          1753 CTTTTCCCAAATGGGAAGAA---GGCGCACCTAGCTTGGACCCACCCACAAGCTGCACTG 1809

Qy          1460 TGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCAC-AGAGTGCCC 1518
                 ||  |||||| || |||||| |||||||||||||||||| |||||||||| | |||||||
Db          1810 TGTGACCTCTCTGTTGCCAGGGTGGGCAAGGGCTCAGCCACTCTGCCCACTAAAGTGCCC 1869

Qy          1519 CCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGAC--GAAC 1576
                 |  | |||||||||||||||  ||||||||||||||  ||| ||||||||| ||  | ||
Db          1870 CACCATGGAACATTCTGGAGTCGGCCATCCCAAATTTCATCGGTCCATAGACACAAGCAC 1929

Qy          1577 AGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCA 1636
                 ||| |||||      ||||||   ||| | | | |||| ||||||| | ||| || |
Db          1930 AGAGTGAGAAACAGGGGCCCAGAAGTGCCACGGAGGGCCCTTTGGTGGGCTGCGCGATGG 1989

Qy          1637 CGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA 1678
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Db          1990 TGGCGTGTGTCATGAAGTGTGAAATCCGAAGTAGAAAAAAAA 2031


RESULT 15
BC023307
LOCUS       BC023307                1615 bp    mRNA    linear   ROD 06-OCT-2003
DEFINITION  Mus musculus neurotrimin, mRNA (cDNA clone MGC:30504
            IMAGE:4480983), complete cds.
ACCESSION   BC023307
VERSION     BC023307.1  GI:23958300
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1615)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1615)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
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  JOURNAL   Submitted (05-FEB-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 41 Row: h Column: 10
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 26986610.
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                     /note="IG; Region: Immunoglobulin"
                     /db_xref="CDD:smart00409"
     misc_feature    485..664
                     /gene="Hnt-pending"
                     /note="IGc2; Region: Immunoglobulin C-2 Type"
                     /db_xref="CDD:smart00408"
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                     /note="IG; Region: Immunoglobulin"
                     /db_xref="CDD:smart00409"
ORIGIN

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  Matches 1234;  Conservative    0;  Mismatches  221;  Indels   25;  Gaps   10;

Qy           214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
                 ||||||||| ||||| ||||||||||||||||| ||||||||||||||||||||||||||
Db           124 AGGAGTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAACGTGACGGT 183

Qy           274 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 333
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Qy           394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
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Qy           694 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 753
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Db           664 GGCGGCACCAGTGGTACGAAGAGTGAAGGTCACCGTGAACTATCCACCATACATCTCAGA 723

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                 ||| ||||| ||||||||||||||||| || |||||||| ||||||||||||||| || ||
Db           724 AGCTAAGGGCACAGGTGTCCCCGTGGGGCAGAAGGGGACTCTGCAGTGTGAAGCTTCCGC 783

Qy           874 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 933
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Qy          1349 TAAAAAA---GAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTT- 1404
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Qy          1405 TCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTG-CAAGCTGCATCGTGCA 1463
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Qy          1464 ACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCAC-AGAGTGCCCCCAC 1522
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ID   AAZ34324 standard; cDNA; 1679 BP.
DE   Human PRO337 nucleotide sequence.
PN   WO9946281-A2.
PD   16-SEP-1999.
PA   (GETH ) GENENTECH INC.
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DE   Human PRO337 nucleotide sequence SEQ ID NO:522.
PN   WO200053756-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
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  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 3
ID   AAC87037 standard; cDNA; 1679 BP.
DE   Nucleotide sequence of human polypeptide PRO337.
PN   WO200077037-A2.
PD   21-DEC-2000.
PA   (GETH ) GENENTECH INC.
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  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 4
ID   AAS21431 standard; cDNA; 1679 BP.
DE   Human cDNA sequence encoding for PRO337 polypeptide.
PN   WO200140466-A2.
PD   07-JUN-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 4;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 5
ID   ABK33598 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO protein, Seq ID No 125.
PN   WO200208288-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
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ID   ABL88099 standard; cDNA; 1679 BP.
DE   Human PRO337 cDNA sequence SEQ ID NO:55.
PN   WO200200690-A2.
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ID   ABL95588 standard; cDNA; 1679 BP.
DE   Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.
PN   WO200208284-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
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RESULT 8
ID   ACA63892 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2002192706-A1.
PD   19-DEC-2002.
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PN   US2003036180-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
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DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003032063-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
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DE   Human secreted and transmembrane PRO polypeptide #37 cDNA.
PN   US2002177553-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
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RESULT 12
ID   ABX89328 standard; cDNA; 1679 BP.
DE   DNA encoding novel secreted and transmembrane protein PRO337.
PN   US2003017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
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RESULT 13
ID   ABX92696 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO337 polypeptide.
PN   US2002169284-A1.
PD   14-NOV-2002.
PA   (GETH ) GENENTECH INC.
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  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 14
ID   ACD41982 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #188.
PN   US2003036179-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
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RESULT 15
ID   ACA60526 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2002177165-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
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  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 16
ID   ACA04516 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 DNA.
PN   US2003032062-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
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  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 17
ID   ACA66437 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO337.
PN   US2003004102-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 18
ID   ACA68559 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088063-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
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  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 19
ID   ACA04211 standard; cDNA; 1679 BP.
DE   Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
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  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 20
ID   ACA65657 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO337.
PN   US2003032057-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
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  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 21
ID   ADA45894 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
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  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 22
ID   ADA76325 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
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RESULT 23
ID   ABT44288 standard; cDNA; 1679 BP.
DE   Human PRO337 cDNA.
PN   US2003050448-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
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RESULT 24
ID   ADA18975 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003054517-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 25
ID   ADA61598 standard; cDNA; 1679 BP.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 26
ID   ADB19383 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 27
ID   ADB27924 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 28
ID   ADA86403 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 29
ID   ADB15967 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 30
ID   ADA47753 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 31
ID   ADA67548 standard; cDNA; 1679 BP.
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DE   Human PRO polynucleotide #188.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 32
ID   ADB30555 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003068794-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 33
ID   ADA85851 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082693-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 34
ID   ADA97063 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082705-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 35
ID   ADA79367 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082763-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 36
ID   ADA87506 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087345-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 37
ID   ADB16708 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087349-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 38
ID   ADA91800 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082694-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 39
ID   ADB14863 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087351-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 40
ID   ADA25061 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
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PN   US2003050241-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 41
ID   ADA47275 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
PN   US2003044844-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 42
ID   ADB18824 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073211-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 43
ID   ADA94039 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077722-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 44
ID   ADB19935 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082691-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 45
ID   ADB13247 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082710-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 46
ID   ACD98611 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003044945-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 47
ID   ACD30038 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003050240-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 48
ID   ADA12722 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO337.
PN   US2003055216-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 49
ID   ADA74501 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003068798-A1.
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PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 50
ID   ADB24734 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077713-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 51
ID   ADA82258 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082701-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 52
ID   ADA75221 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003073216-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 53
ID   ADA85299 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082695-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 54
ID   ADA84747 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 55
ID   ADB30003 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 56
ID   ADA80531 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 57
ID   ADA75773 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082703-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 58
ID   ADA46998 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003073210-A1.
PD   17-APR-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 59
ID   ADB25294 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 60
ID   ADA93470 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077721-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 61
ID   ADB26820 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 62
ID   ADB31107 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 63
ID   ABT44571 standard; cDNA; 1679 BP.
DE   Human PRO337 cDNA.
PN   US2003027988-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 64
ID   ADA61035 standard; cDNA; 1679 BP.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 65
ID   ADB24182 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 66
ID   ADA96511 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082690-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 67
ID   ADA81083 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082702-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 68
ID   ADA95959 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 69
ID   ADB26268 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 70
ID   ADB21753 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 71
ID   ACD82238 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO 337 cDNA.
PN   US2003044934-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 72
ID   ACD29453 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane polypeptide cDNA #133.
PN   US2003049633-A1.
PD   13-MAR-2003.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 73
ID   ADA77532 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003068797-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 74
ID   ADB18272 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003077710-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 75
ID   ADA86955 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082709-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 76
ID   ADA88058 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082700-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
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RESULT 77
ID   ADA46446 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003054516-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 78
ID   ADB28476 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082699-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 79
ID   ADB29028 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082706-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 80
ID   ADA76980 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003059909-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 81
ID   ADA88610 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073213-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 82
ID   ADA97615 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082686-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 83
ID   ADB27372 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003022239-A1.
PD   30-JAN-2003.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 84
ID   ADB22305 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087344-A1.
PD   08-MAY-2003.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 85
ID   ACD30273 standard; cDNA; 1679 BP.
DE   Human cDNA encoding Pro337.
PN   US2003044902-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 86
ID   ABT43944 standard; cDNA; 1679 BP.
DE   Human membrane bound receptor/protein PRO337 cDNA sequence.
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PN   US2003065147-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 87
ID   ADA66996 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003068793-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 88
ID   ADB22857 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077711-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 89
ID   ADB23630 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077712-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 90
ID   ADA92352 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082712-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 91
ID   ADB15415 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087352-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 92
ID   ADB83615 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 93
ID   ADB80721 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088068-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 94
ID   ADB73262 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096968-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 95
ID   ADB38667 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082766-A1.
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PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 96
ID   ADB78344 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092889-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 97
ID   ADB38115 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087347-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 98
ID   ADB66587 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082689-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 99
ID   ADB84992 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003073817-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 100
ID   ADB89667 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082698-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 101
ID   ADB90399 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082762-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 102
ID   ADB39500 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082764-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 103
ID   ADB78098 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092886-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 104
ID   ADB74028 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide sequence #133.
PN   US2003045462-A1.
PD   06-MAR-2003.
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PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 105
ID    ADB87164 standard; cDNA; 1679 BP.
DE    Human PRO polynucleotide #63.
PN    US2003088067-A1.
PD    08-MAY-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 106
ID    ADB84746 standard; cDNA; 1679 BP.
DE    Human PRO polynucleotide #63.
PN    US2003092890-A1.
PD    15-MAY-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 107
ID    ADB47123 standard; cDNA; 1679 BP.
DE    Novel human secreted and transmembrane protein PRO337 cDNA.
PN    US2003082687-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 108
ID    ADB83861 standard; cDNA; 1679 BP.
DE    Novel human secreted and transmembrane protein PRO337 cDNA.
PN    US2003069397-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 109
ID    ADB86730 standard; cDNA; 1679 BP.
DE    Human PRO polynucleotide #188.
PN    US2003082697-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 110
ID    ADB73016 standard; cDNA; 1679 BP.
DE    Novel human secreted and transmembrane protein PRO337 cDNA.
PN    US2003092887-A1.
PD    15-MAY-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 111
ID    ADB76744 standard; cDNA; 1679 BP.
DE    Human PRO polynucleotide sequence #133.
PN    US2003083248-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 112
ID    ADB77335 standard; cDNA; 1679 BP.
DE    Novel human secreted and transmembrane protein PRO337 cDNA.
PN    US2003082696-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 113
ID    ADB34492 standard; cDNA; 1679 BP.
DE    Human PRO polynucleotide SEQ ID NO 375.
PN    US2003077717-A1.
PD    24-APR-2003.
PA    (GETH ) GENENTECH INC.
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  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 114
ID    ADB35596 standard; cDNA; 1679 BP.
DE    Human PRO polynucleotide SEQ ID NO 375.
PN    US2003077719-A1.
PD    24-APR-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 115
ID    ADB33940 standard; cDNA; 1679 BP.
DE    Human PRO polynucleotide SEQ ID NO 375.
PN    US2003077716-A1.
PD    24-APR-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 116
ID    ADB35044 standard; cDNA; 1679 BP.
DE    Human PRO polynucleotide SEQ ID NO 375.
PN    US2003077718-A1.
PD    24-APR-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 117
ID    ADB36148 standard; cDNA; 1679 BP.
DE    Human PRO polynucleotide SEQ ID NO 375.
PN    US2003077720-A1.
PD    24-APR-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 118
ID    ADB46543 standard; cDNA; 1679 BP.
DE    Novel human secreted and transmembrane protein PRO337 cDNA.
PN    US2003082692-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 119
ID    ADC44170 standard; cDNA; 1679 BP.
DE    Human cDNA encoding secreted/transmembrane protein, PRO337.
PN    US2003054986-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 120
ID    ADC61930 standard; cDNA; 1679 BP.
DE    Human cDNA encoding secreted/transmembrane protein, PRO337.
PN    US2003049684-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 121
ID    ADC63894 standard; cDNA; 1679 BP.
DE    Human cDNA encoding secreted/transmembrane protein, PRO337.
PN    US2003054405-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 0;
RESULT 122
ID    ADC66994 standard; cDNA; 1679 BP.
DE    Human cDNA encoding secreted/transmembrane protein, PRO337.
PN    US2003060406-A1.
PD    27-MAR-2003.
PA    (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 123
ID   ADC69118 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003064407-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 124
ID   ADC63178 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003068648-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 125
ID   ADC68243 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003069178-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 126
ID   ADC41563 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003072745-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 127
ID   ADC67618 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003073131-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 128
ID   ADC62554 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003073624-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 129
ID   ADC36854 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003088065-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 130
ID   ADC42187 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003104998-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 131
ID   ADC21844 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
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RESULT 132
ID   ADC50416 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092106-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 133
ID   ADC71963 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 134
ID   ADC59942 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 135
ID   ADC49875 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088064-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 136
ID   ADC49074 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088070-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 137
ID   ADC49591 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088071-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 138
ID   ADC47452 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088072-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 139
ID   ADC52949 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087365-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 140
ID   ADC57303 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087366-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 141
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ID   ADC60494 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 142
ID   ADC50969 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 143
ID   ADC65496 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 144
ID   ADC54594 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 145
ID   ADC53555 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087364-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 146
ID   ADC59078 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087359-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 147
ID   ADC55956 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087360-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 148
ID   ADC58526 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087346-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 149
ID   ADC47197 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105288-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 150
ID   ADD03200 standard; cDNA; 1679 BP.
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DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092104-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 151
ID   ADC90192 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087348-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 152
ID   ADC69611 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194770-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 153
ID   ADC48500 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194773-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 154
ID   ADD10029 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 155
ID   ADC78072 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096972-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 156
ID   ADD04604 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 157
ID   ADD06307 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073816-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 158
ID   ADC80560 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 159
ID   ADD11067 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
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PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 160
ID   ADD10344 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003105011-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 161
ID   ADC47948 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 162
ID   ADC77826 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088066-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 163
ID   ADC80008 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 164
ID   ADD11304 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 165
ID   ADD09477 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 166
ID   ADD50789 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105291-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 167
ID   ADD41190 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 168
ID   ADD52329 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194769-A1.
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PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 169
ID   ADD51035 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 170
ID   ADD53069 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 171
ID   ADD53621 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003203437-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 172
ID   ADD37097 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 173
ID   ADD51777 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 174
ID   ADD02576 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203431-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 175
ID   ADD50516 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096971-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 176
ID   ADD02010 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203430-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 177
ID   ADD54192 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003203432-A1.
PD   30-OCT-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 178
ID   ADD50270 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096970-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 179
ID   ADD51281 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105289-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 180
ID   ADE49556 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003096744-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 181
ID   ADD92509 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199030-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 182
ID   ADD91405 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199055-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 183
ID   ADE04019 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199057-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 184
ID   ADE32316 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194765-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 185
ID   ADE22248 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199056-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 186
ID   ADD79472 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003203428-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 187
ID   ADE35610 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203434-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 188
ID   ADE16724 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203435-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 189
ID   ADD73339 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203436-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 190
ID   ADE42008 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194772-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 191
ID   ADE17825 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199023-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 192
ID   ADD91957 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199053-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 193
ID   ADE33420 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194767-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 194
ID   ADE33972 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194791-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 195
ID   ADD80024 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207417-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 196
ID   ADD93061 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194768-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 197
ID   ADD72697 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003194781-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 198
ID   ADE19481 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199025-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 199
ID   ADE18929 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199026-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 200
ID   ADE43125 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 201
ID   ADD95914 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199059-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 202
ID   ADE22800 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 203
ID   ADD78918 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 204
ID   ADE32868 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
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RESULT 205
ID   ADE42560 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 206
ID   ADE17348 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203433-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 207
ID   ADD80576 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 208
ID   ADD89604 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 209
ID   ADE40888 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 210
ID   ADE04687 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 211
ID   ADE92816 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194777-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 212
ID   ADF47362 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195333-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 213
ID   ADG21525 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 214
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ID   ADG23166 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 215
ID   ADF97501 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 216
ID   ADG80565 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 217
ID   ADG53119 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003216561-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 218
ID   ADG60439 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003206915-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 219
ID   ADG80013 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 220
ID   ADG63784 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
PN   US2003170721-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 221
ID   ADH55305 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207381-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 222
ID   ADH55857 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207379-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 223
ID   ADI61199 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003077700-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 224
ID   ADI64076 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207385-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 225
ID   ADI65025 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207386-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 226
ID   ADI63524 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207387-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 227
ID   ADH81938 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207388-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 228
ID   ADH81386 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207377-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 229
ID   ACD24040 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003032156-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 230
ID   ACA66903 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #63.
PN   US2003036635-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 231
ID   ACD42387 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003040014-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 232
ID   ACD42857 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
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PN   US2003050239-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 233
ID   ACD68655 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003045687-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 234
ID   ACA67181 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003004311-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 235
ID   ADM82555 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087355-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 11;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 236
ID   ADN15954 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087353-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 11;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 237
ID   ADN16583 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087385-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 11;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 238
ID   ADN15402 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087356-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 11;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 239
ID   ADN14850 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087357-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 11;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 240
ID   ADC48828 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092888-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 241
ID   ADC81112 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092115-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 242
ID   ADE20999 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100735-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 243
ID   ADE05843 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100728-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 244
ID   ADD76560 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003100087-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 245
ID   ADD75072 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100712-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 246
ID   ADD75818 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100717-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 247
ID   ADD85050 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100722-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 248
ID   ADD86876 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100738-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 249
ID   ADE20753 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100734-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 250
ID   ADE39050 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096362-A1.
PD   22-MAY-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 251
ID   ADD87924 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003092113-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 252
ID   ADD86328 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203440-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 253
ID   ADE05597 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100727-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 254
ID   ADD73582 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100711-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 255
ID   ADE75776 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003211571-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 256
ID   ADE48856 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003104536-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 257
ID   ADD78422 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100737-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 258
ID   ADE41305 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 259
ID   ADE23352 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092108-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 260
ID   ADE21245 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100736-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 261
ID   ADD77360 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100732-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 262
ID   ADE20507 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100733-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 263
ID   ADD75572 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100064-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 264
ID   ADD74088 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100708-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 265
ID   ADD74334 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100709-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 266
ID   ADD76064 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100718-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 267
ID   ADD85556 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100721-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 268
ID   ADE23904 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092110-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 269
ID   ADE24547 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092111-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 270
ID   ADD87372 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 271
ID   ADE05105 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100726-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 272
ID   ADD75318 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 273
ID   ADD76862 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 274
ID   ADD86630 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 275
ID   ADE89238 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 276
ID   ADE41198 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
PN   US2003104558-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 277
ID   ADD78098 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
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RESULT 278
ID   ADE18377 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194794-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 279
ID   ADE88686 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 280
ID   ADE89957 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003130181-A1.
PD   10-JUL-2003.
PA   (ASHK/) ASHKENAZI A J.
PA   (BAKE/) BAKER K P.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GIRM/) GIRMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (KUOS/) KUO S S.
PA   (NAPI/) NAPIER M A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (SHEL/) SHELTON D L.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 281
ID   ADD77606 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 282
ID   ADD77852 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100730-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 283
ID   ADD85310 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100725-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 284
ID   ADD73842 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 285
ID   ADD74580 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 286
ID   ADD77108 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100716-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 287
ID   ADD85802 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100720-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 288
ID   ADE05351 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100723-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 289
ID   ADD74826 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100724-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 290
ID   ADF61597 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195345-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 291
ID   ADF40289 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003198994-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 292
ID   ADF46085 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195148-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
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RESULT 293
ID   ADE94706 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199027-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 294
ID   ADE91117 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 295
ID   ADE95258 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 296
ID   ADE93368 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 297
ID   ADF24481 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003204055-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 298
ID   ADF40913 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199021-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 299
ID   ADF23857 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203402-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 300
ID   ADF33840 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003194780-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 301
ID   ADF34949 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199029-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 302
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ID   ADF27307 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199436-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 303
ID   ADF27943 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199437-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 304
ID   ADE92264 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 305
ID   ADE90565 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 306
ID   ADF41537 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199435-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 307
ID   ADF33216 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003211091-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 308
ID   ADF25582 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003211092-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 309
ID   ADF26683 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199674-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 310
ID   ADF34472 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003194410-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 311
ID   ADF46709 standard; cDNA; 1679 BP.
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DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195344-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 312
ID   ADE91712 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 313
ID   ADG05638 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096959-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 314
ID   ADG27192 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096962-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 315
ID   ADG02291 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 316
ID   ADG22077 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 317
ID   ADG20147 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 318
ID   ADF98053 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 319
ID   ADG24270 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207426-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 320
ID   ADF98624 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
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PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 321
ID   ADG03455 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 322
ID   ADF99176 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 323
ID   ADG16761 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 324
ID   ADG05220 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 325
ID   ADG19487 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 326
ID   ADG11255 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 327
ID   ADG13324 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 328
ID   ADG08381 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 329
ID   ADG15551 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 330
ID   ADG12034 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 331
ID   ADF96949 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 332
ID   ADG06134 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 333
ID   ADG23718 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 334
ID   ADG04007 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 335
ID   ADG24908 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 336
ID   ADF94591 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 337
ID   ADG07205 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 338
ID   ADG07757 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207356-A1.
PD   06-NOV-2003.
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PA   (GETH ) GENENTECH INC.
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  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 339
ID   ADG06687 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096966-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 340
ID   ADG55252 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 341
ID   ADG60916 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 342
ID   ADG62020 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 343
ID   ADG82221 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 344
ID   ADG57460 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 345
ID   ADG56908 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 346
ID   ADG55804 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 347
ID   ADG58564 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 348
ID   ADG70930 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 349
ID   ADH39031 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096965-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 350
ID   ADG58012 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 351
ID   ADG53596 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 352
ID   ADG71482 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 353
ID   ADG50695 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003207803-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 354
ID   ADG81669 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207805-A1.
PD   06-NOV-2003.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 355
ID   ADH30631 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 356
ID   ADG63633 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
PN   US2003180796-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
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RESULT 357
ID   ADH11998 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 358
ID   ADG50071 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003215905-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 359
ID   ADG51943 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003215908-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 360
ID   ADG52420 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 361
ID   ADG54148 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 362
ID   ADG49447 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003216305-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 363
ID   ADG81117 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 364
ID   ADG56356 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 365
ID   ADH12622 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 366
ID   ADG48823 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003216560-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 367
ID   ADG61468 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 368
ID   ADH28555 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 369
ID   ADG54700 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 370
ID   ADG59740 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 371
ID   ADG51319 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004005312-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 372
ID   ADH43488 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #28.
PN   US2003224984-A1.
PD   04-DEC-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 373
ID   ADG59263 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004005657-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 374
ID   ADG34121 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004006206-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 375
ID   ADG62719 standard; cDNA; 1679 BP.
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DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004006219-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 376
ID   ADI81164 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207361-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 377
ID   ADI33591 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096960-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 378
ID   ADH69685 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2004019183-A1.
PD   29-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 379
ID   ADH25744 standard; cDNA; 1679 BP.
DE   Human PRO337 encoding cDNA SEQ ID NO:522.
PN   EP1386931-A1.
PD   04-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 380
ID   ADG09907 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004009548-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 381
ID   ADI15378 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207382-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 382
ID   ADG09255 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004009547-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 383
ID   ADI14710 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207383-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 384
ID   ADI29846 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096961-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 385
ID   ADI18305 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207349-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 386
ID   ADM27243 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004044179-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 387
ID   ADJ63586 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 388
ID   ADJ77481 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2004038336-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 389
ID   ADK82833 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #28.
PN   US2004043927-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 390
ID   ADK66601 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2004044180-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 391
ID   ADJ65603 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004038335-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 392
ID   ADM27739 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004048333-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 393
ID   ADM17521 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004048332-A1.
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PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 394
ID   ADL07355 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004063921-A1.
PD   01-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 395
ID   ADM42463 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004058424-A1.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 396
ID   ADM28325 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004077064-A1.
PD   22-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 397
ID   ADI95807 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 13;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 398
ID   ADI96359 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207354-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1679;  DB 13;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 399
ID   AAZ47893 standard; cDNA; 1693 BP.
DE   Human protein encoding cDNA SEQ ID NO:3.
PN   WO9958668-A1.
PD   18-NOV-1999.
PA   (ONOY ) ONO PHARM CO LTD.
  Query Match             99.0%;  Score 1661.4;  DB 3;  Length 1693;
  Best Local Similarity   99.9%;  Pred. No. 0;
RESULT 400
ID   AAA88791 standard; cDNA; 2012 BP.
DE   Human SECX cDNA Clone 11753149.0.37.
PN   WO200061754-A2.
PD   19-OCT-2000.
PA   (CURA-) CURAGEN CORP.
  Query Match             97.9%;  Score 1643.4;  DB 3;  Length 2012;
  Best Local Similarity   99.9%;  Pred. No. 0;
RESULT 401
ID   ADD18290 standard; DNA; 2012 BP.
DE   Human molecule (MOL) protein MOL11 DNA sequence.
PN   WO2003003984-A2.
PD   16-JAN-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             97.9%;  Score 1643.4;  DB 10;  Length 2012;
  Best Local Similarity   99.9%;  Pred. No. 0;
RESULT 402
ID   AAA88790 standard; cDNA; 1603 BP.
DE   Human SECX cDNA Clone 11753149.0.6.
PN   WO200061754-A2.
PD   19-OCT-2000.
PA   (CURA-) CURAGEN CORP.
  Query Match             95.4%;  Score 1601.4;  DB 3;  Length 1603;
  Best Local Similarity   99.9%;  Pred. No. 0;
RESULT 403
ID   ADD18288 standard; DNA; 1603 BP.
DE   Human molecule (MOL) protein MOL10 DNA sequence.
PN   WO2003003984-A2.
PD   16-JAN-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             95.4%;  Score 1601.4;  DB 10;  Length 1603;
  Best Local Similarity   99.9%;  Pred. No. 0;
RESULT 404
ID   ABK49272 standard; cDNA; 1873 BP.
DE   Human Kruppel associated DNA binding protein 42 cDNA.
PN   WO200183541-A1.
PD   08-NOV-2001.
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
  Query Match             89.9%;  Score 1509.8;  DB 6;  Length 1873;
  Best Local Similarity   93.1%;  Pred. No. 0;
RESULT 405
ID   AAI57869 standard; cDNA; 1678 BP.
DE   Human polynucleotide SEQ ID NO 72.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             86.8%;  Score 1457;  DB 4;  Length 1678;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 406
ID   ADQ22984 standard; DNA; 3987 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5804.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             85.7%;  Score 1438.4;  DB 12;  Length 3987;
  Best Local Similarity   98.9%;  Pred. No. 0;
RESULT 407
ID   ADQ24601 standard; DNA; 3987 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7421.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             85.7%;  Score 1438.4;  DB 12;  Length 3987;
  Best Local Similarity   98.9%;  Pred. No. 0;
RESULT 408
ID   ABT17390 standard; DNA; 1839 BP.
DE   Human IG gene related nucleic acid SEQ ID No 16.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             85.3%;  Score 1432.8;  DB 8;  Length 1839;
  Best Local Similarity   98.5%;  Pred. No. 0;
RESULT 409
ID   ABX76448 standard; DNA; 1839 BP.
DE   Lung cancer-associated polynucleotide #312.
PN   WO200286443-A2.
PD   31-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
  Query Match             85.3%;  Score 1432.8;  DB 8;  Length 1839;
  Best Local Similarity   98.5%;  Pred. No. 0;
RESULT 410
ID   ADG63208 standard; DNA; 1839 BP.
DE   Human neurotrimin DNA.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             85.3%;  Score 1432.8;  DB 10;  Length 1839;
  Best Local Similarity   98.5%;  Pred. No. 0;
RESULT 411
ID   ADN39137 standard; cDNA; 1839 BP.
DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:455.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
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  Query Match             85.3%;  Score 1432.8;  DB 11;  Length 1839;
  Best Local Similarity   98.5%;  Pred. No. 0;
RESULT 412
ID   ADI21817 standard; cDNA; 2884 BP.
DE   Novel human protein cDNA #76.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match             85.3%;  Score 1432.8;  DB 10;  Length 2884;
  Best Local Similarity   98.5%;  Pred. No. 0;
RESULT 413
ID   ADI35771 standard; DNA; 2129 BP.
DE   Human neurotrimin DNA.
PN   US2003100485-A1.
PD   29-MAY-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             84.5%;  Score 1418.2;  DB 10;  Length 2129;
  Best Local Similarity   97.6%;  Pred. No. 0;
RESULT 414
ID   AAI59655 standard; cDNA; 1690 BP.
DE   Human polynucleotide SEQ ID NO 3644.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             78.3%;  Score 1315;  DB 4;  Length 1690;
  Best Local Similarity   99.8%;  Pred. No. 0;
RESULT 415
ID   ADI21360 standard; cDNA; 1690 BP.
DE   Novel human expressed sequence tag, EST #59.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match             78.3%;  Score 1315;  DB 10;  Length 1690;
  Best Local Similarity   99.8%;  Pred. No. 0;
RESULT 416
ID   AAZ47892 standard; cDNA; 1032 BP.
DE   Human protein encoding cDNA SEQ ID NO:2.
PN   WO9958668-A1.
PD   18-NOV-1999.
PA   (ONOY ) ONO PHARM CO LTD.
  Query Match             61.5%;  Score 1032;  DB 3;  Length 1032;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-262;
RESULT 417
ID   ABT17393 standard; DNA; 1061 BP.
DE   Human IG gene related nucleic acid SEQ ID No 19.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             58.0%;  Score 974;  DB 8;  Length 1061;
  Best Local Similarity   100.0%;  Pred. No. 5e-247;
RESULT 418
ID   AAZ47894 standard; cDNA; 939 BP.
DE   Human protein encoding cDNA SEQ ID NO:5.
PN   WO9958668-A1.
PD   18-NOV-1999.
PA   (ONOY ) ONO PHARM CO LTD.
  Query Match             55.9%;  Score 939;  DB 3;  Length 939;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-238;
RESULT 419
ID   ABT17391 standard; DNA; 1094 BP.
DE   Human IG gene related nucleic acid SEQ ID No 17.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             55.4%;  Score 931;  DB 8;  Length 1094;
  Best Local Similarity   96.7%;  Pred. No. 1.2e-235;
RESULT 420
ID   ADG63210 standard; DNA; 1068 BP.
DE   Human neurotrimin DNA +33bp isoform.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             54.2%;  Score 910.4;  DB 10;  Length 1068;
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  Best Local Similarity   96.6%;  Pred. No. 3.4e-230;
RESULT 421
ID   ABT17392 standard; DNA; 1130 BP.
DE   Human IG gene related nucleic acid SEQ ID No 18.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             53.1%;  Score 891.8;  DB 8;  Length 1130;
  Best Local Similarity   93.2%;  Pred. No. 2.9e-225;
RESULT 422
ID   ADG63212 standard; DNA; 1104 BP.
DE   Human neurotrimin DNA +69bp isoform.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             52.1%;  Score 874.4;  DB 10;  Length 1104;
  Best Local Similarity   93.2%;  Pred. No. 1.2e-220;
RESULT 423
ID   ADG63214 standard; DNA; 1140 BP.
DE   Human neurotrimin DNA +108bp isoform.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             50.7%;  Score 851.8;  DB 10;  Length 1140;
  Best Local Similarity   99.8%;  Pred. No. 1.1e-214;
RESULT 424
ID   AAA44536 standard; cDNA; 832 BP.
DE   Human secreted expressed sequence tag SEQ ID NO:1111.
PN   WO200021991-A1.
PD   20-APR-2000.
PA   (GEMY ) GENETICS INST INC.
  Query Match             47.9%;  Score 803.8;  DB 3;  Length 832;
  Best Local Similarity   99.8%;  Pred. No. 5e-202;
RESULT 425
ID   ADE07017 standard; DNA; 3298 BP.
DE   Novel coding sequence (useful for identifying genetic disorders) #83.
PN   WO2003054152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match             33.6%;  Score 564.2;  DB 10;  Length 3298;
  Best Local Similarity   69.6%;  Pred. No. 2.7e-138;
RESULT 426
ID   AAQ51015 standard; cDNA; 3069 BP.
DE   Rat opioid receptor gene.
PN   WO9321309-A1.
PD   28-OCT-1993.
PA   (LEEN/) LEE N M.
PA   (LOHH/) LOH H H.
PA   (LIPP/) LIPPMAN D.
  Query Match             32.2%;  Score 540.8;  DB 2;  Length 3069;
  Best Local Similarity   71.2%;  Pred. No. 4e-132;
RESULT 427
ID   ABT17409 standard; DNA; 1478 BP.
DE   Human IG gene related nucleic acid SEQ ID No 35.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             32.1%;  Score 539.2;  DB 8;  Length 1478;
  Best Local Similarity   73.0%;  Pred. No. 7.4e-132;
RESULT 428
ID   ABT17406 standard; DNA; 3110 BP.
DE   Human IG gene related nucleic acid SEQ ID No 32.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             32.1%;  Score 539.2;  DB 8;  Length 3110;
  Best Local Similarity   73.0%;  Pred. No. 1.1e-131;
RESULT 429
ID   ADG63206 standard; DNA; 3110 BP.
DE   Opioid-binding protein/cell adhesion molecule-like DNA.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
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  Query Match             32.1%;  Score 539.2;  DB 10;  Length 3110;
  Best Local Similarity   73.0%;  Pred. No. 1.1e-131;
RESULT 430
ID   ABT17408 standard; DNA; 1071 BP.
DE   Human IG gene related nucleic acid SEQ ID No 34.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             32.0%;  Score 537.6;  DB 8;  Length 1071;
  Best Local Similarity   72.9%;  Pred. No. 1.7e-131;
RESULT 431
ID   ABT17407 standard; DNA; 1080 BP.
DE   Human IG gene related nucleic acid SEQ ID No 33.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             32.0%;  Score 537.6;  DB 8;  Length 1080;
  Best Local Similarity   72.9%;  Pred. No. 1.7e-131;
RESULT 432
ID   AAQ51017 standard; cDNA; 2179 BP.
DE   Rat opioid receptor gene.
PN   WO9321309-A1.
PD   28-OCT-1993.
PA   (LEEN/) LEE N M.
PA   (LOHH/) LOH H H.
PA   (LIPP/) LIPPMAN D.
  Query Match             31.1%;  Score 523;  DB 2;  Length 2179;
  Best Local Similarity   72.2%;  Pred. No. 1.7e-127;
RESULT 433
ID   AAQ51016 standard; cDNA; 2337 BP.
DE   Rat opioid receptor gene.
PN   WO9321309-A1.
PD   28-OCT-1993.
PA   (LEEN/) LEE N M.
PA   (LOHH/) LOH H H.
PA   (LIPP/) LIPPMAN D.
  Query Match             31.1%;  Score 523;  DB 2;  Length 2337;
  Best Local Similarity   72.2%;  Pred. No. 1.8e-127;
RESULT 434
ID   AAZ34325 standard; DNA; 503 BP.
DE   Human EST DNA42301.
PN   WO9946281-A2.
PD   16-SEP-1999.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 2;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 435
ID   AAC78591 standard; cDNA; 503 BP.
DE   Human EST DNA42301 nucleotide sequence SEQ ID NO:524.
PN   WO200053756-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 3;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 436
ID   ACA63893 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein DNA42301.
PN   US2002192706-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 8;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 437
ID   ACA72057 standard; DNA; 503 BP.
DE   Human PRO polypeptide associated oligonucleotide SEQ ID NO 524.
PN   US2002177553-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 8;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 438
ID   ABX92697 standard; cDNA; 503 BP.
DE   Human PRO337 EST polynucleotide sequence.
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PN   US2002169284-A1.
PD   14-NOV-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 8;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 439
ID   ACA66438 standard; cDNA; 503 BP.
DE   Human secreted/transmembrane protein EST DNA42301.
PN   US2003004102-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 8;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 440
ID   ADA25063 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein EST DNA42301.
PN   US2003050241-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 9;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 441
ID   ACD30039 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein EST DNA42301.
PN   US2003050240-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 9;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 442
ID   ADA12724 standard; cDNA; 503 BP.
DE   Human secreted/transmembrane polypeptide PRO337 EST.
PN   US2003055216-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 9;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 443
ID   ACD29454 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane polypeptide cDNA #134.
PN   US2003049633-A1.
PD   13-MAR-2003.
  Query Match             30.0%;  Score 503;  DB 9;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 444
ID   ADB74030 standard; cDNA; 503 BP.
DE   Human PRO polynucleotide sequence #134.
PN   US2003045462-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 445
ID   ADB76746 standard; cDNA; 503 BP.
DE   Human PRO polynucleotide sequence #134.
PN   US2003083248-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 446
ID   ADC44172 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003054986-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 447
ID   ADC61932 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003049684-A1.
PD   13-MAR-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 448
ID   ADC63896 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003054405-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 449
ID   ADC66996 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003060406-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 450
ID   ADC69120 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003064407-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 451
ID   ADC63180 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003068648-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 452
ID   ADC68245 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003069178-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 453
ID   ADC41565 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003072745-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 454
ID   ADC67620 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003073131-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 455
ID   ADC62556 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003073624-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 456
ID   ADC42189 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003104998-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 457
ID   ADE49558 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003096744-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 458
ID   ADE35612 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203434-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 459
ID   ADE16726 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203435-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 460
ID   ADD73341 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203436-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 461
ID   ADD72699 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003194781-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 462
ID   ADE17350 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203433-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 463
ID   ADF47364 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195333-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 464
ID   ADG53121 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003216561-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 465
ID   ADG60441 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003206915-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 466
ID   ADI61201 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003077700-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 467
ID   ACD42858 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein EST DNA42301.
PN   US2003050239-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 468
ID   ADE48858 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003104536-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 469
ID   ADE89959 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003130181-A1.
PD   10-JUL-2003.
PA   (ASHK/) ASHKENAZI A J.
PA   (BAKE/) BAKER K P.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GIRM/) GIRMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (KUOS/) KUO S S.
PA   (NAPI/) NAPIER M A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (SHEL/) SHELTON D L.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 470
ID   ADF61599 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195345-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 471
ID   ADF40291 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003198994-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 472
ID   ADF46087 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195148-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 473
ID   ADF24483 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003204055-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 474
ID   ADF40915 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199021-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 475
ID   ADF23859 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203402-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 476
ID   ADF33842 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003194780-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 477
ID   ADF27309 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199436-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 478
ID   ADF27945 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199437-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 479
ID   ADF41539 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199435-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 480
ID   ADF33218 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003211091-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 481
ID   ADF25584 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003211092-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 482
ID   ADF26685 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199674-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 483
ID   ADF34474 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003194410-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 484
ID   ADF46711 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195344-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 485
ID   ADG50697 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003207803-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 486
ID   ADG50073 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003215905-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 487
ID   ADG51945 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003215908-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 488
ID   ADG49449 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003216305-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 489
ID   ADG48825 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003216560-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 490
ID   ADG51321 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004005312-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 491
ID   ADG59265 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004005657-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 492
ID   ADG62721 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004006219-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 493
ID   ADH25746 standard; cDNA; 503 BP.
DE   Human DNA42301 expressed sequence tag (EST) SEQ ID NO:524.
PN   EP1386931-A1.
PD   04-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 494
ID   ADM17523 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004048332-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 495
ID   ADL07357 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004063921-A1.
PD   01-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             30.0%;  Score 503;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-122;
RESULT 496
ID   AAC91321 standard; cDNA; 537 BP.
DE   Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 21.
PN   WO200073509-A2.
PD   07-DEC-2000.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             29.3%;  Score 491.2;  DB 4;  Length 537;
  Best Local Similarity   98.6%;  Pred. No. 2.2e-119;
RESULT 497
ID   ADM47274 standard; DNA; 617 BP.
DE   Oestrogen regulated protein like NOVX 25b gene.
PN   WO2003083039-A2.
PD   09-OCT-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             26.8%;  Score 449.4;  DB 11;  Length 617;
  Best Local Similarity   97.6%;  Pred. No. 2.8e-108;
RESULT 498
ID   AAF93346 standard; cDNA; 452 BP.
DE   Spinal cord tissue cDNA encoding SRT protein SEQ ID 167.
PN   WO200107611-A2.
PD   01-FEB-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 441.2;  DB 5;  Length 452;
  Best Local Similarity   99.1%;  Pred. No. 3.5e-106;
RESULT 499
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ID   ACH15238 standard; cDNA; 437 BP.
DE   Human adult brain cDNA #2450.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             24.1%;  Score 404;  DB 9;  Length 437;
  Best Local Similarity   97.4%;  Pred. No. 2.4e-96;
RESULT 500
ID   AAS78035 standard; cDNA; 484 BP.
DE   DNA encoding novel human diagnostic protein #13839.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             23.6%;  Score 396;  DB 5;  Length 484;
  Best Local Similarity   92.3%;  Pred. No. 3.4e-94;
RESULT 501
ID   ACH46276 standard; cDNA; 409 BP.
DE   Human infant brain cDNA #339.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             21.1%;  Score 353.8;  DB 9;  Length 409;
  Best Local Similarity   98.1%;  Pred. No. 4.6e-83;
RESULT 502
ID   AAL50356 standard; cDNA; 1411 BP.
DE   Human limbic system associated membrane protein 36-85 coding sequence.
PN   CN1345756-A.
PD   24-APR-2002.
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
  Query Match             20.5%;  Score 343.8;  DB 6;  Length 1411;
  Best Local Similarity   62.1%;  Pred. No. 3.8e-80;
RESULT 503
ID   AAT42080 standard; cDNA to mRNA; 1238 BP.
DE   Rat LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             20.4%;  Score 343;  DB 2;  Length 1238;
  Best Local Similarity   62.0%;  Pred. No. 5.8e-80;
RESULT 504
ID   ABX63560 standard; cDNA; 1195 BP.
DE   Human cDNA #560 differentially expressed in activated vascular tissue.
PN   US2002137081-A1.
PD   26-SEP-2002.
PA   (BAND/) BANDMAN O.
  Query Match             20.3%;  Score 341.6;  DB 8;  Length 1195;
  Best Local Similarity   60.1%;  Pred. No. 1.3e-79;
RESULT 505
ID   ADL12674 standard; cDNA; 1195 BP.
DE   Human steroid-induced C3A liver cell cDNA #403.
PN   US6673549-B1.
PD   06-JAN-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             20.3%;  Score 341.6;  DB 12;  Length 1195;
  Best Local Similarity   60.1%;  Pred. No. 1.3e-79;
RESULT 506
ID   AAT42084 standard; cDNA to mRNA; 924 BP.
DE   Human LAMP residues 8-315 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             20.3%;  Score 340.6;  DB 2;  Length 924;
  Best Local Similarity   63.3%;  Pred. No. 2.2e-79;
RESULT 507
ID   AAT42079 standard; cDNA to mRNA; 977 BP.
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DE   Human LAMP residues 8-332 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             20.3%;  Score 340.6;  DB 2;  Length 977;
  Best Local Similarity   63.3%;  Pred. No. 2.2e-79;
RESULT 508
ID   AAT42081 standard; cDNA to mRNA; 1014 BP.
DE   Rat LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             20.3%;  Score 340.6;  DB 2;  Length 1014;
  Best Local Similarity   61.9%;  Pred. No. 2.3e-79;
RESULT 509
ID   ABT17402 standard; DNA; 1017 BP.
DE   Human IG gene related nucleic acid SEQ ID No 28.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             20.3%;  Score 340.6;  DB 8;  Length 1017;
  Best Local Similarity   63.3%;  Pred. No. 2.3e-79;
RESULT 510
ID   ABT17404 standard; DNA; 1017 BP.
DE   Human IG gene related nucleic acid SEQ ID No 30.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             20.3%;  Score 340.6;  DB 8;  Length 1017;
  Best Local Similarity   63.3%;  Pred. No. 2.3e-79;
RESULT 511
ID   AAT42086 standard; cDNA to mRNA; 861 BP.
DE   Human LAMP residues 29-315 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             20.2%;  Score 338.6;  DB 2;  Length 861;
  Best Local Similarity   63.7%;  Pred. No. 7.1e-79;
RESULT 512
ID   AAT42082 standard; cDNA to mRNA; 912 BP.
DE   Human mature LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             20.2%;  Score 338.6;  DB 2;  Length 912;
  Best Local Similarity   63.7%;  Pred. No. 7.3e-79;
RESULT 513
ID   AAT42085 standard; cDNA to mRNA; 945 BP.
DE   Rat LAMP residues 1-315 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             20.1%;  Score 337.4;  DB 2;  Length 945;
  Best Local Similarity   63.1%;  Pred. No. 1.5e-78;
RESULT 514
ID   ABZ76264 standard; cDNA; 1757 BP.
DE   Human GENSET cDNA clone name SLAMP.
PN   WO2003014151-A2.
PD   20-FEB-2003.
PA   (GEST ) GENSET SA.
  Query Match             20.1%;  Score 337.4;  DB 8;  Length 1757;
  Best Local Similarity   63.8%;  Pred. No. 2.1e-78;
RESULT 515
ID   AAT42083 standard; cDNA to mRNA; 930 BP.
DE   Rat mature LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             20.1%;  Score 337;  DB 2;  Length 930;
  Best Local Similarity   62.1%;  Pred. No. 2e-78;
RESULT 516
ID   ABT17403 standard; DNA; 1075 BP.
DE   Human IG gene related nucleic acid SEQ ID No 29.
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PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             20.0%;  Score 335;  DB 8;  Length 1075;
  Best Local Similarity   63.5%;  Pred. No. 7.1e-78;
RESULT 517
ID   AAT42087 standard; cDNA to mRNA; 861 BP.
DE   Rat LAMP residues 29-315 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             19.9%;  Score 333.8;  DB 2;  Length 861;
  Best Local Similarity   63.4%;  Pred. No. 1.3e-77;
RESULT 518
ID   AAT42116 standard; cDNA to mRNA; 1307 BP.
DE   Rat LAMP clone 6c coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             19.8%;  Score 331.8;  DB 2;  Length 1307;
  Best Local Similarity   63.3%;  Pred. No. 5.5e-77;
RESULT 519
ID   AAH34425 standard; cDNA; 1153 BP.
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:1507.
PN   WO200122920-A2.
PD   05-APR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             19.4%;  Score 325.2;  DB 4;  Length 1153;
  Best Local Similarity   62.7%;  Pred. No. 2.9e-75;
RESULT 520
ID   AAC19214 standard; cDNA; 333 BP.
DE   Human secreted protein 5' EST, SEQ ID NO: 23289.
PN   EP1033401-A2.
PD   06-SEP-2000.
PA   (GEST ) GENSET.
  Query Match             18.8%;  Score 316.2;  DB 3;  Length 333;
  Best Local Similarity   97.0%;  Pred. No. 3.7e-73;
RESULT 521
ID   ABT17405 standard; DNA; 898 BP.
DE   Human IG gene related nucleic acid SEQ ID No 31.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             18.7%;  Score 314.6;  DB 8;  Length 898;
  Best Local Similarity   61.6%;  Pred. No. 1.6e-72;
RESULT 522
ID   AAT42094 standard; cDNA to mRNA; 756 BP.
DE   Human LAMP residues 46-294 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             18.1%;  Score 303.6;  DB 2;  Length 756;
  Best Local Similarity   63.5%;  Pred. No. 1.2e-69;
RESULT 523
ID   AAT42095 standard; cDNA to mRNA; 756 BP.
DE   Rat LAMP residues 46-294 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             17.8%;  Score 298.2;  DB 2;  Length 756;
  Best Local Similarity   63.0%;  Pred. No. 3.3e-68;
RESULT 524
ID   AAS78034 standard; cDNA; 443 BP.
DE   DNA encoding novel human diagnostic protein #13838.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             17.7%;  Score 296.8;  DB 5;  Length 443;
  Best Local Similarity   89.6%;  Pred. No. 5.9e-68;
RESULT 525
ID   ABT17401 standard; DNA; 1809 BP.
DE   Human IG gene related nucleic acid SEQ ID No 27.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             16.6%;  Score 279;  DB 8;  Length 1809;
  Best Local Similarity   57.8%;  Pred. No. 6.2e-63;
RESULT 526
ID   ADS82049 standard; DNA; 4891 BP.
DE   Human cancer-associated protein coding sequence #5.
PN   WO2004035789-A1.
PD   29-APR-2004.
PA   (GLDS ) LG LIFE SCI LTD.
  Query Match             16.3%;  Score 274.2;  DB 13;  Length 4891;
  Best Local Similarity   58.6%;  Pred. No. 1.9e-61;
RESULT 527
ID   ABQ82338 standard; cDNA; 1165 BP.
DE   Human NOV12b encoding cDNA SEQ ID NO:25.
PN   WO200262999-A2.
PD   15-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             16.2%;  Score 272.6;  DB 6;  Length 1165;
  Best Local Similarity   58.4%;  Pred. No. 2.4e-61;
RESULT 528
ID   ADI28059 standard; cDNA; 1327 BP.
DE   ECMCAD gene clone 7087904CB1.
PN   WO200202634-A2.
PD   10-JAN-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             16.2%;  Score 272.6;  DB 6;  Length 1327;
  Best Local Similarity   58.4%;  Pred. No. 2.6e-61;
RESULT 529
ID   AAC87055 standard; cDNA; 4834 BP.
DE   Nucleotide sequence of human polypeptide PRO6004.
PN   WO200077037-A2.
PD   21-DEC-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 4;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 530
ID   ABK33536 standard; cDNA; 4834 BP.
DE   cDNA encoding human PRO protein, Seq ID No 1.
PN   WO200208288-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 6;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 531
ID   ACA05014 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003032063-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 8;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 532
ID   ACA60544 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2002177165-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 8;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 533
ID   ACA04534 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 DNA.
PN   US2003032062-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 8;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 534
ID   ACA68497 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088063-A1.
PD   08-MAY-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 8;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 535
ID   ACA65675 standard; cDNA; 4834 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO6004.
PN   US2003032057-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 536
ID   ABT44226 standard; cDNA; 4834 BP.
DE   Human PRO6004 cDNA.
PN   US2003050448-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 537
ID   ADA47301 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003044844-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 538
ID   ABT44509 standard; cDNA; 4834 BP.
DE   Human PRO6004 cDNA.
PN   US2003027988-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 539
ID   ACD82176 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO 6004 cDNA.
PN   US2003044934-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 540
ID   ACD30291 standard; cDNA; 4834 BP.
DE   Human cDNA encoding Pro6004.
PN   US2003044902-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 541
ID   ABT43882 standard; cDNA; 4834 BP.
DE   Human membrane bound receptor/protein PRO6004 cDNA sequence.
PN   US2003065147-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 542
ID   ADB83491 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 543
ID   ADB80597 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088068-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             16.2%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 544
ID   ADB73138 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096968-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 545
ID   ADB78220 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092889-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 546
ID   ADB84868 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003073817-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 547
ID   ADB77974 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092886-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 548
ID   ADB87040 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003088067-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 549
ID   ADB84622 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003092890-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 550
ID   ADB83737 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003069397-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 551
ID   ADB72892 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092887-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 552
ID   ADC36730 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003088065-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 553
ID   ADC21720 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 554
ID   ADC49751 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088064-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 555
ID   ADC48950 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088070-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 556
ID   ADC49467 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088071-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 557
ID   ADC47328 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088072-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 558
ID   ADC47073 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105288-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 559
ID   ADC77948 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096972-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 560
ID   ADD06183 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003073816-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 561
ID   ADC77702 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088066-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 562
ID   ADD50665 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105291-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 563
ID   ADD50911 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 564
ID   ADD50392 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096971-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 565
ID   ADD50146 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096970-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 566
ID   ADD51157 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105289-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 567
ID   ADG63810 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003170721-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 568
ID   ACA66841 standard; cDNA; 4834 BP.
DE   cDNA encoding human PRO polypeptide #1.
PN   US2003036635-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 569
ID   ACD42405 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003040014-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 570
ID   ACD68593 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003045687-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 571
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ID   ADC48704 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092888-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 572
ID   ADE20875 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100735-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 573
ID   ADE05719 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100728-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 574
ID   ADD74948 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100712-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 575
ID   ADD75694 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100717-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 576
ID   ADD84926 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100722-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 577
ID   ADD86752 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100738-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 578
ID   ADE20629 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100734-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 579
ID   ADE38926 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096362-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 580
ID   ADE05473 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100727-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 581
ID   ADD73458 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100711-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 582
ID   ADD78298 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100737-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 583
ID   ADE21121 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100736-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 584
ID   ADD77236 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100732-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 585
ID   ADE20383 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100733-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 586
ID   ADD75448 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100064-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 587
ID   ADD73964 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100708-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 588
ID   ADD74210 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100709-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5e-61;
RESULT 589
ID   ADD75940 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
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PN   US2003100718-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 590
ID   ADD85432 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100721-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 591
ID   ADE04981 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100726-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 592
ID   ADD75194 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 593
ID   ADD76738 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 594
ID   ADD86506 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 595
ID   ADE41224 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003104558-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 596
ID   ADD77974 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 597
ID   ADD77482 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 598
ID   ADD77728 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100730-A1.
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PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 599
ID   ADD85186 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100725-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 600
ID   ADD73718 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 601
ID   ADD74456 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 602
ID   ADD76984 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100716-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 603
ID   ADD85678 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100720-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 604
ID   ADE05227 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100723-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 605
ID   ADD74702 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100724-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 606
ID   ADG05514 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096959-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 607
ID   ADG27068 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096962-A1.
PD   22-MAY-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 608
ID   ADG11131 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 609
ID   ADG11910 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 610
ID   ADF94467 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 611
ID   ADG06563 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096966-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 612
ID   ADH38907 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096965-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 613
ID   ADG63658 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003180796-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 614
ID   ADG33997 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2004006206-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 615
ID   ADI33467 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096960-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 616
ID   ADH69561 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2004019183-A1.
PD   29-JAN-2004.
PA   (GETH ) GENENTECH INC.
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  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 617
ID   ADI29722 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096961-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 618
ID   ADM27119 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2004044179-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 619
ID   ADK66477 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2004044180-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             16.2%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5e-61;
RESULT 620
ID   ABQ82337 standard; cDNA; 1196 BP.
DE   Human NOV12a encoding cDNA SEQ ID NO:23.
PN   WO200262999-A2.
PD   15-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             16.2%;  Score 272.2;  DB 6;  Length 1196;
  Best Local Similarity   58.3%;  Pred. No. 3.2e-61;
RESULT 621
ID   ABN85384 standard; DNA; 1119 BP.
DE   Human NOV6, KILON-like protein, coding sequence.
PN   WO200255704-A2.
PD   18-JUL-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             16.1%;  Score 271;  DB 6;  Length 1119;
  Best Local Similarity   58.3%;  Pred. No. 6.3e-61;
RESULT 622
ID   ADB62841 standard; cDNA; 2383 BP.
DE   Human cDNA encoding clone OCBBF20110210.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match             16.1%;  Score 271;  DB 10;  Length 2383;
  Best Local Similarity   58.3%;  Pred. No. 9.3e-61;
RESULT 623
ID   AAC78596 standard; cDNA; 2840 BP.
DE   Human PRO4993 nucleotide sequence SEQ ID NO:611.
PN   WO200053756-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 3;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 624
ID   ACA63979 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
PN   US2002192706-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 8;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 625
ID   ACA72143 standard; cDNA; 2840 BP.
DE   Human secreted and transmembrane PRO polypeptide #39 cDNA.
PN   US2002177553-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
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  Query Match             16.0%;  Score 269.4;  DB 8;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 626
ID   ABX92783 standard; cDNA; 2840 BP.
DE   cDNA encoding human PRO4993 polypeptide.
PN   US2002169284-A1.
PD   14-NOV-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 8;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 627
ID   ACA66524 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO4993.
PN   US2003004102-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 8;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 628
ID   ADA25149 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
PN   US2003050241-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 9;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 629
ID   ACD30125 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
PN   US2003050240-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 9;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 630
ID   ADA12811 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO4993.
PN   US2003055216-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 9;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 631
ID   ACD29540 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane polypeptide cDNA #139.
PN   US2003049633-A1.
PD   13-MAR-2003.
  Query Match             16.0%;  Score 269.4;  DB 9;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 632
ID   ADB74117 standard; cDNA; 2840 BP.
DE   Human PRO polynucleotide sequence #139.
PN   US2003045462-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 633
ID   ADB76833 standard; cDNA; 2840 BP.
DE   Human PRO polynucleotide sequence #139.
PN   US2003083248-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 634
ID   ADC44259 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003054986-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
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RESULT 635
ID   ADC62019 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003049684-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 636
ID   ADC63983 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003054405-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 637
ID   ADC67083 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003060406-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 638
ID   ADC69207 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003064407-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 639
ID   ADC63267 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003068648-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 640
ID   ADC68332 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003069178-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 641
ID   ADC41652 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003072745-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 642
ID   ADC67707 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003073131-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 643
ID   ADC62643 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003073624-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 644
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ID   ADC42276 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003104998-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 645
ID   ADE49645 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003096744-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 646
ID   ADE35699 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203434-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 647
ID   ADE16813 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203435-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 648
ID   ADD73428 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203436-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 649
ID   ADD72786 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003194781-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 650
ID   ADE17437 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203433-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 651
ID   ADF47451 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195333-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 652
ID   ADG53208 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003216561-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 653
ID   ADG60528 standard; cDNA; 2840 BP.
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DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003206915-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 654
ID   ADI61288 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003077700-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 655
ID   ACD42944 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
PN   US2003050239-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 656
ID   ADE48945 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003104536-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 657
ID   ADE90046 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003130181-A1.
PD   10-JUL-2003.
PA   (ASHK/) ASHKENAZI A J.
PA   (BAKE/) BAKER K P.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GIRM/) GIRMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (KUOS/) KUO S S.
PA   (NAPI/) NAPIER M A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (SHEL/) SHELTON D L.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 658
ID   ADF61686 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195345-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 659
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ID   ADF40378 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003198994-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 660
ID   ADF46174 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195148-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 661
ID   ADF24570 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003204055-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 662
ID   ADF41002 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199021-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 663
ID   ADF23946 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203402-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 664
ID   ADF33929 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003194780-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 665
ID   ADF27396 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199436-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 666
ID   ADF28032 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199437-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 667
ID   ADF41626 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199435-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 668
ID   ADF33305 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003211091-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 669
ID   ADF25671 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003211092-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 670
ID   ADF26772 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199674-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 671
ID   ADF34561 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003194410-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 672
ID   ADF46798 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195344-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 673
ID   ADG50784 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003207803-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 674
ID   ADG50160 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003215905-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 675
ID   ADG52032 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003215908-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 676
ID   ADG49536 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003216305-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 677
ID   ADG48912 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
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PN   US2003216560-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 678
ID   ADG51408 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004005312-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 679
ID   ADG59352 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004005657-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 680
ID   ADG62808 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004006219-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 681
ID   ADM17610 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004048332-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 682
ID   ADL07444 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004063921-A1.
PD   01-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             16.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 2.7e-60;
RESULT 683
ID   ADP28685 standard; DNA; 834 BP.
DE   Human secreted protein encoding sequence SEQ ID #683.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 834;
  Best Local Similarity   59.5%;  Pred. No. 3.5e-58;
RESULT 684
ID   ADH71401 standard; DNA; 926 BP.
DE   Human gene of the invention NOV11i SEQ ID NO:297.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 926;
  Best Local Similarity   59.5%;  Pred. No. 3.7e-58;
RESULT 685
ID   ADH71405 standard; DNA; 927 BP.
DE   Human gene of the invention NOV11k SEQ ID NO:301.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 927;
  Best Local Similarity   59.5%;  Pred. No. 3.7e-58;
RESULT 686
ID   ADH71409 standard; DNA; 946 BP.
DE   Human gene of the invention NOV11m SEQ ID NO:305.
PN   WO2003102155-A2.
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PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 946;
  Best Local Similarity   59.5%;  Pred. No. 3.7e-58;
RESULT 687
ID   ADH71393 standard; DNA; 946 BP.
DE   Human gene of the invention NOV11e SEQ ID NO:289.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 946;
  Best Local Similarity   59.5%;  Pred. No. 3.7e-58;
RESULT 688
ID   ADH71395 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11f SEQ ID NO:291.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 976;
  Best Local Similarity   59.5%;  Pred. No. 3.8e-58;
RESULT 689
ID   ADH71415 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11p SEQ ID NO:311.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 976;
  Best Local Similarity   59.5%;  Pred. No. 3.8e-58;
RESULT 690
ID   ADH71389 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11c SEQ ID NO:285.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 976;
  Best Local Similarity   59.5%;  Pred. No. 3.8e-58;
RESULT 691
ID   ADH71397 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11g SEQ ID NO:293.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 976;
  Best Local Similarity   59.5%;  Pred. No. 3.8e-58;
RESULT 692
ID   ABS71699 standard; DNA; 1017 BP.
DE   DNA encoding human NOV5b protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 6;  Length 1017;
  Best Local Similarity   59.5%;  Pred. No. 3.9e-58;
RESULT 693
ID   ADL35978 standard; cDNA; 1017 BP.
DE   Human NOVX cDNA #12.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
  Query Match             15.5%;  Score 260.4;  DB 11;  Length 1017;
  Best Local Similarity   59.5%;  Pred. No. 3.9e-58;
RESULT 694
ID   ADH71417 standard; DNA; 1030 BP.
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DE   Human gene of the invention NOV11q SEQ ID NO:313.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 1030;
  Best Local Similarity   59.5%;  Pred. No. 3.9e-58;
RESULT 695
ID   ADH71411 standard; DNA; 1033 BP.
DE   Human gene of the invention NOV11n SEQ ID NO:307.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 1033;
  Best Local Similarity   59.5%;  Pred. No. 3.9e-58;
RESULT 696
ID   ADH71387 standard; DNA; 1033 BP.
DE   Human gene of the invention NOV11b SEQ ID NO:283.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 1033;
  Best Local Similarity   59.5%;  Pred. No. 3.9e-58;
RESULT 697
ID   ADH71413 standard; DNA; 1035 BP.
DE   Human gene of the invention NOV11o SEQ ID NO:309.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 260.4;  DB 12;  Length 1035;
  Best Local Similarity   59.5%;  Pred. No. 3.9e-58;
RESULT 698
ID   ABS76364 standard; DNA; 1427 BP.
DE   DNA encoding human immunoglobulin superfamily protein IGSFP-9.
PN   WO200272794-A2.
PD   19-SEP-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             15.5%;  Score 260.4;  DB 6;  Length 1427;
  Best Local Similarity   59.5%;  Pred. No. 4.6e-58;
RESULT 699
ID   AAD47371 standard; DNA; 2653 BP.
DE   Human LP289 DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
  Query Match             15.5%;  Score 260.4;  DB 8;  Length 2653;
  Best Local Similarity   59.5%;  Pred. No. 6.3e-58;
RESULT 700
ID   ABS71698 standard; DNA; 1018 BP.
DE   DNA encoding human NOV5a protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.4%;  Score 258.8;  DB 6;  Length 1018;
  Best Local Similarity   59.4%;  Pred. No. 1e-57;
RESULT 701
ID   ADL35976 standard; cDNA; 1018 BP.
DE   Human NOVX cDNA #11.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
  Query Match             15.4%;  Score 258.8;  DB 11;  Length 1018;
  Best Local Similarity   59.4%;  Pred. No. 1e-57;
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RESULT 702
ID   ADH71399 standard; DNA; 1018 BP.
DE   Human gene of the invention NOV11h SEQ ID NO:295.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.4%;  Score 258.8;  DB 12;  Length 1018;
  Best Local Similarity   59.4%;  Pred. No. 1e-57;
RESULT 703
ID   ABS71700 standard; DNA; 1136 BP.
DE   DNA encoding human NOV5c protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.3%;  Score 257.2;  DB 6;  Length 1136;
  Best Local Similarity   59.3%;  Pred. No. 2.9e-57;
RESULT 704
ID   ADH71403 standard; DNA; 1171 BP.
DE   Human gene of the invention NOV11j SEQ ID NO:299.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.3%;  Score 257.2;  DB 12;  Length 1171;
  Best Local Similarity   59.3%;  Pred. No. 2.9e-57;
RESULT 705
ID   ADH71385 standard; DNA; 1271 BP.
DE   Human gene of the invention NOV11a SEQ ID NO:281.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.3%;  Score 257.2;  DB 12;  Length 1271;
  Best Local Similarity   59.3%;  Pred. No. 3e-57;
RESULT 706
ID   ADH71421 standard; DNA; 1271 BP.
DE   Human gene of the invention NOV11s SEQ ID NO:317.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.3%;  Score 257.2;  DB 12;  Length 1271;
  Best Local Similarity   59.3%;  Pred. No. 3e-57;
RESULT 707
ID   ADH71419 standard; DNA; 1271 BP.
DE   Human gene of the invention NOV11r SEQ ID NO:315.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.2%;  Score 255.6;  DB 12;  Length 1271;
  Best Local Similarity   59.1%;  Pred. No. 8.1e-57;
RESULT 708
ID   AAH87585 standard; DNA; 255 BP.
DE   Human single nucleotide polymorphism containing DNA sequence #2442.
PN   WO9953095-A2.
PD   21-OCT-1999.
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
  Query Match             15.2%;  Score 255;  DB 2;  Length 255;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-57;
RESULT 709
ID   AAX10694 standard; DNA; 251 BP.
DE   Human biallelic polymorphic DNA fragment WI-9617.
PN   WO9820165-A2.
PD   14-MAY-1998.
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
  Query Match             14.9%;  Score 250.6;  DB 2;  Length 251;
  Best Local Similarity   99.6%;  Pred. No. 7.5e-56;
RESULT 710
ID   ABK35606 standard; DNA; 1011 BP.
DE   Gene encoding novel human secreted or membrane-associated protein #25.
PN   WO200204600-A2.
PD   17-JAN-2002.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
  Query Match             14.7%;  Score 246;  DB 6;  Length 1011;
  Best Local Similarity   58.4%;  Pred. No. 2.5e-54;
RESULT 711
ID   ABS71701 standard; DNA; 1169 BP.
DE   DNA encoding human NOV5d protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             14.7%;  Score 246;  DB 6;  Length 1169;
  Best Local Similarity   58.4%;  Pred. No. 2.7e-54;
RESULT 712
ID   ADH71407 standard; DNA; 1169 BP.
DE   Human gene of the invention NOV111 SEQ ID NO:303.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             14.7%;  Score 246;  DB 12;  Length 1169;
  Best Local Similarity   58.4%;  Pred. No. 2.7e-54;
RESULT 713
ID   ABA06475 standard; cDNA; 2813 BP.
DE   Human cDNA SEQ ID NO: 141.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             14.3%;  Score 240.8;  DB 4;  Length 2813;
  Best Local Similarity   58.3%;  Pred. No. 1e-52;
RESULT 714
ID   ABV83812 standard; cDNA; 2813 BP.
DE   Human polynucleotide SEQ ID NO 141.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match             14.3%;  Score 240.8;  DB 6;  Length 2813;
  Best Local Similarity   58.3%;  Pred. No. 1e-52;
RESULT 715
ID   ADH71391 standard; DNA; 760 BP.
DE   Human gene of the invention NOV11d SEQ ID NO:287.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             14.1%;  Score 236.6;  DB 12;  Length 760;
  Best Local Similarity   59.9%;  Pred. No. 6.7e-52;
RESULT 716
ID   AAD47374 standard; DNA; 2601 BP.
DE   Human LP319b DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
  Query Match             13.9%;  Score 234;  DB 8;  Length 2601;
  Best Local Similarity   58.3%;  Pred. No. 6.1e-51;
RESULT 717
ID   ABK35605 standard; DNA; 1056 BP.
DE   Gene encoding novel human secreted or membrane-associated protein #24.
PN   WO200204600-A2.
PD   17-JAN-2002.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
  Query Match             13.8%;  Score 232;  DB 6;  Length 1056;
  Best Local Similarity   58.1%;  Pred. No. 1.3e-50;
RESULT 718
ID   ADL35982 standard; cDNA; 1168 BP.
DE   Human NOVX cDNA #14.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
  Query Match             13.8%;  Score 231.2;  DB 11;  Length 1168;
  Best Local Similarity   58.1%;  Pred. No. 2.2e-50;
RESULT 719
ID   ADL35980 standard; cDNA; 1133 BP.
DE   Human NOVX cDNA #13.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
  Query Match             13.4%;  Score 224.8;  DB 11;  Length 1133;
  Best Local Similarity   59.3%;  Pred. No. 1.1e-48;
RESULT 720
ID   AAS28811 standard; cDNA; 4656 BP.
DE   Human immunoglobulin encoding cDNA SEQ ID No 57.
PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             13.1%;  Score 220.6;  DB 4;  Length 4656;
  Best Local Similarity   57.5%;  Pred. No. 2.9e-47;
RESULT 721
ID   ADB31536 standard; cDNA; 4656 BP.
DE   Human cDNA encoding a novel protein SEQ ID NO 57.
PN   US2003077606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             13.1%;  Score 220.6;  DB 10;  Length 4656;
  Best Local Similarity   57.5%;  Pred. No. 2.9e-47;
RESULT 722
ID   AAS78003 standard; cDNA; 2883 BP.
DE   DNA encoding novel human diagnostic protein #13807.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             13.0%;  Score 217.8;  DB 5;  Length 2883;
  Best Local Similarity   71.1%;  Pred. No. 1.2e-46;
RESULT 723
ID   ADE08816 standard; DNA; 2883 BP.
DE   Novel DNA-related contig nucleotide sequence #60.
PN   WO2003054152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match             13.0%;  Score 217.8;  DB 10;  Length 2883;
  Best Local Similarity   71.1%;  Pred. No. 1.2e-46;
RESULT 724
ID   AAD47372 standard; DNA; 754 BP.
DE   Human LP289 splice variant (LP343) DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
  Query Match             12.6%;  Score 211.4;  DB 8;  Length 754;
  Best Local Similarity   61.1%;  Pred. No. 3.1e-45;
RESULT 725
ID   ADP28686 standard; DNA; 666 BP.
DE   Human secreted protein encoding sequence SEQ ID #684.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
  Query Match             12.5%;  Score 210;  DB 12;  Length 666;
  Best Local Similarity   60.2%;  Pred. No. 6.9e-45;
RESULT 726
ID   AAD47373 standard; DNA; 2597 BP.
DE   Human LP319a DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
  Query Match             12.4%;  Score 208.6;  DB 8;  Length 2597;
  Best Local Similarity   58.1%;  Pred. No. 3.2e-44;
RESULT 727
ID   AAC02777 standard; cDNA; 352 BP.
DE   Human secreted protein 5' EST, SEQ ID NO: 2775.
PN   EP1033401-A2.
PD   06-SEP-2000.
PA   (GEST ) GENSET.
  Query Match             11.5%;  Score 193.6;  DB 3;  Length 352;
  Best Local Similarity   82.5%;  Pred. No. 1.1e-40;
RESULT 728
ID   ABL99899 standard; cDNA; 5666 BP.
DE   Human secretory polynucleotide (sptm) 154.
PN   WO200220756-A2.
PD   14-MAR-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             10.7%;  Score 180.4;  DB 6;  Length 5666;
  Best Local Similarity   56.1%;  Pred. No. 1.4e-36;
RESULT 729
ID   ADG63283 standard; DNA; 540 BP.
DE   Human OBCAM gene exon 2.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             10.5%;  Score 176.6;  DB 10;  Length 540;
  Best Local Similarity   74.9%;  Pred. No. 4.3e-36;
RESULT 730
ID   ADQ83739 standard; cDNA; 919 BP.
DE   Human tumour-associated antigenic target (TAT) cDNA sequence #553.
PN   WO2004060270-A2.
PD   22-JUL-2004.
PA   (GETH ) GENENTECH INC.
PA   (WUTD/) WU T D.
PA   (ZHOU/) ZHOU Y.
  Query Match             10.4%;  Score 175;  DB 12;  Length 919;
  Best Local Similarity   58.0%;  Pred. No. 1.5e-35;
RESULT 731
ID   AAS78037 standard; cDNA; 767 BP.
DE   DNA encoding novel human diagnostic protein #13841.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             10.1%;  Score 170.2;  DB 5;  Length 767;
  Best Local Similarity   95.6%;  Pred. No. 2.5e-34;
RESULT 732
ID   AAF93597 standard; cDNA; 585 BP.
DE   Umbilical vein endothelial cell cDNA encoding SRT protein SEQ ID 418.
PN   WO200107611-A2.
PD   01-FEB-2001.
PA   (GETH ) GENENTECH INC.
  Query Match              9.7%;  Score 163.2;  DB 5;  Length 585;
  Best Local Similarity   62.0%;  Pred. No. 1.6e-32;
RESULT 733
ID   ABS52769 standard; cDNA; 408 BP.
DE   Murine tuberous sclerosis complex 8 (TSC8) DNA.
PN   WO200246475-A2.
PD   13-JUN-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match              9.5%;  Score 160;  DB 6;  Length 408;
  Best Local Similarity   63.7%;  Pred. No. 9.2e-32;
RESULT 734
ID   AAC10355 standard; cDNA; 200 BP.
DE   Human secreted protein 5' EST, SEQ ID NO: 14430.
PN   EP1033401-A2.
PD   06-SEP-2000.
PA   (GEST ) GENSET.
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  Query Match              8.7%;  Score 146;  DB 3;  Length 200;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-28;
RESULT 735
ID   AAS78038 standard; cDNA; 693 BP.
DE   DNA encoding novel human diagnostic protein #13842.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              8.2%;  Score 137.2;  DB 5;  Length 693;
  Best Local Similarity   97.9%;  Pred. No. 1.3e-25;
RESULT 736
ID   ADQ21981 standard; DNA; 125 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 4801.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              6.6%;  Score 110.8;  DB 12;  Length 125;
  Best Local Similarity   97.6%;  Pred. No. 5.3e-19;
RESULT 737
ID   AAS78592 standard; cDNA; 1275 BP.
DE   DNA encoding novel human diagnostic protein #14396.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              6.4%;  Score 107;  DB 5;  Length 1275;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-17;
RESULT 738
ID   AAS71904 standard; cDNA; 1275 BP.
DE   DNA encoding novel human diagnostic protein #7708.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              6.4%;  Score 107;  DB 5;  Length 1275;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-17;
RESULT 739
ID   AAS78036 standard; cDNA; 1275 BP.
DE   DNA encoding novel human diagnostic protein #13840.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              6.4%;  Score 107;  DB 5;  Length 1275;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-17;
RESULT 740
ID   ABX71182 standard; cDNA; 913 BP.
DE   Novel human cDNA sequence #407.
PN   WO200281731-A2.
PD   17-OCT-2002.
PA   (HYSE-) HYSEQ INC.
PA   (GOOD/) GOODRICH R W.
  Query Match              6.3%;  Score 105.6;  DB 8;  Length 913;
  Best Local Similarity   61.1%;  Pred. No. 3.5e-17;
RESULT 741
ID   ADQ54463 standard; DNA; 351 BP.
DE   Novel canine microarray-related DNA sequence SeqID5765.
PN   WO2004063324-A2.
PD   29-JUL-2004.
PA   (GENE-) GENE LOGIC INC.
PA   (PFIZ ) PFIZER PROD INC.
  Query Match              6.2%;  Score 104.6;  DB 13;  Length 351;
  Best Local Similarity   60.8%;  Pred. No. 3.9e-17;
RESULT 742
ID   AAT42088 standard; cDNA to mRNA; 219 BP.
DE   Human LAMP residues 46-118 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match              6.0%;  Score 100;  DB 2;  Length 219;
  Best Local Similarity   67.0%;  Pred. No. 5.1e-16;
RESULT 743
ID   AAT42089 standard; cDNA to mRNA; 219 BP.
DE   Rat LAMP residues 46-118 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
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PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match              5.7%;  Score 95.2;  DB 2;  Length 219;
  Best Local Similarity   65.6%;  Pred. No. 9.6e-15;
RESULT 744
ID   AAS67246 standard; cDNA; 2678 BP.
DE   DNA encoding novel human diagnostic protein #3050.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              5.6%;  Score 94.4;  DB 5;  Length 2678;
  Best Local Similarity   57.1%;  Pred. No. 5.5e-14;
RESULT 745
ID   AAS71723 standard; cDNA; 2678 BP.
DE   DNA encoding novel human diagnostic protein #7527.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              5.6%;  Score 94.4;  DB 5;  Length 2678;
  Best Local Similarity   57.1%;  Pred. No. 5.5e-14;
RESULT 746
ID   AAS64445 standard; cDNA; 3131 BP.
DE   DNA encoding novel human diagnostic protein #249.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              5.6%;  Score 94.4;  DB 5;  Length 3131;
  Best Local Similarity   57.1%;  Pred. No. 6e-14;
RESULT 747
ID   AAS64798 standard; cDNA; 3131 BP.
DE   DNA encoding novel human diagnostic protein #602.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              5.6%;  Score 94.4;  DB 5;  Length 3131;
  Best Local Similarity   57.1%;  Pred. No. 6e-14;
RESULT 748
ID   ADM18382 standard; DNA; 2026 BP.
DE   Human chromosome 11qtel subtelomeric DNA probe SEQ ID NO:6.
PN   WO2004029283-A2.
PD   08-APR-2004.
PA   (CHIL-) CHILDREN'S MERCY HOSPITAL.
  Query Match              5.3%;  Score 89;  DB 12;  Length 2026;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-12;
RESULT 749
ID   ADG63285 standard; DNA; 420 BP.
DE   Human OBCAM gene exon 4.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match              4.7%;  Score 78.6;  DB 10;  Length 420;
  Best Local Similarity   70.5%;  Pred. No. 3.3e-10;
RESULT 750
ID   AAT42090 standard; cDNA to mRNA; 177 BP.
DE   Human LAMP residues 156-204 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match              4.6%;  Score 77.8;  DB 2;  Length 177;
  Best Local Similarity   65.0%;  Pred. No. 3.5e-10;
RESULT 751
ID   AAT42091 standard; cDNA to mRNA; 177 BP.
DE   Rat LAMP residues 156-204 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match              4.6%;  Score 77.8;  DB 2;  Length 177;
  Best Local Similarity   65.0%;  Pred. No. 3.5e-10;
RESULT 752
ID   ADG63287 standard; DNA; 480 BP.
DE   Human OBCAM gene exon 6.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match              4.6%;  Score 76.8;  DB 10;  Length 480;
  Best Local Similarity   70.8%;  Pred. No. 1.1e-09;
RESULT 753
ID   AAS28866 standard; cDNA; 293 BP.
DE   Human immunoglobulin encoding cDNA SEQ ID No 112.
PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              4.3%;  Score 73;  DB 4;  Length 293;
  Best Local Similarity   62.9%;  Pred. No. 8.3e-09;
RESULT 754
ID   ABA06681 standard; cDNA; 293 BP.
DE   Human cDNA SEQ ID NO: 347.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              4.3%;  Score 73;  DB 4;  Length 293;
  Best Local Similarity   62.9%;  Pred. No. 8.3e-09;
RESULT 755
ID   ABV84018 standard; cDNA; 293 BP.
DE   Human polynucleotide SEQ ID NO 347.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match              4.3%;  Score 73;  DB 6;  Length 293;
  Best Local Similarity   62.9%;  Pred. No. 8.3e-09;
RESULT 756
ID   ADB31591 standard; cDNA; 293 BP.
DE   Human cDNA encoding a novel protein SEQ ID NO 112.
PN   US2003077606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              4.3%;  Score 73;  DB 10;  Length 293;
  Best Local Similarity   62.9%;  Pred. No. 8.3e-09;
RESULT 757
ID   ADG63286 standard; DNA; 480 BP.
DE   Human OBCAM gene exon 5.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match              4.3%;  Score 71.4;  DB 10;  Length 480;
  Best Local Similarity   74.4%;  Pred. No. 2.8e-08;
RESULT 758
ID   AAT42092 standard; cDNA to mRNA; 198 BP.
DE   Human LAMP residues 232-297 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match              3.8%;  Score 64.6;  DB 2;  Length 198;
  Best Local Similarity   61.3%;  Pred. No. 1.1e-06;
RESULT 759
ID   AAT42093 standard; cDNA to mRNA; 198 BP.
DE   Rat LAMP residues 232-297 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match              3.8%;  Score 63.4;  DB 2;  Length 198;
  Best Local Similarity   60.7%;  Pred. No. 2.4e-06;
RESULT 760
ID   ADG63282 standard; DNA; 270 BP.
DE   Human OBCAM gene exon 1.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match              3.7%;  Score 61.6;  DB 10;  Length 270;
  Best Local Similarity   88.6%;  Pred. No. 8.3e-06;
RESULT 761
ID   ABN40988 standard; DNA; 60 BP.
DE   Human spliced transcript detection oligonucleotide SEQ ID NO:13736.
PN   WO200210449-A2.
PD   07-FEB-2002.
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PA   (COMP-) COMPUGEN INC.
  Query Match             3.6%;  Score 60;  DB 6;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 1e-05;
RESULT 762
ID   ADA71938 standard; DNA; 2000 BP.
DE   Rice gene, SEQ ID 5263.
PN   WO2003000898-A1.
PD   03-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
  Query Match             3.5%;  Score 58.6;  DB 8;  Length 2000;
  Best Local Similarity   9.5%;  Pred. No. 0.00014;
RESULT 763
ID   ADG63284 standard; DNA; 420 BP.
DE   Human OBCAM gene exon 3.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             3.4%;  Score 57.6;  DB 10;  Length 420;
  Best Local Similarity   65.6%;  Pred. No. 0.00012;
RESULT 764
ID   ACN55172 standard; cDNA; 248 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-030-Q6-K6-C8, SEQ:9953.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             3.4%;  Score 57.2;  DB 13;  Length 248;
  Best Local Similarity   58.0%;  Pred. No. 0.00012;
RESULT 765
ID   ABX47608 standard; cDNA; 399 BP.
DE   Bovine EST associated with lactation/muscle/fat deposition #12773.
PN   US2002137139-A1.
PD   26-SEP-2002.
PA   (BYAT/) BYATT J C.
PA   (MATH/) MATHIALAGAN N.
PA   (TAON/) TAO N.
PA   (WARR/) WARREN W C.
  Query Match             3.4%;  Score 56.6;  DB 8;  Length 399;
  Best Local Similarity   57.7%;  Pred. No. 0.00021;
RESULT 766
ID   ABV56779 standard; cDNA; 247 BP.
DE   Human prostate expression marker cDNA 56770.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.3%;  Score 55.6;  DB 5;  Length 247;
  Best Local Similarity   54.4%;  Pred. No. 0.00031;
RESULT 767
ID   ABK39945 standard; DNA; 6359 BP.
DE   Human chemically pretreated gene sequence #13 strand 2.
PN   WO200202806-A2.
PD   10-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.3%;  Score 55;  DB 6;  Length 6359;
  Best Local Similarity   66.4%;  Pred. No. 0.0023;
RESULT 768
ID   ACH15235 standard; cDNA; 514 BP.
DE   Human adult brain cDNA #2447.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             3.2%;  Score 54.4;  DB 9;  Length 514;
  Best Local Similarity   62.3%;  Pred. No. 0.00093;
RESULT 769
ID   ABL32788 standard; DNA; 6171 BP.
DE   Human immune system associated gene SEQ ID NO: 761.
PN   WO200200928-A2.
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PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.2%;  Score 54.4;  DB 6;  Length 6171;
  Best Local Similarity   61.1%;  Pred. No. 0.0033;
RESULT 770
ID   AAI86998 standard; cDNA; 390 BP.
DE   Human polynucleotide SEQ ID NO 7058.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             3.2%;  Score 53.2;  DB 4;  Length 390;
  Best Local Similarity   58.0%;  Pred. No. 0.0017;
RESULT 771
ID   AAD05318 standard; cDNA; 671 BP.
DE   Human secreted protein-encoding gene 19 cDNA clone HWLFQ64, SEQ ID NO:29.
PN   WO200134626-A1.
PD   17-MAY-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.2%;  Score 53.2;  DB 4;  Length 671;
  Best Local Similarity   60.3%;  Pred. No. 0.0022;
RESULT 772
ID   ABV58693 standard; cDNA; 607 BP.
DE   Human prostate expression marker cDNA 58684.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.2%;  Score 53;  DB 5;  Length 607;
  Best Local Similarity   56.6%;  Pred. No. 0.0024;
RESULT 773
ID   ABV48356 standard; cDNA; 392 BP.
DE   Human prostate expression marker cDNA 48347.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.1%;  Score 52.8;  DB 5;  Length 392;
  Best Local Similarity   57.1%;  Pred. No. 0.0022;
RESULT 774
ID   ADH23363 standard; cDNA; 3351 BP.
DE   Fruit fly PAK4 serine/threonine kinase cDNA.
PN   US2003186254-A1.
PD   02-OCT-2003.
PA   (CELL-) CELL SIGNALING TECHNOLOGY INC.
  Query Match             3.1%;  Score 52.8;  DB 12;  Length 3351;
  Best Local Similarity   58.1%;  Pred. No. 0.0064;
RESULT 775
ID   ABL33589 standard; DNA; 5567 BP.
DE   Human immune system associated gene SEQ ID NO: 1562.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.1%;  Score 52.8;  DB 6;  Length 5567;
  Best Local Similarity   63.3%;  Pred. No. 0.0082;
RESULT 776
ID   ABL92273 standard; DNA; 5567 BP.
DE   Chemically treated DNA repair gene fragment complementary to#41.
PN   WO200181622-A2.
PD   01-NOV-2001.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.1%;  Score 52.8;  DB 6;  Length 5567;
  Best Local Similarity   63.3%;  Pred. No. 0.0082;
RESULT 777
ID   ADA71938 standard; DNA; 2000 BP.
DE   Rice gene, SEQ ID 5263.
PN   WO2003000898-A1.
PD   03-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
  Query Match             3.1%;  Score 52.6;  DB 8;  Length 2000;
  Best Local Similarity   8.4%;  Pred. No. 0.0055;
RESULT 778
ID   ABQ25430 standard; DNA; 579 BP.
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 12021.
PN   WO200218632-A2.
PD   07-MAR-2002.
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PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.1%;  Score 52.4;  DB 6;  Length 579;
  Best Local Similarity   60.6%;  Pred. No. 0.0033;
RESULT 779
ID   ABQ25431 standard; DNA; 579 BP.
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 12022.
PN   WO200218632-A2.
PD   07-MAR-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.1%;  Score 52.4;  DB 6;  Length 579;
  Best Local Similarity   60.6%;  Pred. No. 0.0033;
RESULT 780
ID   ACN81600 standard; DNA; 679 BP.
DE   Breast cancer related marker, seq id 2750.
PN   US2003099974-A1.
PD   29-MAY-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match             3.1%;  Score 52.4;  DB 11;  Length 679;
  Best Local Similarity   55.2%;  Pred. No. 0.0036;
RESULT 781
ID   ABK40004 standard; DNA; 5586 BP.
DE   Human chemically pretreated gene sequence #43 strand 2.
PN   WO200202806-A2.
PD   10-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.1%;  Score 52.4;  DB 6;  Length 5586;
  Best Local Similarity   59.3%;  Pred. No. 0.011;
RESULT 782
ID   ACN52334 standard; cDNA; 571 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-E11, SEQ:7115.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             3.1%;  Score 52.2;  DB 13;  Length 571;
  Best Local Similarity   57.8%;  Pred. No. 0.0038;
RESULT 783
ID   AAL11399 standard; cDNA; 666 BP.
DE   Human breast cancer expressed polynucleotide 3856.
PN   WO200151628-A2.
PD   19-JUL-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.1%;  Score 52.2;  DB 4;  Length 666;
  Best Local Similarity   56.8%;  Pred. No. 0.0041;
RESULT 784
ID   ABL11515 standard; cDNA; 2010 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 29027.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match             3.1%;  Score 52.2;  DB 4;  Length 2010;
  Best Local Similarity   45.6%;  Pred. No. 0.0071;
RESULT 785
ID   AAF72803 standard; DNA; 2057 BP.
DE   Secreted protein gene #5.
PN   WO200107459-A1.
PD   01-FEB-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.1%;  Score 52.2;  DB 4;  Length 2057;
  Best Local Similarity   57.8%;  Pred. No. 0.0072;
RESULT 786
ID   ABS67818 standard; DNA; 3063 BP.
DE   Human receptors and membrane associated protein REMAP-40 gene.
PN   WO200263006-A2.
PD   15-AUG-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             3.1%;  Score 52.2;  DB 6;  Length 3063;
  Best Local Similarity   64.5%;  Pred. No. 0.0088;
RESULT 787
ID   ABL33948 standard; DNA; 18218 BP.
DE   Human immune system associated gene SEQ ID NO: 1921.
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PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.1%;  Score 52.2;  DB 6;  Length 18218;
  Best Local Similarity   60.0%;  Pred. No. 0.022;
RESULT 788
ID   ADS73024 standard; cDNA; 183 BP.
DE   Human kidney tumour specific cDNA, SEQ ID 1621.
PN   US2003109434-A1.
PD   12-JUN-2003.
PA   (CORI-) CORIXA CORP.
  Query Match             3.1%;  Score 52;  DB 7;  Length 183;
  Best Local Similarity   60.7%;  Pred. No. 0.0024;
RESULT 789
ID   ABV58708 standard; cDNA; 484 BP.
DE   Human prostate expression marker cDNA 58699.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.1%;  Score 52;  DB 5;  Length 484;
  Best Local Similarity   58.3%;  Pred. No. 0.0039;
RESULT 790
ID   ABT08076 standard; cDNA; 791 BP.
DE   Human breast specific coding sequence SEQ ID NO: 22.
PN   WO200266607-A2.
PD   29-AUG-2002.
PA   (DIAD-) DIADEXUS INC.
  Query Match             3.1%;  Score 52;  DB 6;  Length 791;
  Best Local Similarity   60.7%;  Pred. No. 0.005;
RESULT 791
ID   ABL32719 standard; DNA; 5739 BP.
DE   Human immune system associated gene SEQ ID NO: 692.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.1%;  Score 52;  DB 6;  Length 5739;
  Best Local Similarity   59.5%;  Pred. No. 0.014;
RESULT 792
ID   ABQ54403 standard; cDNA; 2911 BP.
DE   Human ovarian antigen HAPOE30 cDNA, SEQ ID NO:283.
PN   WO200200677-A1.
PD   03-JAN-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.1%;  Score 51.6;  DB 6;  Length 2911;
  Best Local Similarity   59.6%;  Pred. No. 0.012;
RESULT 793
ID   AAA16619 standard; cDNA; 3508 BP.
DE   Human secreted protein clone lo311_8 nucleotide sequence SEQ ID NO:3.
PN   WO200009552-A1.
PD   24-FEB-2000.
PA   (GEMY ) GENETICS INST INC.
  Query Match             3.1%;  Score 51.6;  DB 3;  Length 3508;
  Best Local Similarity   62.3%;  Pred. No. 0.014;
RESULT 794
ID   ADS89723 standard; DNA; 5759 BP.
DE   Oligonucleotide of the invention SEQ ID NO:739.
PN   WO2004035803-A2.
PD   29-APR-2004.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.1%;  Score 51.6;  DB 13;  Length 5759;
  Best Local Similarity   56.5%;  Pred. No. 0.017;
RESULT 795
ID   ABZ10109 standard; DNA; 8759 BP.
DE   Haematopoietic cell proliferation disorder related DNA sequence #249.
PN   WO200277272-A2.
PD   03-OCT-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.1%;  Score 51.6;  DB 8;  Length 8759;
  Best Local Similarity   56.5%;  Pred. No. 0.022;
RESULT 796
ID   ABZ10237 standard; DNA; 8759 BP.
DE   Haematopoietic cell proliferation disorder related DNA sequence #377.
PN   WO200277272-A2.
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PD   03-OCT-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              3.1%;  Score 51.6;  DB 8;  Length 8759;
  Best Local Similarity   56.5%;  Pred. No. 0.022;
RESULT 797
ID   ADB54213 standard; DNA; 8759 BP.
DE   Pretreated genomic DNA region 137.
PN   WO2003072821-A2.
PD   04-SEP-2003.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              3.1%;  Score 51.6;  DB 10;  Length 8759;
  Best Local Similarity   56.5%;  Pred. No. 0.022;
RESULT 798
ID   ADE84147 standard; DNA; 8759 BP.
DE   Human lymphoid cell proliferative disorder gene derived DNA #83.
PN   WO2003044226-A2.
PD   30-MAY-2003.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              3.1%;  Score 51.6;  DB 10;  Length 8759;
  Best Local Similarity   56.5%;  Pred. No. 0.022;
RESULT 799
ID   ADS89513 standard; DNA; 8759 BP.
DE   Oligonucleotide of the invention SEQ ID NO:529.
PN   WO2004035803-A2.
PD   29-APR-2004.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              3.1%;  Score 51.6;  DB 13;  Length 8759;
  Best Local Similarity   56.5%;  Pred. No. 0.022;
RESULT 800
ID   ABL32784 standard; DNA; 8979 BP.
DE   Human immune system associated gene SEQ ID NO: 757.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              3.1%;  Score 51.6;  DB 6;  Length 8979;
  Best Local Similarity   63.9%;  Pred. No. 0.022;
RESULT 801
ID   ABK31270 standard; DNA; 8979 BP.
DE   Signal transduction associated gene modified DNA #57.
PN   WO200200926-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              3.1%;  Score 51.6;  DB 6;  Length 8979;
  Best Local Similarity   63.9%;  Pred. No. 0.022;
RESULT 802
ID   ABL70231 standard; DNA; 8979 BP.
DE   Chemically treated cell signalling DNA sequence#61.
PN   WO200202807-A2.
PD   10-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              3.1%;  Score 51.6;  DB 6;  Length 8979;
  Best Local Similarity   63.9%;  Pred. No. 0.022;
RESULT 803
ID   AAS61178 standard; DNA; 8979 BP.
DE   Human gene regulation-associated gene oligonucleotide #133.
PN   WO200177375-A2.
PD   18-OCT-2001.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              3.1%;  Score 51.6;  DB 6;  Length 8979;
  Best Local Similarity   63.9%;  Pred. No. 0.022;
RESULT 804
ID   AAI87807 standard; cDNA; 419 BP.
DE   Human polynucleotide SEQ ID NO 7867.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              3.1%;  Score 51.4;  DB 4;  Length 419;
  Best Local Similarity   60.3%;  Pred. No. 0.0052;
RESULT 805
ID   ACN52877 standard; cDNA; 421 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H7, SEQ:7658.
PN   US2004123340-A1.
PD   24-JUN-2004.
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PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match              3.1%;  Score 51.4;  DB 13;  Length 421;
  Best Local Similarity   58.0%;  Pred. No. 0.0052;
RESULT 806
ID   ACN50120 standard; cDNA; 585 BP.
DE   Cotton non-primed seed EST Clone ID: LIB3826-001-Q1-K6-D8, SEQ:4901.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match              3.1%;  Score 51.4;  DB 13;  Length 585;
  Best Local Similarity   58.0%;  Pred. No. 0.0062;
RESULT 807
ID   ABV58626 standard; cDNA; 504 BP.
DE   Human prostate expression marker cDNA 58617.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              3.0%;  Score 51.2;  DB 5;  Length 504;
  Best Local Similarity   57.5%;  Pred. No. 0.0065;
RESULT 808
ID   ABK43454 standard; cDNA; 894 BP.
DE   DNA encoding novel central nervous system protein #34.
PN   WO200155318-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.0%;  Score 51.2;  DB 4;  Length 894;
  Best Local Similarity   66.1%;  Pred. No. 0.0087;
RESULT 809
ID   ADI53841 standard; cDNA; 894 BP.
DE   cDNA encoding novel human protein seq id 44.
PN   US2004018969-A1.
PD   29-JAN-2004.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match              3.0%;  Score 51.2;  DB 12;  Length 894;
  Best Local Similarity   66.1%;  Pred. No. 0.0087;
RESULT 810
ID   AAI83204 standard; cDNA; 386 BP.
DE   Human polynucleotide SEQ ID NO 3264.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              3.0%;  Score 51;  DB 4;  Length 386;
  Best Local Similarity   59.2%;  Pred. No. 0.0064;
RESULT 811
ID   ACN56273 standard; cDNA; 517 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-E7, SEQ:11054.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match              3.0%;  Score 51;  DB 13;  Length 517;
  Best Local Similarity   59.2%;  Pred. No. 0.0074;
RESULT 812
ID   ADJ81646 standard; DNA; 10428 BP.
DE   Human tyrosine phosphatase SHP1 bisulphited genomic DNA SeqID 6.
PN   JP2004000128-A.
PD   08-JAN-2004.
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
  Query Match              3.0%;  Score 51;  DB 12;  Length 10428;
  Best Local Similarity   59.2%;  Pred. No. 0.034;
RESULT 813
ID   ACN87837 standard; DNA; 643 BP.
DE   Breast cancer related marker, seq id 8987.
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PN   US2003099974-A1.
PD   29-MAY-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match              3.0%;  Score 50.8;  DB 11;  Length 643;
  Best Local Similarity   57.8%;  Pred. No. 0.0094;
RESULT 814
ID   ADL41364 standard; DNA; 393 BP.
DE   Human ovarian cancer DNA marker #15254.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              3.0%;  Score 50.6;  DB 5;  Length 393;
  Best Local Similarity   57.1%;  Pred. No. 0.0082;
RESULT 815
ID   ABN98845 standard; DNA; 856 BP.
DE   Arabidopsis thaliana expressed polynucleotide SEQ ID NO 613.
PN   US2002023281-A1.
PD   21-FEB-2002.
PA   (GORL/) GORLACH J.
PA   (ANYY/) AN Y.
PA   (HAMI/) HAMILTON C M.
PA   (PRIC/) PRICE J L.
PA   (RAIN/) RAINES T M.
PA   (YUYY/) YU Y.
PA   (RAME/) RAMEAKA J G.
PA   (PAGE/) PAGE A.
PA   (MATH/) MATHEW A V.
PA   (LEDF/) LEDFORD B L.
PA   (WOES/) WOESSNER J P.
PA   (HAAS/) HAAS W D.
PA   (GARC/) GARCIA C A.
PA   (KRIC/) KRICKER M.
PA   (SLAT/) SLATER T.
PA   (DAVI/) DAVIS K R.
PA   (ALLE/) ALLEN K.
PA   (HOFF/) HOFFMAN N.
PA   (HURB/) HURBAN P.
  Query Match              3.0%;  Score 50.6;  DB 6;  Length 856;
  Best Local Similarity   54.8%;  Pred. No. 0.012;
RESULT 816
ID   AAC63439 standard; cDNA; 876 BP.
DE   Human secreted protein coding sequence SEQ ID NO: 40.
PN   WO200061779-A1.
PD   19-OCT-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.0%;  Score 50.6;  DB 3;  Length 876;
  Best Local Similarity   63.6%;  Pred. No. 0.012;
RESULT 817
ID   ABZ73647 standard; cDNA; 876 BP.
DE   Secreted protein-encoding gene 367 cDNA clone HUSIR18, SEQ ID NO:377.
PN   WO200277013-A2.
PD   03-OCT-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.0%;  Score 50.6;  DB 8;  Length 876;
  Best Local Similarity   63.6%;  Pred. No. 0.012;
RESULT 818
ID   ADA98139 standard; cDNA; 876 BP.
DE   Human secreted protein cDNA sequence #233.
PN   WO2003004623-A2.
PD   16-JAN-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.0%;  Score 50.6;  DB 8;  Length 876;
  Best Local Similarity   63.6%;  Pred. No. 0.012;
RESULT 819
ID   ABZ67241 standard; cDNA; 876 BP.
DE   Human secreted protein encoding cDNA SEQ ID NO 361.
PN   WO200277186-A2.
PD   03-OCT-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.0%;  Score 50.6;  DB 10;  Length 876;
  Best Local Similarity   63.6%;  Pred. No. 0.012;
RESULT 820
ID   ADD71195 standard; cDNA; 2200 BP.
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DE   Human intracellular signalling molecule INTSIG-32 cDNA SEQ ID NO:84.
PN   WO2003039348-A2.
PD   15-MAY-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match              3.0%;  Score 50.6;  DB 10;  Length 2200;
  Best Local Similarity   70.1%;  Pred. No. 0.02;
RESULT 821
ID   ADB79863 standard; DNA; 2924 BP.
DE   Rat myosin heavy chain coding sequence, SEQ ID 103.
PN   EP1279744-A2.
PD   29-JAN-2003.
PA   (WARN ) WARNER LAMBERT CO.
  Query Match              3.0%;  Score 50.6;  DB 10;  Length 2924;
  Best Local Similarity   63.6%;  Pred. No. 0.023;
RESULT 822
ID   ABV25005 standard; cDNA; 4990 BP.
DE   Human prostate expression marker cDNA 24996.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              3.0%;  Score 50.6;  DB 5;  Length 4990;
  Best Local Similarity   58.2%;  Pred. No. 0.03;
RESULT 823
ID   ABV25400 standard; cDNA; 4990 BP.
DE   Human prostate expression marker cDNA 25391.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              3.0%;  Score 50.6;  DB 5;  Length 4990;
  Best Local Similarity   58.2%;  Pred. No. 0.03;
RESULT 824
ID   ACN89861 standard; DNA; 5001 BP.
DE   Breast cancer related marker, seq id 11011.
PN   US2003099974-A1.
PD   29-MAY-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match              3.0%;  Score 50.6;  DB 11;  Length 5001;
  Best Local Similarity   58.2%;  Pred. No. 0.03;
RESULT 825
ID   ABL92257 standard; DNA; 6029 BP.
DE   Chemically treated DNA repair gene fragment complementary to#33.
PN   WO200181622-A2.
PD   01-NOV-2001.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              3.0%;  Score 50.6;  DB 6;  Length 6029;
  Best Local Similarity   57.1%;  Pred. No. 0.033;
RESULT 826
ID   AAD22326 standard; DNA; 6029 BP.
DE   Chemically treated human genomic DNA #16 associated with DNA adducts.
PN   WO200177378-A2.
PD   18-OCT-2001.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              3.0%;  Score 50.6;  DB 6;  Length 6029;
  Best Local Similarity   57.1%;  Pred. No. 0.033;
RESULT 827
ID   ABX41821 standard; cDNA; 272 BP.
DE   Bovine EST associated with lactation/muscle/fat deposition #6986.
PN   US2002137139-A1.
PD   26-SEP-2002.
PA   (BYAT/) BYATT J C.
PA   (MATH/) MATHIALAGAN N.
PA   (TAON/) TAO N.
PA   (WARR/) WARREN W C.
  Query Match              3.0%;  Score 50.4;  DB 8;  Length 272;
  Best Local Similarity   60.0%;  Pred. No. 0.0077;
RESULT 828
ID   AAH71505 standard; cDNA; 310 BP.
DE   Human cervical cancer marker nucleic acid 2779.
PN   WO200142467-A2.
PD   14-JUN-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              3.0%;  Score 50.4;  DB 4;  Length 310;
  Best Local Similarity   56.7%;  Pred. No. 0.0082;
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RESULT 829
ID   ABL33696 standard; DNA; 6668 BP.
DE   Human immune system associated gene SEQ ID NO: 1669.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.0%;  Score 50.4;  DB 6;  Length 6668;
  Best Local Similarity   58.8%;  Pred. No. 0.039;
RESULT 830
ID   ABV19038 standard; cDNA; 201 BP.
DE   Human prostate expression marker cDNA 19029.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 50.2;  DB 5;  Length 201;
  Best Local Similarity   59.8%;  Pred. No. 0.0075;
RESULT 831
ID   AAT76782 standard; DNA; 240 BP.
DE   Staphylococcus aureus exfoliative toxin A gene capture probe.
PN   US5627054-A.
PD   06-MAY-1997.
PA   (USSA ) US SEC OF ARMY.
  Query Match             3.0%;  Score 50.2;  DB 2;  Length 240;
  Best Local Similarity   58.3%;  Pred. No. 0.0082;
RESULT 832
ID   ABV42927 standard; cDNA; 382 BP.
DE   Human prostate expression marker cDNA 42918.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 50.2;  DB 5;  Length 382;
  Best Local Similarity   55.4%;  Pred. No. 0.01;
RESULT 833
ID   ABV34060 standard; cDNA; 383 BP.
DE   Human prostate expression marker cDNA 34051.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 50.2;  DB 5;  Length 383;
  Best Local Similarity   55.4%;  Pred. No. 0.01;
RESULT 834
ID   ABV18980 standard; cDNA; 384 BP.
DE   Human prostate expression marker cDNA 18971.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 50.2;  DB 5;  Length 384;
  Best Local Similarity   48.1%;  Pred. No. 0.01;
RESULT 835
ID   ADI69792 standard; DNA; 384 BP.
DE   Human ovarian cancer DNA marker #2534.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 50.2;  DB 5;  Length 384;
  Best Local Similarity   52.6%;  Pred. No. 0.01;
RESULT 836
ID   ADI76128 standard; DNA; 384 BP.
DE   Human ovarian cancer DNA marker #8870.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 50.2;  DB 5;  Length 384;
  Best Local Similarity   52.6%;  Pred. No. 0.01;
RESULT 837
ID   ABV48817 standard; cDNA; 448 BP.
DE   Human prostate expression marker cDNA 48808.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 50.2;  DB 5;  Length 448;
  Best Local Similarity   59.8%;  Pred. No. 0.011;
RESULT 838
ID   ABL32540 standard; DNA; 6476 BP.
DE   Human immune system associated gene SEQ ID NO: 513.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.0%;  Score 50.2;  DB 6;  Length 6476;
  Best Local Similarity   62.2%;  Pred. No. 0.043;
RESULT 839
ID   ABV59017 standard; cDNA; 325 BP.
DE   Human prostate expression marker cDNA 59008.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 50;  DB 5;  Length 325;
  Best Local Similarity   61.5%;  Pred. No. 0.011;
RESULT 840
ID   ABV50931 standard; cDNA; 464 BP.
DE   Human prostate expression marker cDNA 50922.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 50;  DB 5;  Length 464;
  Best Local Similarity   63.1%;  Pred. No. 0.013;
RESULT 841
ID   ABV54323 standard; cDNA; 471 BP.
DE   Human prostate expression marker cDNA 54314.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 50;  DB 5;  Length 471;
  Best Local Similarity   52.4%;  Pred. No. 0.013;
RESULT 842
ID   ACH45627 standard; cDNA; 520 BP.
DE   Human foetal brain cDNA #6352.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             3.0%;  Score 50;  DB 9;  Length 520;
  Best Local Similarity   53.8%;  Pred. No. 0.014;
RESULT 843
ID   AAC79893 standard; cDNA; 680 BP.
DE   Human secreted protein encoding cDNA for gene 45.
PN   WO200055176-A2.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.0%;  Score 50;  DB 3;  Length 680;
  Best Local Similarity   58.9%;  Pred. No. 0.016;
RESULT 844
ID   AAA61261 standard; DNA; 870 BP.
DE   Human secreted protein gene 2 clone HHFBY53.
PN   WO200029422-A1.
PD   25-MAY-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.0%;  Score 50;  DB 3;  Length 870;
  Best Local Similarity   59.7%;  Pred. No. 0.018;
RESULT 845
ID   ADA39860 standard; cDNA; 870 BP.
DE   Human secreted protein encoding cDNA.
PN   WO2002102993-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.0%;  Score 50;  DB 8;  Length 870;
  Best Local Similarity   59.7%;  Pred. No. 0.018;
RESULT 846
ID   ACC50464 standard; cDNA; 870 BP.
DE   Human secreted protein coding sequence, SEQ ID 131.
PN   WO200295010-A2.
PD   28-NOV-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
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  Query Match             3.0%;  Score 50;  DB 8;  Length 870;
  Best Local Similarity   59.7%;  Pred. No. 0.018;
RESULT 847
ID   ADO62706 standard; DNA; 1971 BP.
DE   Transcription factor G2550 orthologous sequence, SEQ ID 1173.
PN   WO2004031349-A2.
PD   15-APR-2004.
PA   (MEND-) MENDEL BIOTECHNOLOGY INC.
  Query Match             3.0%;  Score 50;  DB 12;  Length 1971;
  Best Local Similarity   67.0%;  Pred. No. 0.027;
RESULT 848
ID   ADQ24914 standard; DNA; 3469 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7734.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             3.0%;  Score 50;  DB 12;  Length 3469;
  Best Local Similarity   56.8%;  Pred. No. 0.036;
RESULT 849
ID   ABN80041 standard; DNA; 5387 BP.
DE   Human chemically modified disease associated gene SEQ ID NO 58.
PN   WO200200927-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.0%;  Score 50;  DB 6;  Length 5387;
  Best Local Similarity   57.8%;  Pred. No. 0.045;
RESULT 850
ID   ABX56303 standard; DNA; 8243 BP.
DE   Human NOV25b CG93858-02 DNA SEQ ID 85.
PN   WO200281625-A2.
PD   17-OCT-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             3.0%;  Score 50;  DB 8;  Length 8243;
  Best Local Similarity   49.7%;  Pred. No. 0.055;
RESULT 851
ID   ABL33999 standard; DNA; 21537 BP.
DE   Human immune system associated gene SEQ ID NO: 1972.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.0%;  Score 50;  DB 6;  Length 21537;
  Best Local Similarity   60.1%;  Pred. No. 0.09;
RESULT 852
ID   ABV49239 standard; cDNA; 311 BP.
DE   Human prostate expression marker cDNA 49230.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 49.8;  DB 5;  Length 311;
  Best Local Similarity   58.4%;  Pred. No. 0.012;
RESULT 853
ID   ABV57904 standard; cDNA; 376 BP.
DE   Human prostate expression marker cDNA 57895.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 49.8;  DB 5;  Length 376;
  Best Local Similarity   58.4%;  Pred. No. 0.013;
RESULT 854
ID   ABV54466 standard; cDNA; 381 BP.
DE   Human prostate expression marker cDNA 54457.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 49.8;  DB 5;  Length 381;
  Best Local Similarity   62.4%;  Pred. No. 0.013;
RESULT 855
ID   ACH39052 standard; cDNA; 465 BP.
DE   Human foetal brain cDNA #419.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
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PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             3.0%;  Score 49.8;  DB 9;  Length 465;
  Best Local Similarity   55.9%;  Pred. No. 0.015;
RESULT 856
ID   ACH22893 standard; cDNA; 506 BP.
DE   Human adult ovary cDNA #1273.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             3.0%;  Score 49.8;  DB 9;  Length 506;
  Best Local Similarity   60.4%;  Pred. No. 0.015;
RESULT 857
ID   ABV56485 standard; cDNA; 543 BP.
DE   Human prostate expression marker cDNA 56476.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 49.8;  DB 5;  Length 543;
  Best Local Similarity   57.3%;  Pred. No. 0.016;
RESULT 858
ID   AAH70126 standard; cDNA; 545 BP.
DE   Human cervical cancer marker nucleic acid 1400.
PN   WO200142467-A2.
PD   14-JUN-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 49.8;  DB 4;  Length 545;
  Best Local Similarity   53.9%;  Pred. No. 0.016;
RESULT 859
ID   ACN53724 standard; cDNA; 571 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-K6-H4, SEQ:8505.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             3.0%;  Score 49.8;  DB 13;  Length 571;
  Best Local Similarity   64.1%;  Pred. No. 0.016;
RESULT 860
ID   AAA26373 standard; cDNA; 1048 BP.
DE   Human secreted protein gene 28 SEQ ID NO:38.
PN   WO200006698-A1.
PD   10-FEB-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.0%;  Score 49.8;  DB 3;  Length 1048;
  Best Local Similarity   59.6%;  Pred. No. 0.022;
RESULT 861
ID   ADL71434 standard; cDNA; 1048 BP.
DE   Novel human secreted protein cDNA seqid 38.
PN   US2004034196-A1.
PD   19-FEB-2004.
PA   (KOMA/) KOMATSOULIS G A.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (DUAN/) DUAN D R.
PA   (MOOR/) MOORE P A.
PA   (SHIY/) SHI Y.
PA   (LAFL/) LAFLEUR D W.
PA   (WEIY/) WEI Y.
  Query Match             3.0%;  Score 49.8;  DB 12;  Length 1048;
  Best Local Similarity   59.6%;  Pred. No. 0.022;
RESULT 862
ID   ADH02701 standard; DNA; 1317 BP.
DE   Human elongation factor EEF1A1 cDNA fragment, SEQ ID NO:7.
PN   WO2003104488-A1.
PD   18-DEC-2003.
PA   (CANC-) CANCER CARE ONTARIO.
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  Query Match             3.0%;  Score 49.8;  DB 12;  Length 1317;
  Best Local Similarity   58.4%;  Pred. No. 0.025;
RESULT 863
ID   ACF34510 standard; DNA; 1833 BP.
DE   Gene encoding angiogenesis protein BNO144.
PN   WO2003027285-A1.
PD   03-APR-2003.
PA   (BION-) BIONOMICS LTD.
  Query Match             3.0%;  Score 49.8;  DB 8;  Length 1833;
  Best Local Similarity   58.4%;  Pred. No. 0.029;
RESULT 864
ID   ADL35468 standard; DNA; 1833 BP.
DE   Human eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) DNA.
PN   WO2004019893-A2.
PD   11-MAR-2004.
PA   (RIGE-) RIGEL PHARM INC.
  Query Match             3.0%;  Score 49.8;  DB 12;  Length 1833;
  Best Local Similarity   58.4%;  Pred. No. 0.029;
RESULT 865
ID   ADS88611 standard; cDNA; 1833 BP.
DE   Human housekeeping gene cDNA sequence SEQ ID NO:154.
PN   WO2004035785-A1.
PD   29-APR-2004.
PA   (NIGA ) NGK INSULATORS LTD.
  Query Match             3.0%;  Score 49.8;  DB 13;  Length 1833;
  Best Local Similarity   58.4%;  Pred. No. 0.029;
RESULT 866
ID   ADJ62805 standard; cDNA; 1837 BP.
DE   Human cDNA differentially expressed in response to docetaxel #75.
PN   US2004018527-A1.
PD   29-JAN-2004.
PA   (CHAN/) CHANG J C.
PA   (OCON/) O'CONNELL P.
  Query Match             3.0%;  Score 49.8;  DB 12;  Length 1837;
  Best Local Similarity   58.4%;  Pred. No. 0.029;
RESULT 867
ID   ADP10528 standard; DNA; 1837 BP.
DE   Reference mRNA sequences for marker probe #205.
PN   WO2004042346-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
  Query Match             3.0%;  Score 49.8;  DB 12;  Length 1837;
  Best Local Similarity   58.4%;  Pred. No. 0.029;
RESULT 868
ID   AAF18296 standard; DNA; 2044 BP.
DE   Lung cancer associated polynucleotide sequence SEQ ID 315.
PN   WO200055180-A2.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
  Query Match             3.0%;  Score 49.8;  DB 3;  Length 2044;
  Best Local Similarity   57.3%;  Pred. No. 0.031;
RESULT 869
ID   AAA95790 standard; cDNA; 2045 BP.
DE   Apoptosis related gene 1 clone HLDOK36.
PN   WO200056752-A2.
PD   28-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.0%;  Score 49.8;  DB 3;  Length 2045;
  Best Local Similarity   57.3%;  Pred. No. 0.031;
RESULT 870
ID   AAH33283 standard; cDNA; 2045 BP.
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:339.
PN   WO200122920-A2.
PD   05-APR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.0%;  Score 49.8;  DB 4;  Length 2045;
  Best Local Similarity   57.3%;  Pred. No. 0.031;
RESULT 871
ID   AAV63189 standard; cDNA; 2496 BP.
DE   cDNA from clone cr1162_25 which encodes a secreted protein.
PN   WO9844113-A1.
PD   08-OCT-1998.
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PA   (GEMY ) GENETICS INST INC.
  Query Match             3.0%;  Score 49.8;  DB 2;  Length 2496;
  Best Local Similarity   60.9%;  Pred. No. 0.034;
RESULT 872
ID   ABQ92039 standard; cDNA; 2496 BP.
DE   Human polynucleotide SEQ ID NO 36.
PN   US2002065394-A1.
PD   30-MAY-2002.
PA   (JACO/) JACOBS K.
PA   (MCCO/) MCCOY J M.
PA   (LAVA/) LAVALLIE E R.
PA   (COLL/) COLLINS-RACIE L A.
PA   (EVAN/) EVANS C.
PA   (MERB/) MERBERG D.
PA   (TREA/) TREACY M.
PA   (SPAU/) SPAULDING V.
  Query Match             3.0%;  Score 49.8;  DB 6;  Length 2496;
  Best Local Similarity   60.9%;  Pred. No. 0.034;
RESULT 873
ID   ADI03925 standard; DNA; 2496 BP.
DE   Human B7-L1 polypeptide encoding DNA.
PN   WO2003105887-A1.
PD   24-DEC-2003.
PA   (AMHP ) WYETH.
  Query Match             3.0%;  Score 49.8;  DB 12;  Length 2496;
  Best Local Similarity   60.9%;  Pred. No. 0.034;
RESULT 874
ID   AAF91859 standard; cDNA; 3436 BP.
DE   Human secreted protein-encoding gene 2 cDNA clone HDPFB02, SEQ ID NO:12.
PN   WO200118022-A1.
PD   15-MAR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.0%;  Score 49.8;  DB 4;  Length 3436;
  Best Local Similarity   59.6%;  Pred. No. 0.04;
RESULT 875
ID   AAS00767 standard; cDNA; 3436 BP.
DE   Human B7-H3 cDNA clone.
PN   WO200118021-A1.
PD   15-MAR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (MAYO-) MAYO CLINIC.
  Query Match             3.0%;  Score 49.8;  DB 4;  Length 3436;
  Best Local Similarity   59.6%;  Pred. No. 0.04;
RESULT 876
ID   ADA39737 standard; cDNA; 3436 BP.
DE   Human secreted protein encoding cDNA.
PN   WO2002102993-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.0%;  Score 49.8;  DB 8;  Length 3436;
  Best Local Similarity   59.6%;  Pred. No. 0.04;
RESULT 877
ID   ADC73453 standard; DNA; 3436 BP.
DE   Human secreted protein-related DNA - SEQ ID 86.
PN   WO2003038063-A2.
PD   08-MAY-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.0%;  Score 49.8;  DB 10;  Length 3436;
  Best Local Similarity   59.6%;  Pred. No. 0.04;
RESULT 878
ID   ABL32345 standard; DNA; 7346 BP.
DE   Human immune system associated gene SEQ ID NO: 318.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.0%;  Score 49.8;  DB 6;  Length 7346;
  Best Local Similarity   59.6%;  Pred. No. 0.059;
RESULT 879
ID   ABN80102 standard; DNA; 8712 BP.
DE   Human chemically modified disease associated gene SEQ ID NO 119.
PN   WO200200927-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
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  Query Match             3.0%;  Score 49.8;  DB 6;  Length 8712;
  Best Local Similarity   60.9%;  Pred. No. 0.064;
RESULT 880
ID   AAI92106 standard; cDNA; 425 BP.
DE   Human polynucleotide SEQ ID NO 12166.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             3.0%;  Score 49.6;  DB 4;  Length 425;
  Best Local Similarity   57.9%;  Pred. No. 0.016;
RESULT 881
ID   ACN60136 standard; cDNA; 481 BP.
DE   Cotton gynoecium tissue EST Clone ID: LIB3829-018-Q6-K6-C5, SEQ:14917.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             3.0%;  Score 49.6;  DB 13;  Length 481;
  Best Local Similarity   59.0%;  Pred. No. 0.017;
RESULT 882
ID   ADQ22716 standard; DNA; 1486 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5536.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             3.0%;  Score 49.6;  DB 12;  Length 1486;
  Best Local Similarity   58.6%;  Pred. No. 0.03;
RESULT 883
ID   ACC59907 standard; cDNA; 1678 BP.
DE   Human REMAP-20 encoding cDNA SEQ ID NO:56.
PN   WO2003025130-A2.
PD   27-MAR-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             3.0%;  Score 49.6;  DB 9;  Length 1678;
  Best Local Similarity   59.0%;  Pred. No. 0.032;
RESULT 884
ID   ADL63386 standard; DNA; 2161 BP.
DE   Human ovarian cancer DNA marker #21598.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             3.0%;  Score 49.6;  DB 5;  Length 2161;
  Best Local Similarity   56.9%;  Pred. No. 0.036;
RESULT 885
ID   ADG32748 standard; DNA; 2870 BP.
DE   Human DNA differentially expressed in patients with SLE SeqID72.
PN   WO2003090694-A2.
PD   06-NOV-2003.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
  Query Match             3.0%;  Score 49.6;  DB 10;  Length 2870;
  Best Local Similarity   61.7%;  Pred. No. 0.041;
RESULT 886
ID   ADD18806 standard; DNA; 3232 BP.
DE   Human disease related protein DNA sequence SeqID238.
PN   WO2003018621-A2.
PD   06-MAR-2003.
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
  Query Match             3.0%;  Score 49.6;  DB 10;  Length 3232;
  Best Local Similarity   60.3%;  Pred. No. 0.044;
RESULT 887
ID   ADH61306 standard; DNA; 3420 BP.
DE   INTSIG encoding DNA 7512389CB1, SEQ ID 23.
PN   WO2004001005-A2.
PD   31-DEC-2003.
PA   (INCY-) INCYTE CORP.
  Query Match             3.0%;  Score 49.6;  DB 12;  Length 3420;
  Best Local Similarity   59.0%;  Pred. No. 0.045;
RESULT 888
ID   ABL33518 standard; DNA; 5520 BP.
DE   Human immune system associated gene SEQ ID NO: 1491.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.0%;  Score 49.6;  DB 6;  Length 5520;
  Best Local Similarity   59.0%;  Pred. No. 0.058;
RESULT 889
ID   ABL32677 standard; DNA; 6015 BP.
DE   Human immune system associated gene SEQ ID NO: 650.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             3.0%;  Score 49.6;  DB 6;  Length 6015;
  Best Local Similarity   63.3%;  Pred. No. 0.06;
RESULT 890
ID   AAI87537 standard; cDNA; 366 BP.
DE   Human polynucleotide SEQ ID NO 7597.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 49.4;  DB 4;  Length 366;
  Best Local Similarity   61.1%;  Pred. No. 0.017;
RESULT 891
ID   ABV56666 standard; cDNA; 408 BP.
DE   Human prostate expression marker cDNA 56657.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 49.4;  DB 5;  Length 408;
  Best Local Similarity   54.9%;  Pred. No. 0.017;
RESULT 892
ID   AAI82260 standard; cDNA; 412 BP.
DE   Human polynucleotide SEQ ID NO 2320.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 49.4;  DB 4;  Length 412;
  Best Local Similarity   63.8%;  Pred. No. 0.018;
RESULT 893
ID   ABV45890 standard; cDNA; 438 BP.
DE   Human prostate expression marker cDNA 45881.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 49.4;  DB 5;  Length 438;
  Best Local Similarity   62.6%;  Pred. No. 0.018;
RESULT 894
ID   AAI82206 standard; cDNA; 480 BP.
DE   Human polynucleotide SEQ ID NO 2266.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 49.4;  DB 4;  Length 480;
  Best Local Similarity   54.0%;  Pred. No. 0.019;
RESULT 895
ID   ACH25146 standard; cDNA; 561 BP.
DE   Human adult ovary cDNA #3526.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             2.9%;  Score 49.4;  DB 9;  Length 561;
  Best Local Similarity   58.5%;  Pred. No. 0.02;
RESULT 896
ID   ABV58690 standard; cDNA; 579 BP.
DE   Human prostate expression marker cDNA 58681.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 49.4;  DB 5;  Length 579;
  Best Local Similarity   58.5%;  Pred. No. 0.021;
RESULT 897
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ID   AAL20340 standard; cDNA; 622 BP.
DE   Human breast cancer expressed polynucleotide 12797.
PN   WO200151628-A2.
PD   19-JUL-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49.4;  DB 4;  Length 622;
  Best Local Similarity   57.4%;  Pred. No. 0.022;
RESULT 898
ID   AAC80551 standard; cDNA; 658 BP.
DE   Human secreted protein gene 21 SEQ ID NO:31.
PN   WO200058467-A1.
PD   05-OCT-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              2.9%;  Score 49.4;  DB 3;  Length 658;
  Best Local Similarity   57.4%;  Pred. No. 0.022;
RESULT 899
ID   AAH35003 standard; cDNA; 788 BP.
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:2085.
PN   WO200122920-A2.
PD   05-APR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              2.9%;  Score 49.4;  DB 4;  Length 788;
  Best Local Similarity   58.5%;  Pred. No. 0.024;
RESULT 900
ID   AAS02414 standard; cDNA; 797 BP.
DE   Human secreted protein, cDNA #20.
PN   WO200123546-A1.
PD   05-APR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              2.9%;  Score 49.4;  DB 4;  Length 797;
  Best Local Similarity   58.5%;  Pred. No. 0.024;
RESULT 901
ID   ABV28953 standard; cDNA; 1603 BP.
DE   Human prostate expression marker cDNA 28944.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49.4;  DB 5;  Length 1603;
  Best Local Similarity   64.3%;  Pred. No. 0.035;
RESULT 902
ID   ABV22100 standard; cDNA; 1603 BP.
DE   Human prostate expression marker cDNA 22091.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49.4;  DB 5;  Length 1603;
  Best Local Similarity   64.3%;  Pred. No. 0.035;
RESULT 903
ID   ABV23114 standard; cDNA; 1603 BP.
DE   Human prostate expression marker cDNA 23105.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49.4;  DB 5;  Length 1603;
  Best Local Similarity   64.3%;  Pred. No. 0.035;
RESULT 904
ID   ABV27940 standard; cDNA; 1603 BP.
DE   Human prostate expression marker cDNA 27931.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49.4;  DB 5;  Length 1603;
  Best Local Similarity   64.3%;  Pred. No. 0.035;
RESULT 905
ID   AAS31262 standard; cDNA; 2645 BP.
DE   Human cDNA encoding a novel extracellular matrix protein, Seq ID No 76.
PN   WO200155368-A1.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              2.9%;  Score 49.4;  DB 4;  Length 2645;
  Best Local Similarity   58.5%;  Pred. No. 0.045;
RESULT 906
ID   ABQ66586 standard; cDNA; 2645 BP.
DE   Human polynucleotide SEQ ID NO 76.
PN   US2002042386-A1.
PD   11-APR-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match              2.9%;  Score 49.4;  DB 6;  Length 2645;
  Best Local Similarity   58.5%;  Pred. No. 0.045;
RESULT 907
ID   ADC10608 standard; cDNA; 2645 BP.
DE   Human cDNA from extracellular matrix gene 66.
PN   US2003059875-A1.
PD   27-MAR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              2.9%;  Score 49.4;  DB 10;  Length 2645;
  Best Local Similarity   58.5%;  Pred. No. 0.045;
RESULT 908
ID   ADQ23227 standard; DNA; 3480 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 6047.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              2.9%;  Score 49.4;  DB 12;  Length 3480;
  Best Local Similarity   57.4%;  Pred. No. 0.052;
RESULT 909
ID   ADQ24537 standard; DNA; 3480 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7357.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              2.9%;  Score 49.4;  DB 12;  Length 3480;
  Best Local Similarity   57.4%;  Pred. No. 0.052;
RESULT 910
ID   AAI88514 standard; cDNA; 389 BP.
DE   Human polynucleotide SEQ ID NO 8574.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              2.9%;  Score 49.2;  DB 4;  Length 389;
  Best Local Similarity   57.0%;  Pred. No. 0.019;
RESULT 911
ID   AAI88643 standard; cDNA; 396 BP.
DE   Human polynucleotide SEQ ID NO 8703.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              2.9%;  Score 49.2;  DB 4;  Length 396;
  Best Local Similarity   57.0%;  Pred. No. 0.019;
RESULT 912
ID   AAI87424 standard; cDNA; 429 BP.
DE   Human polynucleotide SEQ ID NO 7484.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              2.9%;  Score 49.2;  DB 4;  Length 429;
  Best Local Similarity   60.0%;  Pred. No. 0.02;
RESULT 913
ID   ABV58527 standard; cDNA; 442 BP.
DE   Human prostate expression marker cDNA 58518.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49.2;  DB 5;  Length 442;
  Best Local Similarity   57.0%;  Pred. No. 0.021;
RESULT 914
ID   ACH25161 standard; cDNA; 448 BP.
DE   Human adult ovary cDNA #3541.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             2.9%;  Score 49.2;  DB 9;  Length 448;
  Best Local Similarity   59.1%;  Pred. No. 0.021;
RESULT 915
ID   AAI84689 standard; cDNA; 453 BP.
DE   Human polynucleotide SEQ ID NO 4749.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 49.2;  DB 4;  Length 453;
  Best Local Similarity   60.4%;  Pred. No. 0.021;
RESULT 916
ID   ABV58840 standard; cDNA; 539 BP.
DE   Human prostate expression marker cDNA 58831.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 49.2;  DB 5;  Length 539;
  Best Local Similarity   59.2%;  Pred. No. 0.023;
RESULT 917
ID   ABV56624 standard; cDNA; 544 BP.
DE   Human prostate expression marker cDNA 56615.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 49.2;  DB 5;  Length 544;
  Best Local Similarity   60.4%;  Pred. No. 0.023;
RESULT 918
ID   ABV58620 standard; cDNA; 554 BP.
DE   Human prostate expression marker cDNA 58611.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 49.2;  DB 5;  Length 554;
  Best Local Similarity   61.9%;  Pred. No. 0.023;
RESULT 919
ID   ABV58414 standard; cDNA; 575 BP.
DE   Human prostate expression marker cDNA 58405.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 49.2;  DB 5;  Length 575;
  Best Local Similarity   57.0%;  Pred. No. 0.023;
RESULT 920
ID   AAH71551 standard; cDNA; 621 BP.
DE   Human cervical cancer marker nucleic acid 2825.
PN   WO200142467-A2.
PD   14-JUN-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 49.2;  DB 4;  Length 621;
  Best Local Similarity   57.0%;  Pred. No. 0.024;
RESULT 921
ID   AAH34312 standard; cDNA; 712 BP.
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:1394.
PN   WO200122920-A2.
PD   05-APR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             2.9%;  Score 49.2;  DB 4;  Length 712;
  Best Local Similarity   59.2%;  Pred. No. 0.026;
RESULT 922
ID   ADJ80203 standard; cDNA; 877 BP.
DE   Novel human nucleic acid-associated protein coding sequence #21.
PN   WO2003038052-A2.
PD   08-MAY-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             2.9%;  Score 49.2;  DB 10;  Length 877;
  Best Local Similarity   59.2%;  Pred. No. 0.029;
RESULT 923
ID   AAK58876 standard; cDNA; 1503 BP.
DE   Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3936.
PN   WO200157182-A2.
PD   09-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
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  Query Match             2.9%;  Score 49.2;  DB 4;  Length 1503;
  Best Local Similarity   59.6%;  Pred. No. 0.038;
RESULT 924
ID   ABA93758 standard; cDNA; 1537 BP.
DE   Human testis derived cDNA clone tes3_22124.
PN   WO200198454-A2.
PD   27-DEC-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
  Query Match             2.9%;  Score 49.2;  DB 6;  Length 1537;
  Best Local Similarity   63.6%;  Pred. No. 0.039;
RESULT 925
ID   ADQ22988 standard; DNA; 1576 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5808.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             2.9%;  Score 49.2;  DB 12;  Length 1576;
  Best Local Similarity   57.0%;  Pred. No. 0.039;
RESULT 926
ID   ADQ23425 standard; DNA; 2408 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 6245.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             2.9%;  Score 49.2;  DB 12;  Length 2408;
  Best Local Similarity   61.9%;  Pred. No. 0.048;
RESULT 927
ID   ABZ10224 standard; DNA; 2501 BP.
DE   Haematopoietic cell proliferation disorder related DNA sequence #364.
PN   WO200277272-A2.
PD   03-OCT-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 49.2;  DB 8;  Length 2501;
  Best Local Similarity   58.0%;  Pred. No. 0.049;
RESULT 928
ID   ADQ08601 standard; DNA; 3030 BP.
DE   Ciona intestinalis nervous system associated gene SeqID3.
PN   JP2004057127-A.
PD   26-FEB-2004.
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
  Query Match             2.9%;  Score 49.2;  DB 12;  Length 3030;
  Best Local Similarity   60.4%;  Pred. No. 0.054;
RESULT 929
ID   AAX33181 standard; DNA; 6644 BP.
DE   Base sequence of the plasmid pRx-ires-bsr.
PN   WO9913073-A2.
PD   18-MAR-1999.
PA   (RPRG-) RPR GENCELL ASIA PACIFIC INC.
  Query Match             2.9%;  Score 49.2;  DB 2;  Length 6644;
  Best Local Similarity   60.4%;  Pred. No. 0.081;
RESULT 930
ID   ABK40051 standard; DNA; 7058 BP.
DE   Human chemically pretreated gene sequence #67 strand 1.
PN   WO200202806-A2.
PD   10-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 49.2;  DB 6;  Length 7058;
  Best Local Similarity   63.6%;  Pred. No. 0.083;
RESULT 931
ID   AAX33182 standard; DNA; 7372 BP.
DE   Base sequence of the plasmid pRx-Bcl-xl-bsr.
PN   WO9913073-A2.
PD   18-MAR-1999.
PA   (RPRG-) RPR GENCELL ASIA PACIFIC INC.
  Query Match             2.9%;  Score 49.2;  DB 2;  Length 7372;
  Best Local Similarity   60.4%;  Pred. No. 0.085;
RESULT 932
ID   AAX33180 standard; DNA; 7797 BP.
DE   Cowpox virus bsr full length gene sequence.
PN   WO9913073-A2.
PD   18-MAR-1999.
PA   (RPRG-) RPR GENCELL ASIA PACIFIC INC.
  Query Match             2.9%;  Score 49.2;  DB 2;  Length 7797;
  Best Local Similarity   60.4%;  Pred. No. 0.088;
RESULT 933
ID   AAX33184 standard; DNA; 7996 BP.
DE   Base sequence of the plasmid pRx-Bcl 2-i-hCD 25.
PN   WO9913073-A2.
PD   18-MAR-1999.
PA   (RPRG-) RPR GENCELL ASIA PACIFIC INC.
  Query Match              2.9%;  Score 49.2;  DB 2;  Length 7996;
  Best Local Similarity   60.4%;  Pred. No. 0.089;
RESULT 934
ID   ABK28222 standard; DNA; 11394 BP.
DE   DNA transcription associated complementary genomic DNA #48.
PN   WO200192565-A2.
PD   06-DEC-2001.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 49.2;  DB 6;  Length 11394;
  Best Local Similarity   57.0%;  Pred. No. 0.11;
RESULT 935
ID   ABZ10104 standard; DNA; 35962 BP.
DE   Haematopoietic cell proliferation disorder related DNA sequence #244.
PN   WO200277272-A2.
PD   03-OCT-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 49.2;  DB 8;  Length 35962;
  Best Local Similarity   58.0%;  Pred. No. 0.19;
RESULT 936
ID   AAS07790 standard; DNA; 256 BP.
DE   Cervical cancer pre-malignant condition DNA marker #89.
PN   WO200142792-A2.
PD   14-JUN-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49;  DB 4;  Length 256;
  Best Local Similarity   59.0%;  Pred. No. 0.018;
RESULT 937
ID   ACN55002 standard; cDNA; 342 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-K6-A9, SEQ:9783.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match              2.9%;  Score 49;  DB 13;  Length 342;
  Best Local Similarity   57.5%;  Pred. No. 0.02;
RESULT 938
ID   ABV58528 standard; cDNA; 347 BP.
DE   Human prostate expression marker cDNA 58519.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49;  DB 5;  Length 347;
  Best Local Similarity   57.5%;  Pred. No. 0.02;
RESULT 939
ID   AAI84446 standard; cDNA; 348 BP.
DE   Human polynucleotide SEQ ID NO 4506.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              2.9%;  Score 49;  DB 4;  Length 348;
  Best Local Similarity   59.9%;  Pred. No. 0.021;
RESULT 940
ID   AAI85202 standard; cDNA; 390 BP.
DE   Human polynucleotide SEQ ID NO 5262.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              2.9%;  Score 49;  DB 4;  Length 390;
  Best Local Similarity   58.6%;  Pred. No. 0.022;
RESULT 941
ID   ACN53426 standard; cDNA; 403 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-K6-F9, SEQ:8207.
PN   US2004123340-A1.
PD   24-JUN-2004.
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PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match              2.9%;  Score 49;  DB 13;  Length 403;
  Best Local Similarity   57.5%;  Pred. No. 0.022;
RESULT 942
ID   ACH23125 standard; cDNA; 426 BP.
DE   Human adult ovary cDNA #1505.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match              2.9%;  Score 49;  DB 9;  Length 426;
  Best Local Similarity   58.6%;  Pred. No. 0.023;
RESULT 943
ID   ABV57380 standard; cDNA; 429 BP.
DE   Human prostate expression marker cDNA 57371.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49;  DB 5;  Length 429;
  Best Local Similarity   59.9%;  Pred. No. 0.023;
RESULT 944
ID   ABV56638 standard; cDNA; 469 BP.
DE   Human prostate expression marker cDNA 56629.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49;  DB 5;  Length 469;
  Best Local Similarity   58.6%;  Pred. No. 0.024;
RESULT 945
ID   ACN51887 standard; cDNA; 469 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-C10, SEQ:6668.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match              2.9%;  Score 49;  DB 13;  Length 469;
  Best Local Similarity   57.5%;  Pred. No. 0.024;
RESULT 946
ID   ACN58415 standard; cDNA; 469 BP.
DE   Cotton gynoecium tissue EST Clone ID: LIB3829-009-Q6-K6-H8, SEQ:13196.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match              2.9%;  Score 49;  DB 13;  Length 469;
  Best Local Similarity   57.5%;  Pred. No. 0.024;
RESULT 947
ID   ABV57020 standard; cDNA; 472 BP.
DE   Human prostate expression marker cDNA 57011.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49;  DB 5;  Length 472;
  Best Local Similarity   55.6%;  Pred. No. 0.024;
RESULT 948
ID   ABV54546 standard; cDNA; 541 BP.
DE   Human prostate expression marker cDNA 54537.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 49;  DB 5;  Length 541;
  Best Local Similarity   58.6%;  Pred. No. 0.026;
RESULT 949
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ID   ACN53890 standard; cDNA; 547 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-F10, SEQ:8671.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             2.9%;  Score 49;  DB 13;  Length 547;
  Best Local Similarity   56.2%;  Pred. No. 0.026;
RESULT 950
ID   ABQ52063 standard; DNA; 553 BP.
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 38654.
PN   WO200218632-A2.
PD   07-MAR-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 49;  DB 6;  Length 553;
  Best Local Similarity   62.3%;  Pred. No. 0.026;
RESULT 951
ID   ABQ52062 standard; DNA; 553 BP.
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 38653.
PN   WO200218632-A2.
PD   07-MAR-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 49;  DB 6;  Length 553;
  Best Local Similarity   62.3%;  Pred. No. 0.026;
RESULT 952
ID   ADR63596 standard; cDNA; 1041 BP.
DE   Cotton cDNA sequence, SEQ ID 4377.
PN   US2004181830-A1.
PD   16-SEP-2004.
PA   (KOVA/) KOVALIC D K.
PA   (ZHOU/) ZHOU Y.
PA   (CAOY/) CAO Y.
  Query Match             2.9%;  Score 49;  DB 13;  Length 1041;
  Best Local Similarity   58.6%;  Pred. No. 0.036;
RESULT 953
ID   ADQ24168 standard; DNA; 1698 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 6988.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             2.9%;  Score 49;  DB 12;  Length 1698;
  Best Local Similarity   61.2%;  Pred. No. 0.046;
RESULT 954
ID   ADM47920 standard; DNA; 1882 BP.
DE   Polynucleotide sequence #338 useful in producing transgenic plants.
PN   US2003233670-A1.
PD   18-DEC-2003.
PA   (EDGE/) EDGERTON M D.
PA   (CHOM/) CHOMET P S.
PA   (LACC/) LACCETTI L B.
  Query Match             2.9%;  Score 49;  DB 12;  Length 1882;
  Best Local Similarity   59.9%;  Pred. No. 0.048;
RESULT 955
ID   AAA23441 standard; cDNA; 1954 BP.
DE   cDNA encoding human secreted protein vc51_1, SEQ ID NO:37.
PN   WO200011015-A1.
PD   02-MAR-2000.
PA   (ALPH-) ALPHAGENE INC.
  Query Match             2.9%;  Score 49;  DB 3;  Length 1954;
  Best Local Similarity   59.9%;  Pred. No. 0.049;
RESULT 956
ID   ACN88781 standard; DNA; 2024 BP.
DE   Breast cancer related marker, seq id 9931.
PN   US2003099974-A1.
PD   29-MAY-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match             2.9%;  Score 49;  DB 11;  Length 2024;
  Best Local Similarity   58.6%;  Pred. No. 0.05;
RESULT 957
ID   AAZ43781 standard; cDNA; 2685 BP.
DE   Human fetal brain cDNA clone vb6_1.
PN   WO9955721-A1.
PD   04-NOV-1999.
PA   (ALPH-) ALPHAGENE INC.
  Query Match             2.9%;  Score 49;  DB 3;  Length 2685;
  Best Local Similarity   59.9%;  Pred. No. 0.058;
RESULT 958
ID   ADQ24699 standard; DNA; 2936 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7519.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             2.9%;  Score 49;  DB 12;  Length 2936;
  Best Local Similarity   57.5%;  Pred. No. 0.06;
RESULT 959
ID   ADQ24532 standard; DNA; 2936 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7352.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             2.9%;  Score 49;  DB 12;  Length 2936;
  Best Local Similarity   57.5%;  Pred. No. 0.06;
RESULT 960
ID   ABQ54675 standard; cDNA; 3044 BP.
DE   Human ovarian antigen HVCAE76 cDNA, SEQ ID NO:555.
PN   WO200200677-A1.
PD   03-JAN-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             2.9%;  Score 49;  DB 6;  Length 3044;
  Best Local Similarity   59.0%;  Pred. No. 0.062;
RESULT 961
ID   ABL33662 standard; DNA; 5845 BP.
DE   Human immune system associated gene SEQ ID NO: 1635.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 49;  DB 6;  Length 5845;
  Best Local Similarity   59.9%;  Pred. No. 0.086;
RESULT 962
ID   ADL45710 standard; DNA; 5930 BP.
DE   Human ovarian cancer DNA marker #19600.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 49;  DB 5;  Length 5930;
  Best Local Similarity   58.6%;  Pred. No. 0.086;
RESULT 963
ID   ABL34058 standard; DNA; 6012 BP.
DE   Human immune system associated gene SEQ ID NO: 2031.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 49;  DB 6;  Length 6012;
  Best Local Similarity   59.9%;  Pred. No. 0.087;
RESULT 964
ID   ABL32411 standard; DNA; 6161 BP.
DE   Human immune system associated gene SEQ ID NO: 384.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 49;  DB 6;  Length 6161;
  Best Local Similarity   64.6%;  Pred. No. 0.088;
RESULT 965
ID   ABL32806 standard; DNA; 6211 BP.
DE   Human immune system associated gene SEQ ID NO: 779.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 49;  DB 6;  Length 6211;
  Best Local Similarity   59.9%;  Pred. No. 0.088;
RESULT 966
ID   ABL33050 standard; DNA; 6522 BP.
DE   Human immune system associated gene SEQ ID NO: 1023.
PN   WO200200928-A2.
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PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match               2.9%;  Score 49;  DB 6;  Length 6522;
  Best Local Similarity   59.9%;  Pred. No. 0.09;
RESULT 967
ID   ABL32118 standard; DNA; 11416 BP.
DE   Human immune system associated gene SEQ ID NO: 91.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match               2.9%;  Score 49;  DB 6;  Length 11416;
  Best Local Similarity   59.9%;  Pred. No. 0.12;
RESULT 968
ID   ABL70135 standard; DNA; 11416 BP.
DE   Chemically treated cell signalling DNA sequence#13.
PN   WO200202807-A2.
PD   10-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match               2.9%;  Score 49;  DB 6;  Length 11416;
  Best Local Similarity   59.9%;  Pred. No. 0.12;
RESULT 969
ID   AAS61063 standard; DNA; 11416 BP.
DE   Human gene regulation-associated gene oligonucleotide #18.
PN   WO200177375-A2.
PD   18-OCT-2001.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match               2.9%;  Score 49;  DB 6;  Length 11416;
  Best Local Similarity   59.9%;  Pred. No. 0.12;
RESULT 970
ID   ABL34072 standard; DNA; 40862 BP.
DE   Human immune system associated gene SEQ ID NO: 2045.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match               2.9%;  Score 49;  DB 6;  Length 40862;
  Best Local Similarity   59.9%;  Pred. No. 0.23;
RESULT 971
ID   ADI72102 standard; DNA; 299 BP.
DE   Human ovarian cancer DNA marker #4844.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match               2.9%;  Score 48.8;  DB 5;  Length 299;
  Best Local Similarity   56.0%;  Pred. No. 0.021;
RESULT 972
ID   ADL37251 standard; DNA; 299 BP.
DE   Human ovarian cancer DNA marker #11141.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match               2.9%;  Score 48.8;  DB 5;  Length 299;
  Best Local Similarity   56.0%;  Pred. No. 0.021;
RESULT 973
ID   ABV49426 standard; cDNA; 308 BP.
DE   Human prostate expression marker cDNA 49417.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match               2.9%;  Score 48.8;  DB 5;  Length 308;
  Best Local Similarity   57.1%;  Pred. No. 0.022;
RESULT 974
ID   ABV55289 standard; cDNA; 313 BP.
DE   Human prostate expression marker cDNA 55280.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match               2.9%;  Score 48.8;  DB 5;  Length 313;
  Best Local Similarity   63.8%;  Pred. No. 0.022;
RESULT 975
ID   ABV04395 standard; cDNA; 326 BP.
DE   Human prostate expression marker cDNA 4386.
PN   WO200160860-A2.
PD   23-AUG-2001.
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PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match               2.9%;  Score 48.8;  DB 5;  Length 326;
  Best Local Similarity   61.2%;  Pred. No. 0.022;
RESULT 976
ID   AAI89034 standard; cDNA; 413 BP.
DE   Human polynucleotide SEQ ID NO 9094.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match               2.9%;  Score 48.8;  DB 4;  Length 413;
  Best Local Similarity   57.1%;  Pred. No. 0.025;
RESULT 977
ID   AAI91775 standard; cDNA; 421 BP.
DE   Human polynucleotide SEQ ID NO 11835.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match               2.9%;  Score 48.8;  DB 4;  Length 421;
  Best Local Similarity   60.6%;  Pred. No. 0.026;
RESULT 978
ID   ACN56150 standard; cDNA; 436 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-N6-D9, SEQ:10931.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match               2.9%;  Score 48.8;  DB 13;  Length 436;
  Best Local Similarity   53.7%;  Pred. No. 0.026;
RESULT 979
ID   ABV19606 standard; cDNA; 446 BP.
DE   Human prostate expression marker cDNA 19597.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match               2.9%;  Score 48.8;  DB 5;  Length 446;
  Best Local Similarity   59.2%;  Pred. No. 0.026;
RESULT 980
ID   AAI80552 standard; cDNA; 448 BP.
DE   Human polynucleotide SEQ ID NO 612.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match               2.9%;  Score 48.8;  DB 4;  Length 448;
  Best Local Similarity   59.3%;  Pred. No. 0.026;
RESULT 981
ID   ACN45690 standard; cDNA; 486 BP.
DE   Cotton primed seed EST Clone ID: LIB3825-007-Q1-K6-F5, SEQ:471.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match               2.9%;  Score 48.8;  DB 13;  Length 486;
  Best Local Similarity   62.1%;  Pred. No. 0.027;
RESULT 982
ID   ABV23693 standard; cDNA; 489 BP.
DE   Human prostate expression marker cDNA 23684.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match               2.9%;  Score 48.8;  DB 5;  Length 489;
  Best Local Similarity   59.3%;  Pred. No. 0.028;
RESULT 983
ID   ABV29562 standard; cDNA; 489 BP.
DE   Human prostate expression marker cDNA 29553.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match               2.9%;  Score 48.8;  DB 5;  Length 489;
  Best Local Similarity   59.3%;  Pred. No. 0.028;
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RESULT 984
ID   ABV58114 standard; cDNA; 510 BP.
DE   Human prostate expression marker cDNA 58105.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 48.8;  DB 5;  Length 510;
  Best Local Similarity   59.3%;  Pred. No. 0.028;
RESULT 985
ID   AAC74364 standard; cDNA; 639 BP.
DE   Human secreted protein gene 28 SEQ ID NO:38.
PN   WO200058340-A2.
PD   05-OCT-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              2.9%;  Score 48.8;  DB 3;  Length 639;
  Best Local Similarity   63.8%;  Pred. No. 0.032;
RESULT 986
ID   AAD05366 standard; cDNA; 655 BP.
DE   Human secreted protein-encoding gene 19 cDNA clone HWLFQ64, SEQ ID NO:77.
PN   WO200134626-A1.
PD   17-MAY-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              2.9%;  Score 48.8;  DB 4;  Length 655;
  Best Local Similarity   62.1%;  Pred. No. 0.032;
RESULT 987
ID   AAH34055 standard; cDNA; 673 BP.
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:1137.
PN   WO200122920-A2.
PD   05-APR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              2.9%;  Score 48.8;  DB 4;  Length 673;
  Best Local Similarity   59.3%;  Pred. No. 0.032;
RESULT 988
ID   ABZ76269 standard; cDNA; 836 BP.
DE   Human GENSET cDNA clone name NBART.
PN   WO2003014151-A2.
PD   20-FEB-2003.
PA   (GEST ) GENSET SA.
  Query Match              2.9%;  Score 48.8;  DB 8;  Length 836;
  Best Local Similarity   59.3%;  Pred. No. 0.036;
RESULT 989
ID   ADQ22074 standard; DNA; 980 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 4894.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              2.9%;  Score 48.8;  DB 12;  Length 980;
  Best Local Similarity   57.1%;  Pred. No. 0.039;
RESULT 990
ID   AAV70895 standard; cDNA; 1813 BP.
DE   cDNA encoding an allelic varaint of human Zcytor5.
PN   WO9849307-A1.
PD   05-NOV-1998.
PA   (ZYMO ) ZYMOGENETICS INC.
  Query Match              2.9%;  Score 48.8;  DB 2;  Length 1813;
  Best Local Similarity   56.1%;  Pred. No. 0.053;
RESULT 991
ID   ABL33879 standard; DNA; 5378 BP.
DE   Human immune system associated gene SEQ ID NO: 1852.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.8;  DB 6;  Length 5378;
  Best Local Similarity   57.1%;  Pred. No. 0.093;
RESULT 992
ID   ABQ67094 standard; DNA; 83391 BP.
DE   Human angiogenesis associated polynucleotide SEQ ID NO 124.
PN   WO200246454-A2.
PD   13-JUN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.8;  DB 6;  Length 83391;
  Best Local Similarity   58.1%;  Pred. No. 0.37;
RESULT 993
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ID   ADI72391 standard; DNA; 291 BP.
DE   Human ovarian cancer DNA marker #5133.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 48.6;  DB 5;  Length 291;
  Best Local Similarity   52.2%;  Pred. No. 0.024;
RESULT 994
ID   ADL37534 standard; DNA; 291 BP.
DE   Human ovarian cancer DNA marker #11424.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 48.6;  DB 5;  Length 291;
  Best Local Similarity   52.2%;  Pred. No. 0.024;
RESULT 995
ID   ABV49069 standard; cDNA; 320 BP.
DE   Human prostate expression marker cDNA 49060.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 48.6;  DB 5;  Length 320;
  Best Local Similarity   56.5%;  Pred. No. 0.025;
RESULT 996
ID   AAI86367 standard; cDNA; 379 BP.
DE   Human polynucleotide SEQ ID NO 6427.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              2.9%;  Score 48.6;  DB 4;  Length 379;
  Best Local Similarity   54.9%;  Pred. No. 0.027;
RESULT 997
ID   ACH19935 standard; cDNA; 423 BP.
DE   Human adult lung cDNA #938.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match              2.9%;  Score 48.6;  DB 9;  Length 423;
  Best Local Similarity   52.5%;  Pred. No. 0.029;
RESULT 998
ID   ABV38062 standard; cDNA; 425 BP.
DE   Human prostate expression marker cDNA 38053.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 48.6;  DB 5;  Length 425;
  Best Local Similarity   57.6%;  Pred. No. 0.029;
RESULT 999
ID   ABV47755 standard; cDNA; 471 BP.
DE   Human prostate expression marker cDNA 47746.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 48.6;  DB 5;  Length 471;
  Best Local Similarity   58.7%;  Pred. No. 0.031;
RESULT 1000
ID   ACN54837 standard; cDNA; 489 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-K6-D11, SEQ:9618.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match              2.9%;  Score 48.6;  DB 13;  Length 489;
  Best Local Similarity   57.6%;  Pred. No. 0.031;
RESULT 1001
ID   ABV17965 standard; cDNA; 816 BP.
DE   Human prostate expression marker cDNA 17956.
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PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 48.6;  DB 5;  Length 816;
  Best Local Similarity   58.7%;  Pred. No. 0.04;
RESULT 1002
ID   ABA93702 standard; cDNA; 835 BP.
DE   Human signal transduction cDNA clone amy2_10h17.
PN   WO200198454-A2.
PD   27-DEC-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
  Query Match              2.9%;  Score 48.6;  DB 6;  Length 835;
  Best Local Similarity   61.4%;  Pred. No. 0.041;
RESULT 1003
ID   AAC98083 standard; cDNA; 1377 BP.
DE   Human colon cancer antigen nucleotide sequence SEQ ID NO:93.
PN   WO200055351-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              2.9%;  Score 48.6;  DB 3;  Length 1377;
  Best Local Similarity   58.3%;  Pred. No. 0.053;
RESULT 1004
ID   ABX92004 standard; cDNA; 1808 BP.
DE   Lung specific nucleic acid (LSNA) #46.
PN   WO200268633-A2.
PD   06-SEP-2002.
PA   (DIAD-) DIADEXUS INC.
  Query Match              2.9%;  Score 48.6;  DB 6;  Length 1808;
  Best Local Similarity   58.7%;  Pred. No. 0.06;
RESULT 1005
ID   ABS57347 standard; cDNA; 1851 BP.
DE   cDNA encoding human cancer cell growth suppressing protein PP6068.
PN   CN1351080-A.
PD   29-MAY-2002.
PA   (SHAN-) SHANGHAI INST ONCOLOGY.
  Query Match              2.9%;  Score 48.6;  DB 6;  Length 1851;
  Best Local Similarity   58.7%;  Pred. No. 0.061;
RESULT 1006
ID   AAD06011 standard; DNA; 2034 BP.
DE   Human neuronal apoptosis regulated candidate (NARC) 10C DNA.
PN   WO200131007-A2.
PD   03-MAY-2001.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match              2.9%;  Score 48.6;  DB 4;  Length 2034;
  Best Local Similarity   56.6%;  Pred. No. 0.064;
RESULT 1007
ID   ABS56722 standard; cDNA; 2034 BP.
DE   Human NARC10 cDNA.
PN   WO200281516-A2.
PD   17-OCT-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match              2.9%;  Score 48.6;  DB 8;  Length 2034;
  Best Local Similarity   56.6%;  Pred. No. 0.064;
RESULT 1008
ID   ADJ57918 standard; cDNA; 2034 BP.
DE   Human NARC 10C cDNA.
PN   US2004009553-A1.
PD   15-JAN-2004.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match              2.9%;  Score 48.6;  DB 12;  Length 2034;
  Best Local Similarity   56.6%;  Pred. No. 0.064;
RESULT 1009
ID   ADQ23617 standard; DNA; 2050 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 6437.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              2.9%;  Score 48.6;  DB 12;  Length 2050;
  Best Local Similarity   60.0%;  Pred. No. 0.064;
RESULT 1010
ID   ABL32778 standard; DNA; 5532 BP.
DE   Human immune system associated gene SEQ ID NO: 751.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.6;  DB 6;  Length 5532;
  Best Local Similarity   63.0%;  Pred. No. 0.11;
RESULT 1011
ID   ABL32911 standard; DNA; 8946 BP.
DE   Human immune system associated gene SEQ ID NO: 884.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.6;  DB 6;  Length 8946;
  Best Local Similarity   57.6%;  Pred. No. 0.14;
RESULT 1012
ID   AAS46704 standard; DNA; 14615 BP.
DE   Tumour suppressor gene derived chemically modified sequence #427.
PN   WO200168912-A2.
PD   20-SEP-2001.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.6;  DB 4;  Length 14615;
  Best Local Similarity   57.6%;  Pred. No. 0.17;
RESULT 1013
ID   ABX47137 standard; cDNA; 341 BP.
DE   Bovine EST associated with lactation/muscle/fat deposition #12302.
PN   US2002137139-A1.
PD   26-SEP-2002.
PA   (BYAT/) BYATT J C.
PA   (MATH/) MATHIALAGAN N.
PA   (TAON/) TAO N.
PA   (WARR/) WARREN W C.
  Query Match              2.9%;  Score 48.4;  DB 8;  Length 341;
  Best Local Similarity   62.3%;  Pred. No. 0.029;
RESULT 1014
ID   AAI87525 standard; cDNA; 367 BP.
DE   Human polynucleotide SEQ ID NO 7585.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              2.9%;  Score 48.4;  DB 4;  Length 367;
  Best Local Similarity   64.0%;  Pred. No. 0.03;
RESULT 1015
ID   AAI84785 standard; cDNA; 388 BP.
DE   Human polynucleotide SEQ ID NO 4845.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              2.9%;  Score 48.4;  DB 4;  Length 388;
  Best Local Similarity   60.8%;  Pred. No. 0.031;
RESULT 1016
ID   ADL43635 standard; DNA; 388 BP.
DE   Human ovarian cancer DNA marker #17525.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 48.4;  DB 5;  Length 388;
  Best Local Similarity   57.1%;  Pred. No. 0.031;
RESULT 1017
ID   AAI89093 standard; cDNA; 415 BP.
DE   Human polynucleotide SEQ ID NO 9153.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              2.9%;  Score 48.4;  DB 4;  Length 415;
  Best Local Similarity   65.4%;  Pred. No. 0.032;
RESULT 1018
ID   ABV56837 standard; cDNA; 432 BP.
DE   Human prostate expression marker cDNA 56828.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 48.4;  DB 5;  Length 432;
  Best Local Similarity   64.0%;  Pred. No. 0.033;
RESULT 1019
ID   ABX47746 standard; cDNA; 442 BP.
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DE   Bovine EST associated with lactation/muscle/fat deposition #12911.
PN   US2002137139-A1.
PD   26-SEP-2002.
PA   (BYAT/) BYATT J C.
PA   (MATH/) MATHIALAGAN N.
PA   (TAON/) TAO N.
PA   (WARR/) WARREN W C.
  Query Match              2.9%;  Score 48.4;  DB 8;  Length 442;
  Best Local Similarity   66.0%;  Pred. No. 0.033;
RESULT 1020
ID   ABV56778 standard; cDNA; 451 BP.
DE   Human prostate expression marker cDNA 56769.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match              2.9%;  Score 48.4;  DB 5;  Length 451;
  Best Local Similarity   60.8%;  Pred. No. 0.034;
RESULT 1021
ID   ACN45855 standard; cDNA; 608 BP.
DE   Cotton primed seed EST Clone ID: LIB3825-009-Q1-K6-G7, SEQ:636.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match              2.9%;  Score 48.4;  DB 13;  Length 608;
  Best Local Similarity   57.1%;  Pred. No. 0.039;
RESULT 1022
ID   ACN53565 standard; cDNA; 619 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-C10, SEQ:8346.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match              2.9%;  Score 48.4;  DB 13;  Length 619;
  Best Local Similarity   57.1%;  Pred. No. 0.04;
RESULT 1023
ID   AAA59475 standard; DNA; 1117 BP.
DE   Nucleotide sequence of a soybean type III glutathione-S-transferase.
PN   WO200047728-A2.
PD   17-AUG-2000.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
  Query Match              2.9%;  Score 48.4;  DB 3;  Length 1117;
  Best Local Similarity   58.6%;  Pred. No. 0.053;
RESULT 1024
ID   ADQ22714 standard; DNA; 1661 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5534.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 1661;
  Best Local Similarity   68.4%;  Pred. No. 0.065;
RESULT 1025
ID   ADH72103 standard; DNA; 2136 BP.
DE   Human gene of the invention NOV43b SEQ ID NO:999.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 2136;
  Best Local Similarity   49.4%;  Pred. No. 0.074;
RESULT 1026
ID   ACA10119 standard; cDNA; 2153 BP.
DE   Human NOVX polynucleotide #9.
PN   WO200290504-A2.
PD   14-NOV-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match              2.9%;  Score 48.4;  DB 8;  Length 2153;
  Best Local Similarity   49.4%;  Pred. No. 0.074;
RESULT 1027
ID   ADH72101 standard; DNA; 2153 BP.
DE   Human gene of the invention NOV43a SEQ ID NO:997.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 2153;
  Best Local Similarity   49.4%;  Pred. No. 0.074;
RESULT 1028
ID   ADO08270 standard; cDNA; 2153 BP.
DE   Human NOVX polynucleotide #9.
PN   US2004018594-A1.
PD   29-JAN-2004.
PA   (ALSO/) ALSOBROOK J P.
PA   (ANDE/) ANDERSON D W.
PA   (BOLD/) BOLDOG F L.
PA   (BURG/) BURGESS C E.
PA   (CASM/) CASMAN S J.
PA   (CHAP/) CHAPOVAL A.
PA   (EDIN/) EDINGER S R.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (GUNT/) GUNTHER E.
PA   (GUOX/) GUO X S.
PA   (KEKU/) KEKUDA R.
PA   (LEPL/) LEPLEY D M.
PA   (LILL/) LI L.
PA   (LIUX/) LIU X.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLER C E.
PA   (MILL/) MILLET I.
PA   (PADI/) PADIGARU M.
PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
PA   (RIEG/) RIEGER D K.
PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (SPYT/) SPYTEK K A.
PA   (TAUP/) TAUPIER R J.
PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
PA   (ZERH/) ZERHUSEN B D.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 2153;
  Best Local Similarity   49.4%;  Pred. No. 0.074;
RESULT 1029
ID   ADQ25384 standard; DNA; 2176 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 8204.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 2176;
  Best Local Similarity   58.2%;  Pred. No. 0.075;
RESULT 1030
ID   ADQ22511 standard; DNA; 2179 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5331.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 2179;
  Best Local Similarity   60.8%;  Pred. No. 0.075;
RESULT 1031
ID   ADQ22185 standard; DNA; 2857 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5005.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 2857;
  Best Local Similarity   57.8%;  Pred. No. 0.086;
RESULT 1032
ID   AAS68120 standard; cDNA; 3910 BP.
DE   DNA encoding novel human diagnostic protein #3924.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              2.9%;  Score 48.4;  DB 5;  Length 3910;
  Best Local Similarity   49.4%;  Pred. No. 0.1;
RESULT 1033
ID   ADQ23023 standard; DNA; 4046 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5843.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 4046;
  Best Local Similarity   58.2%;  Pred. No. 0.1;
RESULT 1034
ID   AAI72024 standard; cDNA; 4073 BP.
DE   Human thrombospondin protein, BTL.012, coding sequence.
PN   WO200174852-A2.
PD   11-OCT-2001.
PA   (FARB ) BAYER CORP.
  Query Match              2.9%;  Score 48.4;  DB 6;  Length 4073;
  Best Local Similarity   49.4%;  Pred. No. 0.1;
RESULT 1035
ID   ADB54096 standard; DNA; 4316 BP.
DE   Pretreated genomic DNA region 20.
PN   WO2003072821-A2.
PD   04-SEP-2003.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 10;  Length 4316;
  Best Local Similarity   62.3%;  Pred. No. 0.11;
RESULT 1036
ID   ADB54224 standard; DNA; 4316 BP.
DE   Pretreated genomic DNA region 148.
PN   WO2003072821-A2.
PD   04-SEP-2003.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 10;  Length 4316;
  Best Local Similarity   62.3%;  Pred. No. 0.11;
RESULT 1037
ID   ADS89522 standard; DNA; 4316 BP.
DE   Oligonucleotide of the invention SEQ ID NO:538.
PN   WO2004035803-A2.
PD   29-APR-2004.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 13;  Length 4316;
  Best Local Similarity   62.3%;  Pred. No. 0.11;
RESULT 1038
ID   ADS89248 standard; DNA; 4316 BP.
DE   Oligonucleotide of the invention SEQ ID NO:264.
PN   WO2004035803-A2.
PD   29-APR-2004.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 13;  Length 4316;
  Best Local Similarity   62.3%;  Pred. No. 0.11;
RESULT 1039
ID   ABL32921 standard; DNA; 5195 BP.
DE   Human immune system associated gene SEQ ID NO: 894.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 6;  Length 5195;
  Best Local Similarity   62.3%;  Pred. No. 0.12;
RESULT 1040
ID   ADL93996 standard; cDNA; 5877 BP.
DE   Human G-coupled protein receptor-related gene #44.
PN   US2004006205-A1.
PD   08-JAN-2004.
PA   (LILL/) LI L.
PA   (GERL/) GERLACH V.
PA   (LIUX/) LIU X.
PA   (MILL/) MILLER C E.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PENA/) PENA C E A.
PA   (SHEN/) SHENOY S G.
PA   (ZHON/) ZHONG H.
PA   (SMIT/) SMITHSON G.
PA   (CASM/) CASMAN S J.
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PA   (BOLD/) BOLDOG F L.
PA   (VOSS/) VOSS E Z.
PA   (VERN/) VERNET C A.
PA   (MACD/) MACDOUGALL J R.
PA   (RAST/) RASTELLI L.
PA   (ANDE/) ANDERSON D W.
PA   (ZHON/) ZHONG M.
PA   (MEZE/) MEZES P S.
PA   (FURT/) FURTAK K.
PA   (PATT/) PATTURAJAN M.
PA   (BURG/) BURGESS C E.
PA   (MALY/) MALYANKAR U M.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (EDIN/) EDINGER S.
PA   (MAZU/) MAZUR A.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 5877;
  Best Local Similarity   49.4%;  Pred. No. 0.12;
RESULT 1041
ID   ADE16057 standard; DNA; 5935 BP.
DE   G-coupled protein receptor related polypeptide DNA, SEQ ID No 87.
PN   WO200283841-A2.
PD   24-OCT-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match              2.9%;  Score 48.4;  DB 10;  Length 5935;
  Best Local Similarity   49.4%;  Pred. No. 0.12;
RESULT 1042
ID   ABL33679 standard; DNA; 6070 BP.
DE   Human immune system associated gene SEQ ID NO: 1652.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 6;  Length 6070;
  Best Local Similarity   54.5%;  Pred. No. 0.13;
RESULT 1043
ID   ABL34579 standard; DNA; 6070 BP.
DE   Human metastasis associated gene SEQ ID NO: 132.
PN   WO200177376-A2.
PD   18-OCT-2001.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 6;  Length 6070;
  Best Local Similarity   54.5%;  Pred. No. 0.13;
RESULT 1044
ID   ABL70372 standard; DNA; 6070 BP.
DE   Chemically treated cell signalling DNA sequence complementary to#131.
PN   WO200202807-A2.
PD   10-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 6;  Length 6070;
  Best Local Similarity   54.5%;  Pred. No. 0.13;
RESULT 1045
ID   ABQ67130 standard; DNA; 6070 BP.
DE   Human angiogenesis associated polynucleotide SEQ ID NO 160.
PN   WO200246454-A2.
PD   13-JUN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 6;  Length 6070;
  Best Local Similarity   54.5%;  Pred. No. 0.13;
RESULT 1046
ID   ADS99840 standard; DNA; 6070 BP.
DE   Complement of bisulphite treated metastasis-associated human gene #66.
PN   US2003148327-A1.
PD   07-AUG-2003.
PA   (OLEK/) OLEK A.
PA   (PIEP/) PIEPENBROCK C.
PA   (BERL/) BERLIN K.
  Query Match              2.9%;  Score 48.4;  DB 7;  Length 6070;
  Best Local Similarity   54.5%;  Pred. No. 0.13;
RESULT 1047
ID   ABX56304 standard; DNA; 6343 BP.
DE   Human NOV25c CG56914-03 DNA SEQ ID 87.
PN   WO200281625-A2.
PD   17-OCT-2002.
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PA   (CURA-) CURAGEN CORP.
  Query Match              2.9%;  Score 48.4;  DB 8;  Length 6343;
  Best Local Similarity   49.4%;  Pred. No. 0.13;
RESULT 1048
ID   ADH72107 standard; DNA; 6343 BP.
DE   Human gene of the invention NOV43d SEQ ID NO:1003.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 6343;
  Best Local Similarity   49.4%;  Pred. No. 0.13;
RESULT 1049
ID   ABL33356 standard; DNA; 6577 BP.
DE   Human immune system associated gene SEQ ID NO: 1329.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 6;  Length 6577;
  Best Local Similarity   58.2%;  Pred. No. 0.13;
RESULT 1050
ID   ABL70561 standard; DNA; 6577 BP.
DE   Chemically treated cell signalling DNA sequence#226.
PN   WO200202807-A2.
PD   10-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 6;  Length 6577;
  Best Local Similarity   58.2%;  Pred. No. 0.13;
RESULT 1051
ID   AAS61221 standard; DNA; 6577 BP.
DE   Human gene regulation-associated gene oligonucleotide #176.
PN   WO200177375-A2.
PD   18-OCT-2001.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 6;  Length 6577;
  Best Local Similarity   58.2%;  Pred. No. 0.13;
RESULT 1052
ID   ABK34027 standard; DNA; 6944 BP.
DE   Human DNA for staging of Astrocytomas, complement, #57.
PN   WO200202808-A2.
PD   10-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 6;  Length 6944;
  Best Local Similarity   62.3%;  Pred. No. 0.13;
RESULT 1053
ID   ADA20447 standard; DNA; 6944 BP.
DE   Prostate tumour related genomic DNA complement sample #56.
PN   WO2002103042-A2.
PD   27-DEC-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 8;  Length 6944;
  Best Local Similarity   62.3%;  Pred. No. 0.13;
RESULT 1054
ID   ADA84254 standard; DNA; 6944 BP.
DE   Human renal/prostate carcinoma associated DNA SEQ ID NO:112.
PN   WO2002103041-A2.
PD   27-DEC-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 8;  Length 6944;
  Best Local Similarity   62.3%;  Pred. No. 0.13;
RESULT 1055
ID   ADQ22776 standard; DNA; 7281 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5596.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 7281;
  Best Local Similarity   57.1%;  Pred. No. 0.14;
RESULT 1056
ID   ADS89706 standard; DNA; 7467 BP.
DE   Oligonucleotide of the invention SEQ ID NO:722.
PN   WO2004035803-A2.
PD   29-APR-2004.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 13;  Length 7467;
  Best Local Similarity   60.8%;  Pred. No. 0.14;
RESULT 1057
ID   ADK60477 standard; DNA; 8546 BP.
DE   Angiogenesis differentially expressed gene GS-N52.
PN   FR2836687-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 8546;
  Best Local Similarity   49.4%;  Pred. No. 0.15;
RESULT 1058
ID   ADK60778 standard; DNA; 8546 BP.
DE   Angiogenesis differentially expressed gene GS-N52.
PN   FR2836686-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 8546;
  Best Local Similarity   49.4%;  Pred. No. 0.15;
RESULT 1059
ID   ADP73100 standard; DNA; 8546 BP.
DE   Angiogenesis inhibitor human DNA sequence, GS-N52.
PN   FR2843753-A1.
PD   27-FEB-2004.
PA   (GENE/) GENE S.
PA   (ALMS/) AL M S.
  Query Match              2.9%;  Score 48.4;  DB 12;  Length 8546;
  Best Local Similarity   49.4%;  Pred. No. 0.15;
RESULT 1060
ID   ADS09799 standard; DNA; 8546 BP.
DE   Human therapeutic DNA - SEQ ID 36.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
  Query Match              2.9%;  Score 48.4;  DB 13;  Length 8546;
  Best Local Similarity   49.4%;  Pred. No. 0.15;
RESULT 1061
ID   ABL33068 standard; DNA; 9117 BP.
DE   Human immune system associated gene SEQ ID NO: 1041.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 6;  Length 9117;
  Best Local Similarity   62.3%;  Pred. No. 0.15;
RESULT 1062
ID   ADF50896 standard; DNA; 11097 BP.
DE   Chemically modified promoter region of human melastatin gene (SeqID 4).
PN   EP1344832-A1.
PD   17-SEP-2003.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 10;  Length 11097;
  Best Local Similarity   62.3%;  Pred. No. 0.17;
RESULT 1063
ID   ADF50894 standard; DNA; 11097 BP.
DE   Chemically modified promoter region of human melastatin gene (SeqID 2).
PN   EP1344832-A1.
PD   17-SEP-2003.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match              2.9%;  Score 48.4;  DB 10;  Length 11097;
  Best Local Similarity   62.3%;  Pred. No. 0.17;
RESULT 1064
ID   ADO08272 standard; cDNA; 15659 BP.
DE   Human NOVX polynucleotide #10.
PN   US2004018594-A1.
PD   29-JAN-2004.
PA   (ALSO/) ALSOBROOK J P.
PA   (ANDE/) ANDERSON D W.
PA   (BOLD/) BOLDOG F L.
PA   (BURG/) BURGESS C E.
PA   (CASM/) CASMAN S J.
PA   (CHAP/) CHAPOVAL A.
PA   (EDIN/) EDINGER S R.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (GUNT/) GUNTHER E.
PA   (GUOX/) GUO X S.
PA   (KEKU/) KEKUDA R.
PA   (LEPL/) LEPLEY D M.
PA   (LILL/) LI L.
PA   (LIUX/) LIU X.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLER C E.
PA   (MILL/) MILLET I.
PA   (PADI/) PADIGARU M.
PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
PA   (RIEG/) RIEGER D K.
PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (SPYT/) SPYTEK K A.
PA   (TAUP/) TAUPIER R J.
PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
PA   (ZERH/) ZERHUSEN B D.
  Query Match             2.9%;  Score 48.4;  DB 12;  Length 15659;
  Best Local Similarity   49.4%;  Pred. No. 0.2;
RESULT 1065
ID   ACA10120 standard; cDNA; 15660 BP.
DE   Human NOVX polynucleotide #10.
PN   WO200290504-A2.
PD   14-NOV-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             2.9%;  Score 48.4;  DB 8;  Length 15660;
  Best Local Similarity   49.4%;  Pred. No. 0.2;
RESULT 1066
ID   ADH72105 standard; DNA; 15660 BP.
DE   Human gene of the invention NOV43c SEQ ID NO:1001.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             2.9%;  Score 48.4;  DB 12;  Length 15660;
  Best Local Similarity   49.4%;  Pred. No. 0.2;
RESULT 1067
ID   ABQ86156 standard; DNA; 16908 BP.
DE   Novel human gene. SEQ ID 27.
PN   WO200250105-A1.
PD   27-JUN-2002.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
  Query Match             2.9%;  Score 48.4;  DB 6;  Length 16908;
  Best Local Similarity   49.4%;  Pred. No. 0.21;
RESULT 1068
ID   ADK60455 standard; DNA; 18207 BP.
DE   Angiogenesis differentially expressed gene GS-N29.
PN   FR2836687-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
  Query Match             2.9%;  Score 48.4;  DB 12;  Length 18207;
  Best Local Similarity   49.4%;  Pred. No. 0.22;
RESULT 1069
ID   ADK60756 standard; DNA; 18207 BP.
DE   Angiogenesis differentially expressed gene GS-N29.
PN   FR2836686-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
  Query Match             2.9%;  Score 48.4;  DB 12;  Length 18207;
  Best Local Similarity   49.4%;  Pred. No. 0.22;
RESULT 1070
ID   ADP73078 standard; DNA; 18207 BP.
DE   Angiogenesis inhibitor human DNA sequence, GS-N29.
PN   FR2843753-A1.
PD   27-FEB-2004.
PA   (GENE/) GENE S.
PA   (ALMS/) AL M S.
  Query Match             2.9%;  Score 48.4;  DB 12;  Length 18207;
  Best Local Similarity   49.4%;  Pred. No. 0.22;
RESULT 1071
ID   ADQ22570 standard; DNA; 18248 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5390.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             2.9%;  Score 48.4;  DB 12;  Length 18248;
  Best Local Similarity   49.4%;  Pred. No. 0.22;
RESULT 1072
ID   ABL37453 standard; cDNA; 153 BP.
DE   Human colon tumour antigen polynucleotide SEQ ID NO:1042.
PN   WO200196388-A2.
PD   20-DEC-2001.
PA   (CORI-) CORIXA CORP.
  Query Match             2.9%;  Score 48.2;  DB 6;  Length 153;
  Best Local Similarity   59.3%;  Pred. No. 0.022;
RESULT 1073
ID   AAH70080 standard; cDNA; 268 BP.
DE   Human cervical cancer marker nucleic acid 1354.
PN   WO200142467-A2.
PD   14-JUN-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48.2;  DB 4;  Length 268;
  Best Local Similarity   51.9%;  Pred. No. 0.029;
RESULT 1074
ID   ACN45531 standard; cDNA; 272 BP.
DE   Cotton primed seed EST Clone ID: LIB3825-003-Q1-K6-E5, SEQ:312.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             2.9%;  Score 48.2;  DB 13;  Length 272;
  Best Local Similarity   63.2%;  Pred. No. 0.03;
RESULT 1075
ID   ABV58763 standard; cDNA; 317 BP.
DE   Human prostate expression marker cDNA 58754.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48.2;  DB 5;  Length 317;
  Best Local Similarity   57.7%;  Pred. No. 0.032;
RESULT 1076
ID   ACN50558 standard; cDNA; 325 BP.
DE   Cotton mature seed EST Clone ID: LIB3827-002-Q1-K6-E8, SEQ:5339.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             2.9%;  Score 48.2;  DB 13;  Length 325;
  Best Local Similarity   62.2%;  Pred. No. 0.032;
RESULT 1077
ID   AAL23694 standard; cDNA; 359 BP.
DE   Human breast cancer expressed polynucleotide 16151.
PN   WO200151628-A2.
PD   19-JUL-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48.2;  DB 4;  Length 359;
  Best Local Similarity   61.6%;  Pred. No. 0.034;
RESULT 1078
ID   ADL37765 standard; DNA; 385 BP.
DE   Human ovarian cancer DNA marker #11655.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48.2;  DB 5;  Length 385;
  Best Local Similarity   53.5%;  Pred. No. 0.035;
RESULT 1079
ID   ADI72626 standard; DNA; 385 BP.
DE   Human ovarian cancer DNA marker #5368.
PN   WO200170979-A2.
PD   27-SEP-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48.2;  DB 5;  Length 385;
  Best Local Similarity   53.5%;  Pred. No. 0.035;
RESULT 1080
ID   AAI84791 standard; cDNA; 390 BP.
DE   Human polynucleotide SEQ ID NO 4851.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 48.2;  DB 4;  Length 390;
  Best Local Similarity   57.7%;  Pred. No. 0.035;
RESULT 1081
ID   AAI83999 standard; cDNA; 411 BP.
DE   Human polynucleotide SEQ ID NO 4059.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 48.2;  DB 4;  Length 411;
  Best Local Similarity   60.2%;  Pred. No. 0.036;
RESULT 1082
ID   AAI88617 standard; cDNA; 416 BP.
DE   Human polynucleotide SEQ ID NO 8677.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 48.2;  DB 4;  Length 416;
  Best Local Similarity   58.9%;  Pred. No. 0.037;
RESULT 1083
ID   AAI89032 standard; cDNA; 416 BP.
DE   Human polynucleotide SEQ ID NO 9092.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 48.2;  DB 4;  Length 416;
  Best Local Similarity   61.6%;  Pred. No. 0.037;
RESULT 1084
ID   ABV49374 standard; cDNA; 453 BP.
DE   Human prostate expression marker cDNA 49365.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48.2;  DB 5;  Length 453;
  Best Local Similarity   63.2%;  Pred. No. 0.038;
RESULT 1085
ID   ACN57722 standard; cDNA; 492 BP.
DE   Cotton gynoecium tissue EST Clone ID: LIB3829-005-Q6-N6-B12, SEQ:12503.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             2.9%;  Score 48.2;  DB 13;  Length 492;
  Best Local Similarity   60.2%;  Pred. No. 0.04;
RESULT 1086
ID   ABV57520 standard; cDNA; 504 BP.
DE   Human prostate expression marker cDNA 57511.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48.2;  DB 5;  Length 504;
  Best Local Similarity   58.9%;  Pred. No. 0.04;
RESULT 1087
ID   ACN55029 standard; cDNA; 518 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-K6-D8, SEQ:9810.
PN   US2004123340-A1.
PD   24-JUN-2004.
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PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             2.9%;  Score 48.2;  DB 13;  Length 518;
  Best Local Similarity   55.3%;  Pred. No. 0.041;
RESULT 1088
ID   ACN60563 standard; cDNA; 585 BP.
DE   Cotton gynoecium tissue EST Clone ID: LIB3829-025-Q6-K6-B11, SEQ:15344.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             2.9%;  Score 48.2;  DB 13;  Length 585;
  Best Local Similarity   56.7%;  Pred. No. 0.043;
RESULT 1089
ID   ACN62771 standard; cDNA; 594 BP.
DE   Cotton carpel wall/septum EST Clone ID: LIB3831-001-Q1-K6-C5, SEQ:17552.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             2.9%;  Score 48.2;  DB 13;  Length 594;
  Best Local Similarity   61.6%;  Pred. No. 0.044;
RESULT 1090
ID   AAD34114 standard; cDNA; 921 BP.
DE   Human secreted protein-encoding gene 9 cDNA clone HE8NQ42, SEQ ID NO:19.
PN   WO200222654-A1.
PD   21-MAR-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             2.9%;  Score 48.2;  DB 6;  Length 921;
  Best Local Similarity   63.2%;  Pred. No. 0.055;
RESULT 1091
ID   AAD54409 standard; cDNA; 990 BP.
DE   Lolium perenne defensin a (LpDEFa) cDNA.
PN   WO200288359-A1.
PD   07-NOV-2002.
PA   (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA   (AGRE-) AGRESEARCH LTD.
  Query Match             2.9%;  Score 48.2;  DB 8;  Length 990;
  Best Local Similarity   54.1%;  Pred. No. 0.057;
RESULT 1092
ID   AAL57070 standard; DNA; 1040 BP.
DE   Human G-protein coupled receptor GAVE18 DNA sequence.
PN   WO2003042399-A2.
PD   22-MAY-2003.
PA   (AVET ) AVENTIS PHARM INC.
  Query Match             2.9%;  Score 48.2;  DB 9;  Length 1040;
  Best Local Similarity   63.2%;  Pred. No. 0.058;
RESULT 1093
ID   ADG73631 standard; cDNA; 1259 BP.
DE   Human cDNA of the invention SEQ ID NO:16.
PN   CN1369506-A.
PD   18-SEP-2002.
PA   (SHAN-) SHANGHAI INST ONCOLOGY.
  Query Match             2.9%;  Score 48.2;  DB 10;  Length 1259;
  Best Local Similarity   65.1%;  Pred. No. 0.064;
RESULT 1094
ID   ADF94940 standard; cDNA; 1311 BP.
DE   Human gene 8-derived ACRP30-like cDNA, SEQ ID NO:36.
PN   WO2003031586-A2.
PD   17-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (BLON/) BLONDEL O.
PA   (RUBE/) RUBEN S M.
  Query Match             2.9%;  Score 48.2;  DB 10;  Length 1311;
  Best Local Similarity   62.2%;  Pred. No. 0.065;
RESULT 1095
ID   ABS53034 standard; DNA; 2038 BP.
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DE   Arabidopsis thaliana squalene epoxidase polynucleotide #4.
PN   WO200261072-A2.
PD   08-AUG-2002.
PA   (MONS ) MONSANTO TECHNOLOGY LLC.
  Query Match             2.9%;  Score 48.2;  DB 6;  Length 2038;
  Best Local Similarity   58.9%;  Pred. No. 0.082;
RESULT 1096
ID   ADQ23275 standard; DNA; 3056 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 6095.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             2.9%;  Score 48.2;  DB 12;  Length 3056;
  Best Local Similarity   63.2%;  Pred. No. 0.1;
RESULT 1097
ID   ABL33751 standard; DNA; 7037 BP.
DE   Human immune system associated gene SEQ ID NO: 1724.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 48.2;  DB 6;  Length 7037;
  Best Local Similarity   60.2%;  Pred. No. 0.15;
RESULT 1098
ID   ABL32448 standard; DNA; 7238 BP.
DE   Human immune system associated gene SEQ ID NO: 421.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 48.2;  DB 6;  Length 7238;
  Best Local Similarity   60.2%;  Pred. No. 0.16;
RESULT 1099
ID   ABL32332 standard; DNA; 8895 BP.
DE   Human immune system associated gene SEQ ID NO: 305.
PN   WO200200928-A2.
PD   03-JAN-2002.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 48.2;  DB 6;  Length 8895;
  Best Local Similarity   58.9%;  Pred. No. 0.17;
RESULT 1100
ID   ABL34492 standard; DNA; 11996 BP.
DE   Human metastasis associated gene SEQ ID NO: 45.
PN   WO200177376-A2.
PD   18-OCT-2001.
PA   (EPIG-) EPIGENOMICS AG.
  Query Match             2.9%;  Score 48.2;  DB 6;  Length 11996;
  Best Local Similarity   65.1%;  Pred. No. 0.2;
RESULT 1101
ID   ADS99753 standard; DNA; 11996 BP.
DE   Bisulphite treated human gene associated with metastasis #23.
PN   US2003148327-A1.
PD   07-AUG-2003.
PA   (OLEK/) OLEK A.
PA   (PIEP/) PIEPENBROCK C.
PA   (BERL/) BERLIN K.
  Query Match             2.9%;  Score 48.2;  DB 7;  Length 11996;
  Best Local Similarity   65.1%;  Pred. No. 0.2;
RESULT 1102
ID   ACN50958 standard; cDNA; 139 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-002-Q1-N6-E3, SEQ:5739.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             2.9%;  Score 48;  DB 13;  Length 139;
  Best Local Similarity   64.3%;  Pred. No. 0.024;
RESULT 1103
ID   ABX46273 standard; cDNA; 239 BP.
DE   Bovine EST associated with lactation/muscle/fat deposition #11438.
PN   US2002137139-A1.
PD   26-SEP-2002.
PA   (BYAT/) BYATT J C.
PA   (MATH/) MATHIALAGAN N.
PA   (TAON/) TAO N.
PA   (WARR/) WARREN W C.
  Query Match             2.9%;  Score 48;  DB 8;  Length 239;
  Best Local Similarity   59.6%;  Pred. No. 0.031;
RESULT 1104
ID   ABX42739 standard; cDNA; 241 BP.
DE   Bovine EST associated with lactation/muscle/fat deposition #7904.
PN   US2002137139-A1.
PD   26-SEP-2002.
PA   (BYAT/) BYATT J C.
PA   (MATH/) MATHIALAGAN N.
PA   (TAON/) TAO N.
PA   (WARR/) WARREN W C.
  Query Match             2.9%;  Score 48;  DB 8;  Length 241;
  Best Local Similarity   59.6%;  Pred. No. 0.031;
RESULT 1105
ID   ADS72366 standard; cDNA; 269 BP.
DE   Human kidney tumour specific cDNA, SEQ ID 963.
PN   US2003109434-A1.
PD   12-JUN-2003.
PA   (CORI-) CORIXA CORP.
  Query Match             2.9%;  Score 48;  DB 7;  Length 269;
  Best Local Similarity   56.2%;  Pred. No. 0.033;
RESULT 1106
ID   ABX43930 standard; cDNA; 283 BP.
DE   Bovine EST associated with lactation/muscle/fat deposition #9095.
PN   US2002137139-A1.
PD   26-SEP-2002.
PA   (BYAT/) BYATT J C.
PA   (MATH/) MATHIALAGAN N.
PA   (TAON/) TAO N.
PA   (WARR/) WARREN W C.
  Query Match             2.9%;  Score 48;  DB 8;  Length 283;
  Best Local Similarity   64.3%;  Pred. No. 0.034;
RESULT 1107
ID   ABV56758 standard; cDNA; 323 BP.
DE   Human prostate expression marker cDNA 56749.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48;  DB 5;  Length 323;
  Best Local Similarity   56.2%;  Pred. No. 0.036;
RESULT 1108
ID   ABX38490 standard; cDNA; 373 BP.
DE   Bovine EST associated with lactation/muscle/fat deposition #3655.
PN   US2002137139-A1.
PD   26-SEP-2002.
PA   (BYAT/) BYATT J C.
PA   (MATH/) MATHIALAGAN N.
PA   (TAON/) TAO N.
PA   (WARR/) WARREN W C.
  Query Match             2.9%;  Score 48;  DB 8;  Length 373;
  Best Local Similarity   58.3%;  Pred. No. 0.039;
RESULT 1109
ID   AAI89019 standard; cDNA; 386 BP.
DE   Human polynucleotide SEQ ID NO 9079.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 48;  DB 4;  Length 386;
  Best Local Similarity   64.3%;  Pred. No. 0.04;
RESULT 1110
ID   AAI85430 standard; cDNA; 401 BP.
DE   Human polynucleotide SEQ ID NO 5490.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 48;  DB 4;  Length 401;
  Best Local Similarity   55.6%;  Pred. No. 0.041;
RESULT 1111
ID   AAI85304 standard; cDNA; 404 BP.
DE   Human polynucleotide SEQ ID NO 5364.
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PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 48;  DB 4;  Length 404;
  Best Local Similarity   64.3%;  Pred. No. 0.041;
RESULT 1112
ID   AAI83194 standard; cDNA; 407 BP.
DE   Human polynucleotide SEQ ID NO 3254.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 48;  DB 4;  Length 407;
  Best Local Similarity   64.3%;  Pred. No. 0.041;
RESULT 1113
ID   AAI83744 standard; cDNA; 408 BP.
DE   Human polynucleotide SEQ ID NO 3804.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 48;  DB 4;  Length 408;
  Best Local Similarity   57.9%;  Pred. No. 0.041;
RESULT 1114
ID   ABV59282 standard; cDNA; 452 BP.
DE   Human prostate expression marker cDNA 59273.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48;  DB 5;  Length 452;
  Best Local Similarity   64.3%;  Pred. No. 0.043;
RESULT 1115
ID   AAI82085 standard; cDNA; 466 BP.
DE   Human polynucleotide SEQ ID NO 2145.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 48;  DB 4;  Length 466;
  Best Local Similarity   64.3%;  Pred. No. 0.044;
RESULT 1116
ID   AAI88612 standard; cDNA; 478 BP.
DE   Human polynucleotide SEQ ID NO 8672.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             2.9%;  Score 48;  DB 4;  Length 478;
  Best Local Similarity   64.3%;  Pred. No. 0.044;
RESULT 1117
ID   ACN61416 standard; cDNA; 490 BP.
DE   Cotton gynoecium tissue EST Clone ID: LIB3829-015-Q1-N6-H1, SEQ:16197.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             2.9%;  Score 48;  DB 13;  Length 490;
  Best Local Similarity   49.6%;  Pred. No. 0.045;
RESULT 1118
ID   ABV58419 standard; cDNA; 515 BP.
DE   Human prostate expression marker cDNA 58410.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48;  DB 5;  Length 515;
  Best Local Similarity   56.2%;  Pred. No. 0.046;
RESULT 1119
ID   ABV57482 standard; cDNA; 533 BP.
DE   Human prostate expression marker cDNA 57473.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48;  DB 5;  Length 533;
  Best Local Similarity   56.2%;  Pred. No. 0.047;
RESULT 1120
ID   ABV58372 standard; cDNA; 540 BP.
DE   Human prostate expression marker cDNA 58363.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48;  DB 5;  Length 540;
  Best Local Similarity   56.2%;  Pred. No. 0.047;
RESULT 1121
ID   ABV58085 standard; cDNA; 585 BP.
DE   Human prostate expression marker cDNA 58076.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48;  DB 5;  Length 585;
  Best Local Similarity   56.2%;  Pred. No. 0.049;
RESULT 1122
ID   ADF76609 standard; cDNA; 602 BP.
DE   Novel human secreted and transmembrane protein cDNA SeqID 283.
PN   WO2003072035-A2.
PD   04-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 10;  Length 602;
  Best Local Similarity   60.9%;  Pred. No. 0.05;
RESULT 1123
ID   ADL83210 standard; cDNA; 602 BP.
DE   Human PRO52174 cDNA, SEQ ID 412.
PN   WO2004024097-A2.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 12;  Length 602;
  Best Local Similarity   60.9%;  Pred. No. 0.05;
RESULT 1124
ID   ADL91506 standard; cDNA; 602 BP.
DE   Human immune-related polypeptide PRO52174-encoding cDNA, SEQ ID NO:21.
PN   WO2004024072-A2.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 12;  Length 602;
  Best Local Similarity   60.9%;  Pred. No. 0.05;
RESULT 1125
ID   ADM41666 standard; cDNA; 602 BP.
DE   PRO52174 cDNA, associated with B-cell activation.
PN   WO2004024069-A2.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 12;  Length 602;
  Best Local Similarity   60.9%;  Pred. No. 0.05;
RESULT 1126
ID   ABV43916 standard; cDNA; 606 BP.
DE   Human prostate expression marker cDNA 43907.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             2.9%;  Score 48;  DB 5;  Length 606;
  Best Local Similarity   58.3%;  Pred. No. 0.05;
RESULT 1127
ID   ACN54555 standard; cDNA; 627 BP.
DE   Cotton androecium tissue EST Clone ID: LIB3828-024-Q6-K6-C2, SEQ:9336.
PN   US2004123340-A1.
PD   24-JUN-2004.
PA   (DEIK/) DEIKMAN J.
PA   (FENG/) FENG P C C.
PA   (FINC/) FINCHER K L.
PA   (ZIEG/) ZIEGLER T E.
  Query Match             2.9%;  Score 48;  DB 13;  Length 627;
  Best Local Similarity   64.3%;  Pred. No. 0.051;
RESULT 1128
ID   ADP04748 standard; cDNA; 1352 BP.
DE   Sea squirt cDNA with tissue specific expression in development Seq 343.
PN   JP2004057129-A.
PD   26-FEB-2004.
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
  Query Match             2.9%;  Score 48;  DB 12;  Length 1352;
  Best Local Similarity   59.6%;  Pred. No. 0.075;
RESULT 1129
ID   ADG32734 standard; DNA; 1483 BP.
DE   Human DNA differentially expressed in patients with SLE SeqID58.
PN   WO2003090694-A2.
PD   06-NOV-2003.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
  Query Match             2.9%;  Score 48;  DB 10;  Length 1483;
  Best Local Similarity   59.6%;  Pred. No. 0.079;
RESULT 1130
ID   AAI72316 standard; cDNA; 1637 BP.
DE   Human transporter protein cDNA.
PN   WO200202635-A2.
PD   10-JAN-2002.
PA   (APPL-) APPLERA CORP.
  Query Match             2.9%;  Score 48;  DB 6;  Length 1637;
  Best Local Similarity   58.3%;  Pred. No. 0.083;
RESULT 1131
ID   AAZ90632 standard; DNA; 1690 BP.
DE   Human adipose tissue protein #2 encoding DNA.
PN   JP2000037190-A.
PD   08-FEB-2000.
PA   (NISB ) JAPAN TOBACCO INC.
  Query Match             2.9%;  Score 48;  DB 3;  Length 1690;
  Best Local Similarity   64.3%;  Pred. No. 0.084;
RESULT 1132
ID   AAD32523 standard; DNA; 1726 BP.
DE   Human B7-H10 gene.
PN   WO200202587-A1.
PD   10-JAN-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             2.9%;  Score 48;  DB 6;  Length 1726;
  Best Local Similarity   59.6%;  Pred. No. 0.085;
RESULT 1133
ID   AAX52252 standard; DNA; 1984 BP.
DE   Protein PRO271 cDNA clone DNA39423-1182.
PN   WO9914328-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 2;  Length 1984;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1134
ID   ADC78532 standard; cDNA; 1984 BP.
DE   Human PRO271 cDNA.
PN   WO200015796-A2.
PD   23-MAR-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 3;  Length 1984;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1135
ID   ADR18008 standard; cDNA; 1984 BP.
DE   Human secreted/transmembrane protein cDNA, #42.
PN   US2004147017-A1.
PD   29-JUL-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI C J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (MATH/) MATHER J P.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             2.9%;  Score 48;  DB 13;  Length 1984;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1136
ID   AAF72410 standard; cDNA; 1985 BP.
DE   Human PRO271 cDNA.
PN   WO200104311-A1.
PD   18-JAN-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 4;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1137
ID   AAS45938 standard; cDNA; 1985 BP.
DE   Human DNA encoding PRO polypeptide sequence #14.
PN   WO200168848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 4;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1138
ID   ACA60174 standard; cDNA; 1985 BP.
DE   Human cDNA for secreted/transmembrane protein PRO271.
PN   US2003003530-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1139
ID   ACA89388 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003036141-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1140
ID   ACA73398 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036146-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1141
ID   ACA05713 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036162-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1142
ID   ACA66547 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO protein #14.
PN   US2003036137-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1143
ID   ACD07574 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2002197671-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1144
ID   ACF20122 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
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PN   US2003040063-A1.
PD   27-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1145
ID   ACF19508 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040064-A1.
PD   27-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1146
ID   ACD21796 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003027267-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1147
ID   ACF12961 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003036160-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1148
ID   ACD25064 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003044925-A1.
PD   06-MAR-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1149
ID   ACF00113 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054474-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1150
ID   ACA72170 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003032114-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1151
ID   ACD04694 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003032101-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1152
ID   ACD18155 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036124-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1153
ID   ACD08162 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003040054-A1.
PD   27-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1154
ID   ABX71622 standard; cDNA; 1985 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO271.
PN   US2002132240-A1.
PD   19-SEP-2002.
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PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1155
ID   ACA88596 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003036133-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1156
ID   ACA70038 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036134-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1157
ID   ACD12260 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003022294-A1.
PD   30-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1158
ID   ACC74175 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003027275-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1159
ID   ACD15803 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003027324-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1160
ID   ACD25371 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003036118-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1161
ID   ACD17848 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036123-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1162
ID   ACC88135 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003036148-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1163
ID   ACD21489 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003040060-A1.
PD   27-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1164
ID   ACD18556 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003044916-A1.
PD   06-MAR-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1165
ID   ACH06954 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane polypeptide PRO271 cDNA.
PN   US2003044839-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1166
ID   ABX98166 standard; cDNA; 1985 BP.
DE   Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.
PN   US2003036156-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1167
ID   ACD13917 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003032117-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1168
ID   ACD09697 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036128-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1169
ID   ACC88442 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003027266-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1170
ID   ACD21182 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003054483-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1171
ID   ABX75554 standard; cDNA; 1985 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO271.
PN   US2003022298-A1.
PD   30-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1172
ID   ABX97757 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003032102-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1173
ID   ACA97233 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003036117-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1174
ID   ACA57696 standard; cDNA; 1985 BP.
DE   Human PRO271 cDNA.
PN   US2003036143-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
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RESULT 1175
ID   ACD14224 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003032130-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1176
ID   ACC91007 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003032138-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1177
ID   ACC88749 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003036132-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1178
ID   ACD06946 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003008353-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1179
ID   ACA67397 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003017542-A1.
PD   23-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1180
ID   ACC81452 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003032137-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1181
ID   ACC89056 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003027269-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1182
ID   ACC86412 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003027268-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1183
ID   ACC89670 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003027274-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1184
ID   ACC92849 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003032135-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
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RESULT 1185
ID   ACA72477 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003022295-A1.
PD   30-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1186
ID   ACA88995 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003022297-A1.
PD   30-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1187
ID   ACA69731 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003032105-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1188
ID   ACA96874 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003032123-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1189
ID   ACA90870 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003032108-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1190
ID   ACA70652 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003032111-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1191
ID   ACA95162 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003032119-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1192
ID   ACC86105 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003027263-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1193
ID   ACC89977 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003027271-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1194
ID   ACD12585 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036125-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1195
ID   ACF19815 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040068-A1.
PD   27-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1196
ID   ABX76759 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003027280-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1197
ID   ABX96191 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein cDNA, #40.
PN   US2002160374-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1198
ID   ACA73091 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003022300-A1.
PD   30-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1199
ID   ACA05512 standard; cDNA; 1985 BP.
DE   cDNA encoding human secreted protein PRO271.
PN   US2003023054-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1200
ID   ACA68634 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003036136-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1201
ID   ACA74478 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003036138-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1202
ID   ACA70345 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003032109-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1203
ID   ACD14531 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003040066-A1.
PD   27-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1204
ID   ACD20179 standard; cDNA; 1985 BP.
DE   Human secreted / transmembrane polypeptide PRO271 cDNA.
PN   US2003036060-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1205
ID   ACA68203 standard; cDNA; 1985 BP.
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DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003032104-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1206
ID   ABX98668 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003036157-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1207
ID   ACC81145 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003032120-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1208
ID   ACA95469 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003036155-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1209
ID   ACD04387 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003022296-A1.
PD   30-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1210
ID   ACC87828 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003027281-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1211
ID   ACF12490 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040058-A1.
PD   27-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1212
ID   ACA96205 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003017540-A1.
PD   23-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1213
ID   ACA64979 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003032106-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1214
ID   ACA73705 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003032129-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1215
ID   ACA74117 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003032131-A1.
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PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1216
ID   ACA96512 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003032103-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1217
ID   ACD10618 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003032107-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1218
ID   ACC91314 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003032139-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1219
ID   ACD02649 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003022301-A1.
PD   30-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1220
ID   ACC87214 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003036165-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1221
ID   ACC85798 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003027262-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1222
ID   ACA65286 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003032110-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1223
ID   ACA94103 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036142-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1224
ID   ACA97847 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003036145-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1225
ID   ACA91349 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003036154-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1226
ID   ACA90563 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003036153-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1227
ID   ACD16110 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003044931-A1.
PD   06-MAR-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1228
ID   ACD17271 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036150-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1229
ID   ACC91928 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040069-A1.
PD   27-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1230
ID   ACA74785 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003022293-A1.
PD   30-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1231
ID   ACA91656 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003032128-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1232
ID   ACA71300 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003032116-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1233
ID   ACC90700 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003032122-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1234
ID   ACA65710 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO protein #14.
PN   US2003036139-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1235
ID   ACA54982 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003017463-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1236
ID   ACA94855 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003017541-A1.
PD   23-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1237
ID   ACD16417 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003017543-A1.
PD   23-JAN-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1238
ID   ACD15496 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036152-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1239
ID   ABX16599 standard; cDNA; 1985 BP.
DE   Human cDNA encoding secreted/transmembrane protein #14.
PN   US2002127584-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 8;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1240
ID   ACA97540 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003032115-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1241
ID   ACA98989 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003032140-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1242
ID   ACC91621 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040076-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1243
ID   ACD11032 standard; cDNA; 1985 BP.
DE   Novel human secreted and transmembrane protein PRO271 cDNA.
PN   US2003008352-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1244
ID   ACD14882 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003044922-A1.
PD   06-MAR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1245
ID   ACD19817 standard; cDNA; 1985 BP.
DE   Human secreted / transmembrane polypeptide PRO271 cDNA.
PN   US2003027143-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
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RESULT 1246
ID   ACD11646 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003032118-A1.
PD   13-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1247
ID   ACC95775 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003036135-A1.
PD   20-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1248
ID   ACF16338 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054455-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1249
ID   ACF02456 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049741-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1250
ID   ACF02763 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049743-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1251
ID   ACF21350 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049769-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1252
ID   ACF10034 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068743-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1253
ID   ACF77927 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054479-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1254
ID   ACD46632 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068685-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1255
ID   ACD49395 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068725-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1256
ID   ACF28162 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068752-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1257
ID   ACD88852 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068682-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1258
ID   ACD84247 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003068701-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1259
ID   ACD99021 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003068755-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1260
ID   ADA77779 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003073180-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1261
ID   ACF48763 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104539-A1.
PD   05-JUN-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1262
ID   ADB29417 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein cDNA, #42.
PN   US2003092002-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1263
ID   ACD09083 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036131-A1.
PD   20-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1264
ID   ACF11876 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040075-A1.
PD   27-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1265
ID   ACF41110 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054459-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1266
ID   ACF15724 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003044930-A1.
PD   06-MAR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1267
ID   ACF16031 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040071-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1268
ID   ACD31858 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003054471-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1269
ID   ACF18666 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064452-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1270
ID   ACF09113 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068705-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1271
ID   ACF78234 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054473-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1272
ID   ACF51833 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064440-A1.
PD   03-APR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1273
ID   ACF26320 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068704-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1274
ID   ACF24113 standard; cDNA; 1985 BP.
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DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068722-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1275
ID   ACF63424 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073183-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1276
ID   ACF50298 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104549-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1277
ID   ACH07769 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049749-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1278
ID   ACF13575 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064462-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1279
ID   ACD41501 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003065159-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1280
ID   ACF31914 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1281
ID   ACF23192 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1282
ID   ACF39882 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064463-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1283
ID   ACD45404 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
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PN   US2003064451-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1284
ID   ACF53061 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068721-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1285
ID   ACF27241 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068699-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1286
ID   ACF45079 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068707-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1287
ID   ACF29697 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073175-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1288
ID   ACD89773 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068695-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1289
ID   ACD84554 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003068703-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1290
ID   ACD98714 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003068732-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1291
ID   ACF77006 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003082717-A1.
PD   01-MAY-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1292
ID   ACF76699 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104548-A1.
PD   05-JUN-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1293
ID   ACF49684 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104542-A1.
PD   05-JUN-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1294
ID   ACF49991 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104543-A1.
PD   05-JUN-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1295
ID   ACD09390 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036127-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1296
ID   ACD08469 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003040061-A1.
PD   27-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1297
ID   ACF12183 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003036130-A1.
PD   20-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1298
ID   ACC94691 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054468-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1299
ID   ACD22410 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003054470-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1300
ID   ACF15110 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003044917-A1.
PD   06-MAR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1301
ID   ACC97205 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003044929-A1.
PD   06-MAR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1302
ID   ADA18273 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein cDNA, #42.
PN   US2003039971-A1.
PD   27-FEB-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1303
ID   ACD66964 standard; cDNA; 1985 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO271.
PN   US2003045693-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1304
ID   ACC92235 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003059880-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1305
ID   ACF13882 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064465-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1306
ID   ACF14189 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054478-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1307
ID   ACF09420 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068718-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1308
ID   ACD45711 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003064454-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1309
ID   ACD47860 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003064461-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1310
ID   ACD67591 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003068724-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1311
ID   ACF25399 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068727-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1312
ID   ACF29083 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068772-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1313
ID   ACD84861 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068714-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1314
ID   ACD83940 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003068758-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1315
ID   ACD87931 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068776-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1316
ID   ACF30618 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003069407-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1317
ID   ACF32221 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104555-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1318
ID   ACH11881 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003049768-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1319
ID   ACH12188 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003049771-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1320
ID   ACD40580 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003032134-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
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RESULT 1321
ID   ACF18052 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054481-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1322
ID   ACF08499 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049778-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1323
ID   ACF31300 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049782-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1324
ID   ACF52140 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054476-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1325
ID   ACD50009 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068733-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1326
ID   ACF38712 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068692-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1327
ID   ACF26627 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068709-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1328
ID   ACF24727 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068716-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1329
ID   ACF46307 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068740-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1330
ID   ACF27855 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068751-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1331
ID   ACD89159 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068684-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1332
ID   ACF63731 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073179-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1333
ID   ACF60371 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003087374-A1.
PD   08-MAY-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1334
ID   ACH12495 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003049773-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1335
ID   ACH09918 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049777-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1336
ID   ACD03773 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003040055-A1.
PD   27-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1337
ID   ACD10311 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036164-A1.
PD   20-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1338
ID   ACD11953 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003040074-A1.
PD   27-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1339
ID   ACD83125 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #38.
PN   US2003044793-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1340
ID   ACF42338 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054480-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1341
ID   ADA16248 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein cDNA, #42.
PN   US2003049621-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1342
ID   ACF18359 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003059885-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1343
ID   ACF02149 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049740-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1344
ID   ACF21657 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049770-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1345
ID   ACF10341 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073169-A1.
PD   17-APR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1346
ID   ACF33793 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064457-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1347
ID   ACF44755 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068711-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1348
ID   ACD90387 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049745-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
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RESULT 1349
ID   ACD91000 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049751-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1350
ID   ACF30311 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003067478-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1351
ID   ACD87010 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068773-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1352
ID   ACF60064 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073185-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1353
ID   ACF46614 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003087373-A1.
PD   08-MAY-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1354
ID   ACF75471 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003096353-A1.
PD   22-MAY-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1355
ID   ADA79571 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003073173-A1.
PD   17-APR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1356
ID   ACF17131 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054458-A1.
PD   20-MAR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1357
ID   ACF22885 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003059886-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1358
ID   ACF07885 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049758-A1.
PD   13-MAR-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1359
ID   ACF08192 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049772-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1360
ID   ACF40496 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064448-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1361
ID   ACF53675 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064456-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1362
ID   ACD46939 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068693-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1363
ID   ACF47842 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068735-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1364
ID   ACF47228 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068753-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1365
ID   ACF46000 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068742-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1366
ID   ACD86089 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068756-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1367
ID   ACF52447 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003082715-A1.
PD   01-MAY-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
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  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1368
ID   ACF52754 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003082716-A1.
PD   01-MAY-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1369
ID   ACF64747 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068737-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1370
ID   ACF76392 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104547-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1371
ID   ACF61292 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003096359-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1372
ID   ACF61599 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003100061-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1373
ID   ACD30630 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003032125-A1.
PD   13-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1374
ID   ACD31551 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003054454-A1.
PD   20-MAR-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1375
ID   ACD32472 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003054477-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1376
ID   ACF17438 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054460-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1377
ID   ACF07271 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
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PN   US2003049753-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1378
ID   ACF20429 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049763-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1379
ID   ACF21043 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073172-A1.
PD   17-APR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1380
ID   ACF20736 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073172-A1.
PD   17-APR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1381
ID   ACD47553 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068700-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1382
ID   ACF47535 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068736-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1383
ID   ACF53368 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068679-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1384
ID   ACD86703 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068767-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1385
ID   ACH04951 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003073182-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1386
ID   ACF44448 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104557-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1387
ID   ADA42393 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein cDNA, #42.
PN   US2003054401-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1388
ID   ADA81298 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003092121-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1389
ID   ACD22103 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003027276-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1390
ID   ACD24450 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003044920-A1.
PD   06-MAR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1391
ID   ACD39653 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003027265-A1.
PD   06-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1392
ID   ACD39960 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003054461-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1393
ID   ACF13268 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064446-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1394
ID   ACF03070 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049744-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1395
ID   ACD23303 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #38.
PN   US2003064367-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1396
ID   ACF78541 standard; cDNA; 1985 BP.
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DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049783-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1397
ID   ACF11262 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073171-A1.
PD   17-APR-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1398
ID   ACF50605 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003032121-A1.
PD   13-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1399
ID   ACF34100 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064458-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1400
ID   ACD46325 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003064460-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1401
ID   ACD48167 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003064464-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1402
ID   ACF27548 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068702-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1403
ID   ACF24420 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068734-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1404
ID   ACD85475 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068719-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1405
ID   ACD90080 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068729-A1.
PD   10-APR-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1406
ID   ACD83633 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003068738-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1407
ID   ACF49070 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104540-A1.
PD   05-JUN-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1408
ID   ACH07155 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049742-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1409
ID   ACH07462 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049747-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1410
ID   ACH08076 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049750-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1411
ID   ACH11267 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003049766-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1412
ID   ACH11574 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003049767-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1413
ID   ACH10225 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049779-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1414
ID   ACF01228 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040059-A1.
PD   27-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
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RESULT 1415
ID   ACF40803 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040078-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1416
ID   ACD24143 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003044918-A1.
PD   06-MAR-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1417
ID   ACD31244 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003032132-A1.
PD   13-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1418
ID   ACF17745 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054462-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1419
ID   ACF32528 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064445-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1420
ID   ACF40189 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064449-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1421
ID   ACF48149 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064441-A1.
PD   03-APR-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1422
ID   ACF38098 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068696-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1423
ID   ACF25034 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068712-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1424
ID   ACF26934 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068730-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1425
ID   ACF29390 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073174-A1.
PD   17-APR-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1426
ID   ACD87624 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068775-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1427
ID   ACF76085 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104545-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1428
ID   ACF49377 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104541-A1.
PD   05-JUN-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1429
ID   ACF43834 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104554-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1430
ID   ACH06179 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003049762-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1431
ID   ACH06486 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003049765-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1432
ID   ADA83096 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049752-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1433
ID   ACC92542 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003032133-A1.
PD   13-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
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RESULT 1434
ID   ACC93156 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003032136-A1.
PD   13-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1435
ID   ACF19201 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003036129-A1.
PD   20-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1436
ID   ACD12892 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003040053-A1.
PD   27-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1437
ID   ACF06350 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040057-A1.
PD   27-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1438
ID   ACC94384 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054467-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1439
ID   ACC97812 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003044932-A1.
PD   06-MAR-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1440
ID   ACC94077 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003027270-A1.
PD   06-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1441
ID   ACF42031 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054469-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1442
ID   ACD30937 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003032126-A1.
PD   13-FEB-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1443
ID   ACD42966 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003054463-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
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RESULT 1444
ID   ACD43273 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003054466-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1445
ID   ACF14803 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003059879-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1446
ID   ACF01535 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049738-A1.
PD   13-MAR-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1447
ID   ACF31607 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064469-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1448
ID   ACD67284 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003064453-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1449
ID   ACD48474 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003064466-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1450
ID   ACD48781 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003064468-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1451
ID   ACF51219 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068760-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1452
ID   ACF53982 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068769-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1453
ID   ACF25706 standard; cDNA; 1985 BP.
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DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003045700-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1454
ID   ACF39019 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068698-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1455
ID   ACF28776 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068759-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1456
ID   ACD90693 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049748-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1457
ID   ACD86396 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068765-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1458
ID   ACH05258 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003049754-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1459
ID   ACF65054 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068688-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1460
ID   ADB20139 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003082767-A1.
PD   01-MAY-2003.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1461
ID   ACF43527 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104552-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1462
ID   ACH08997 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049774-A1.
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PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1463
ID   ACH09304 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049775-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1464
ID   ADA78391 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003073181-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1465
ID   ACF09727 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068720-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1466
ID   ACF50912 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068739-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1467
ID   ACF23806 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068763-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1468
ID   ACD88238 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003068689-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1469
ID   ACH09611 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049776-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1470
ID   ACH10532 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049780-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1471
ID   ACD11339 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003036126-A1.
PD   20-FEB-2003.
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  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1472
ID   ACC96389 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003044924-A1.
PD   06-MAR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1473
ID   ACC98419 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003044927-A1.
PD   06-MAR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1474
ID   ADA16672 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein cDNA, #42.
PN   US2003039969-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1475
ID   ACF41724 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040072-A1.
PD   27-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1476
ID   ACF16645 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003040073-A1.
PD   27-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1477
ID   ADA13101 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein cDNA, #42.
PN   US2003049622-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1478
ID   ACD32165 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003054475-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1479
ID   ACD30323 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003032124-A1.
PD   13-FEB-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1480
ID   ACD41194 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003064467-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1481
ID   ACF07578 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003049759-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1482
ID   ACF30993 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003064455-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1483
ID   ACF77313 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003054465-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1484
ID   ACF10955 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073170-A1.
PD   17-APR-2003.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1485
ID   ACF32835 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003073176-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1486
ID   ACF26013 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068717-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1487
ID   ACD83326 standard; cDNA; 1985 BP.
DE   Human PRO polynucleotide #14.
PN   US2003068728-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1488
ID   ACF23499 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003068764-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1489
ID   ACF42913 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104550-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1490
ID   ACF43220 standard; cDNA; 1985 BP.
DE   Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN   US2003104551-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1491
ID   ACH05872 standard; cDNA; 1985 BP.
DE   cDNA encoding human PRO polypeptide #14.
PN   US2003049761-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
  Best Local Similarity   56.2%;  Pred. No. 0.091;
RESULT 1492
ID   ACH08690 standard; cDNA; 1985 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #14.
PN   US2003049757-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.9%;  Score 48;  DB 9;  Length 1985;
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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      Pred. No. is the number of results predicted by chance to have a
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  205    44.4    2.6   1051  4  US-09-358-055B-10            Sequence 10, Appl
  206    44.4    2.6   1051  4  US-09-893-238-10             Sequence 10, Appl
  207    44.4    2.6   1134  3  US-09-248-335-29             Sequence 29, Appl
  208    44.4    2.6   1141  4  US-09-800-729-78             Sequence 78, Appl
  209    44.4    2.6   2327  4  US-10-066-130-20             Sequence 20, Appl
  210    44.4    2.6   2674  4  US-10-066-130-19             Sequence 19, Appl
  211    44.4    2.6   2771  4  US-10-066-130-18             Sequence 18, Appl
  212    44.4    2.6   4456  3  US-09-095-443-1              Sequence 1, Appli
  213    44.4    2.6   5860  4  US-10-066-130-17             Sequence 17, Appl
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c 215    44.4    2.6   9646  3  US-09-034-756-1              Sequence 1, Appli
c 216    44.4    2.6  12980  3  US-08-811-566-5              Sequence 5, Appli
c 217    44.4    2.6  12980  3  US-09-034-756-5              Sequence 5, Appli
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  219    44.2    2.6    244  4  US-09-621-976-484            Sequence 484, App
  220    44.2    2.6    272  4  US-09-270-767-11902          Sequence 11902, A
  221    44.2    2.6    318  4  US-09-621-976-10247          Sequence 10247, A
  222    44.2    2.6   1066  1  US-08-157-101A-4             Sequence 4, Appli
  223    44.2    2.6   1193  3  US-09-372-422A-23            Sequence 23, Appl
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  225    44.2    2.6   1801  4  US-09-439-410A-3             Sequence 3, Appli
  226    44.2    2.6   1925  4  US-09-148-545-128            Sequence 128, App
  227    44.2    2.6   2202  3  US-09-465-558-59             Sequence 59, Appl
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  231      44    2.6    186  4  US-09-513-999C-18897         Sequence 18897, A
  232      44    2.6    240  4  US-09-621-976-1324           Sequence 1324, Ap
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  234      44    2.6    882  4  US-09-311-021-107            Sequence 107, App
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  236      44    2.6   1882  3  US-09-370-253-1              Sequence 1, Appli
  237      44    2.6   1921  2  US-08-557-128-11             Sequence 11, Appl
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  239      44    2.6   2269  3  US-09-243-560B-1             Sequence 1, Appli
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  242    43.8    2.6   1248  4  US-09-489-847-101            Sequence 101, App
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    264    43.4    2.6     552  4  US-10-012-542-111         Sequence 111, App
    265    43.4    2.6     552  4  US-10-115-123-111         Sequence 111, App
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    274    43.4    2.6   49931  4  US-09-949-016-13729       Sequence 13729, A
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c 981      39    2.3   8001  4  US-09-539-601-28         Sequence 28, Appl
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c 983      39    2.3   8638  4  US-10-029-907-7          Sequence 7, Appli
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ALIGNMENTS

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RESULT 1
US-09-700-397-2
; Sequence 2, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
;  APPLICANT:  Ono Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION:   No. 6664383el Polypeptides, cDNA encoding the same, and use of
;  FILE REFERENCE:   Q61459
;  CURRENT APPLICATION NUMBER: US/09/700,397
;  CURRENT FILING DATE:  2001-01-05
;  PRIOR APPLICATION NUMBER:   JP 10-131815
;  PRIOR FILING DATE:   1998-05-14
;  PRIOR APPLICATION NUMBER:   PCT/JP99/02485
;  PRIOR FILING DATE:   1999-05-13
;  NUMBER OF SEQ ID NOS:   19
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 1693
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Clone OC001 derived from human brain
;   NAME/KEY: CDS
;   LOCATION: (130)..(1161)
;   NAME/KEY: sig_peptide
;   LOCATION: (130)..(213)
;   NAME/KEY: mat_peptide
;   LOCATION: (214)..()
US-09-700-397-2

  Query Match             99.0%;  Score 1661.4;  DB 4;  Length 1693;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1673;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

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RESULT 2
US-09-700-397-1
; Sequence 1, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
;  APPLICANT:  Ono Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION:   No. 6664383el Polypeptides, cDNA encoding the same, and use of
;  FILE REFERENCE:   Q61459
;  CURRENT APPLICATION NUMBER: US/09/700,397
;  CURRENT FILING DATE:  2001-01-05
;  PRIOR APPLICATION NUMBER:   JP 10-131815
;  PRIOR FILING DATE:   1998-05-14
;  PRIOR APPLICATION NUMBER:   PCT/JP99/02485
;  PRIOR FILING DATE:   1999-05-13
;  NUMBER OF SEQ ID NOS:   19
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1032
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-700-397-1

  Query Match             61.5%;  Score 1032;  DB 4;  Length 1032;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-273;
  Matches 1032;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720

Qy        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780

Qy        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840

Qy        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900

Qy       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960

Qy       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020

Qy       1154 CTTCTCAAATTT 1165
              ||||||||||||
Db       1021 CTTCTCAAATTT 1032

RESULT 3
US-09-700-397-5
; Sequence 5, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
;  APPLICANT:  Ono Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION:   No. 6664383el Polypeptides, cDNA encoding the same, and use of
;  FILE REFERENCE:   Q61459
;  CURRENT APPLICATION NUMBER: US/09/700,397
;  CURRENT FILING DATE:  2001-01-05
;  PRIOR APPLICATION NUMBER:   JP 10-131815
;  PRIOR FILING DATE:   1998-05-14
;  PRIOR APPLICATION NUMBER:   PCT/JP99/02485
;  PRIOR FILING DATE:   1999-05-13
;  NUMBER OF SEQ ID NOS:   19
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 939
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-700-397-5

  Query Match             55.9%;  Score 939;  DB 4;  Length 939;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-247;
  Matches  939;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 CGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAG 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAG 60

Qy        287 AGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGC 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGC 120

Qy        347 AGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTG 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTG 180

Qy        407 AGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGC 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGC 240

Qy        467 CCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATT 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATT 300

Qy        527 GTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC 360

Qy        587 AATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACAC 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACAC 420

Qy        647 ATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATC 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATC 480

Qy        707 ACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTG 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTG 540

Qy        767 GTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACA 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACA 600

Qy        827 GGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCA 886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCA 660

Qy        887 GAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTG 946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTG 720

Qy        947 GAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGG 1006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGG 780

Qy       1007 AACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTT 1066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTT 840

Qy       1067 GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGG 1126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGG 900

Qy       1127 CTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 1165
              |||||||||||||||||||||||||||||||||||||||
Db        901 CTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 939

RESULT 4
US-08-414-657D-3
; Sequence 3, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;     APPLICANT:  Levitt, Pat
;     APPLICANT:  Pimenta, Aurea
;     APPLICANT:  Fischer, Itzhak
;     APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1238 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  56...1069
;      OTHER INFORMATION:
US-08-414-657D-3

  Query Match             20.4%;  Score 343;  DB 2;  Length 1238;
  Best Local Similarity   62.0%;  Pred. No. 9.5e-84;
  Matches  598;  Conservative    0;  Mismatches  355;  Indels   12;  Gaps    3;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
              |||   |  |||| ||||||| ||||||| |||      ||   |  ||  | ||||||
Db        121 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 174

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
              | | || ||  ||||||||||| |  |||| |||||||||     | ||  ||  |  | |
Db        175 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 234

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
                  ||||||||| | ||||||     ||||| |||  |||||  | ||||||||||  ||
Db        235 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 294

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
              ||| ||||| || |  ||   ||    |        | | |||||| ||   ||||||||
Db        295 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 354

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
               |||||||| ||||| || ||  | ||||| ||||| || |||||| |  |  | || ||
Db        355 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 414

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
              |||||||   ||  || | ||||| |||||  | || || ||     | || || || ||
Db        415 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 474

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
              | || |  | ||||| || | |||| | | |||   |||||| || | ||  | || ||
Db        475 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 534
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Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
               |||    | || ||||||||| |  | ||    |     |  ||||   | ||||| ||
Db        535 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 594

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
              |||  |||| || |  |||||||| |||| |||||||||  | || |||||||  ||  |
Db        595 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 654

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
              ||| || ||  || |  | |  ||      ||| |||||||| ||||||||||||||
Db        655 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 714

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
              |||  ||||  | ||| | |  |  | | ||   |||| | |   | ||  | |||||
Db        715 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 774

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
              ||||||||| || ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db        775 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 831

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
                |    || ||  |  |  |  | | ||       ||  ||     | |   |   |||
Db        832 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 891

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
               ||| ||||  |  |||| || ||||| || || |||||  |||||||||| |||  |||
Db        892 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 951

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 1104
              |||||||||| |  | || ||  | || ||  | || ||    |  | ||||||  |
Db        952 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAG---AGGAATCAACGGATCCAT 1008

Qy       1105 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1164
               ||   ||| |      | ||||||||| |        | ||   ||| ||   |||||
Db       1009 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCCTTCTCAGCAAATG 1068

Qy       1165 TTGAT 1169
              || ||
Db       1069 TTAAT 1073


RESULT 5
US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1238 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  56...1069
;      OTHER INFORMATION:
US-09-135-080-3

  Query Match             20.4%;  Score 343;  DB 3;  Length 1238;
  Best Local Similarity   62.0%;  Pred. No. 9.5e-84;
  Matches  598;  Conservative    0;  Mismatches  355;  Indels   12;  Gaps    3;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
              |||   |  |||| ||||||| |||||||  |||      ||   |  ||  | ||||||
Db        121 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 174

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
              | | || ||  |||||||||| |  |||| |||||||||     | ||  ||  |  | |
Db        175 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 234

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
                  ||||||||| | ||||||     |||| |||  |||||  | ||||||||||  ||
Db        235 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 294

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
              ||| ||||| || |  ||   ||    |        | | |||||| ||   ||||||||
Db        295 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 354

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
               |||||||| ||||| || ||  | ||||| ||||| || |||||| |  |  | || ||
Db        355 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 414

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
              |||||||   ||  || | ||||| |||||  | || || ||     | || || || ||
Db        415 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 474

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
              | || |  | ||||| || | |||| | | |||   |||||| || | |||  | || ||
Db        475 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 534

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
               |||    | || ||||||||| |  | ||    |     |  ||||   | ||||| ||
Db        535 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 594

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
              |||  |||| || |  ||||||||| |||| ||||||||  | || |||||||  ||  |
Db        595 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 654

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
              ||| || ||  || |  | |  ||      ||| |||||||| ||||||||||||||
Db        655 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 714

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
              |||  ||||  | ||| | |  |  | | ||   |||| | | |   | ||  | |||||
Db        715 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 774

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
              ||||||||| || ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db        775 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 831

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
                |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db        832 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 891

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
               ||| ||||  |  |||| || ||||| || || |||||  |||||||||| |||  |||
Db        892 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 951

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 1104
              |||||||||| |  | || ||  | || ||  | || ||    |  | ||||||  |
Db        952 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAG---AGGAATCAACGGATCCAT 1008

Qy       1105 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1164
               ||   ||| |      | ||||||||| |        | ||   ||| ||   |||||
Db       1009 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCCTTCTCAGCAAATG 1068

Qy       1165 TTGAT 1169
              || ||
Db       1069 TTAAT 1073

RESULT 6
US-09-976-594-403
; Sequence 403, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 403
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 1640555CB1
US-09-976-594-403

  Query Match             20.3%;  Score 341.6;  DB 4;  Length 1195;
  Best Local Similarity   60.1%;  Pred. No. 2.3e-83;
  Matches  626;  Conservative    0;  Mismatches  404;  Indels   12;  Gaps    3;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
              |||   |  |||| |||| || |||||||  |||      ||   |  ||  | ||||||
Db         66 TCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 119

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
              | | || ||  |||||||||| |  |||| ||||||||||  | | ||  ||  |  | |
Db        120 CATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTC 179

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
                 |||||||||| | |||||      |||| | | ||||||  ||||||||||||  ||
Db        180 AAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCT 239

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
              ||| || || || |  ||   ||    |        | | |||||| ||   ||||||||
Db        240 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAA 299

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
               |||||||| ||||| |||||  | ||||| ||||| || |||||| |  |  | || ||
Db        300 GGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAA 359

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
              ||||||    ||  || | || || |||||  | || || ||     | || || || ||
Db        360 GACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGA 419

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
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              | || |  | ||||| || | |||  | |  ||   |||||| || | |||  | || ||
Db        420 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGA 479

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
               |||    | || ||||||||| |  | || |  |     |  ||||   | ||||| ||
Db        480 ACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 539

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
              |||  |||| || |  |||||||| |||||||||||||  | || |||||||  ||  |
Db        540 ATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGC 599

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
              ||| || ||  || || | |  ||      ||| |||||||| ||||||||||| ||
Db        600 CAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCAC 659

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
               ||  ||||| ||||| | |  |  | | ||   |||| | | |   ||||  |  ||||
Db        660 TATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGA 719

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
               ||||| ||||| ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db        720 GGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 776

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
                |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db        777 TAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 836

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
               ||| ||||  |  |||| || ||||||||  || |||||  |||||||||||||   |||
Db        837 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCAC 896

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 1104
              |||||||||| |  | || ||  | || ||  | || ||    |  |  || ||  |
Db        897 CAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAG---AGGAATAAATGGATCCAT 953

Qy       1105 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1164
               ||   ||| |      | ||||||||| |        |  |   ||| ||   |||||
Db        954 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCATCTCTGCTCTGCCTTCTCAGCAAATG 1013

Qy       1165 TTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACA 1224
              || ||   |     | ||    |      |||     |    |    |  |||  | |
Db       1014 TTAATAGAATAAAAATTTAAAAATAATTTAAAAAACACACAAAAATGCGTCACACAGAAT 1073

Qy       1225 ACAGCAATGGCAACACCGACAG 1246
              ||||  |  |  | || || ||
Db       1074 ACAGAGAGAGAGAGACAGAGAG 1095
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RESULT 7
US-08-414-657D-7
; Sequence 7, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  924 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...924
;      OTHER INFORMATION:
US-08-414-657D-7

  Query Match             20.3%;  Score 340.6;  DB 2;  Length 924;
  Best Local Similarity   63.3%;  Pred. No. 3.7e-83;
  Matches  558;  Conservative    0;  Mismatches  314;  Indels    9;  Gaps    2;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
              |||   |  |||| |||| || |||||||  |||      ||   |  ||  | ||||||
Db         45 TCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 98

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
              | | || ||  |||||||||| |  |||| ||||||||||  | | ||  ||  |  | |
Db         99 CATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTC 158

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
                 |||||||||| | |||||      |||| | | ||||||  ||||||||||||  ||
Db        159 AAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCT 218

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
              ||| || || || |  ||   ||    |        | | |||||| ||   ||||||||
Db        219 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAA 278

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
               |||||||| ||||| |||||  | ||||| ||||| || |||||| |  |  | || ||
Db        279 GGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAA 338

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
              ||||||    ||  || | || || |||||  | || || ||     | || || || ||
Db        339 GACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGA 398

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
              | || |  | ||||| || | |||  | |  ||   |||||| || | |||  | || ||
Db        399 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGA 458

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
               |||    | || ||||||||| |  | || |  |     |  ||||   | ||||| ||
Db        459 ACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 518

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
              |||  |||| || |  |||||||| |||||||||||||  | || |||||||  ||  |
Db        519 ATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGC 578

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
              ||| || ||  || || | |  ||      ||| |||||||| ||||||||||| ||
Db        579 CAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCAC 638

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
               ||  ||||| ||||| | |  |  | | ||   |||| | | |   ||||  |  ||||
Db        639 TATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGA 698
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Qy         865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
                ||||| ||||| ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db         699 GGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 755

Qy         925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
                 |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db         756 TAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 815

Qy         985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
                ||| ||||  |  |||| || |||||||| || |||||  |||||||||||||   |||
Db         816 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCAC 875

Qy        1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
               |||||||||| |  | || ||  | || ||  | || || |
Db         876 CAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 916


RESULT 8
US-08-414-657D-1
; Sequence 1, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  2...976
;      OTHER INFORMATION:
US-08-414-657D-1

  Query Match             20.3%;  Score 340.6;  DB 2;  Length 977;
  Best Local Similarity   63.3%;  Pred. No. 3.8e-83;
  Matches  558;  Conservative    0;  Mismatches  314;  Indels    9;  Gaps    2;
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Qy         205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
               |||   |  |||| |||| || |||||||  |||      ||   |  ||  | ||||||
Db          46 TCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 99

Qy         265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
               | | || ||  |||||||||| |  |||| ||||||||||  | | ||  ||  |  | |
Db         100 CATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTC 159

Qy         325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
                  |||||||||| | |||||      |||| | | ||||||  ||||||||||||  ||
Db         160 AAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCT 219

Qy         385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
               ||| || || || |  ||   ||    |        | | |||||| ||   ||||||||
Db         220 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAA 279

Qy         445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
                |||||||| ||||| |||||  | ||||| ||||| || |||||| |  |  | || ||
Db         280 GGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAA 339

Qy         505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
               ||||||    ||  || | || || |||||  | || || ||     | || || || ||
Db         340 GACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGA 399

Qy         565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
               | || |  | ||||| || | |||  | |  ||   |||||| || | |||  | || ||
Db         400 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGA 459

Qy         625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
                |||    | || ||||||||| |  | || |  |     |  ||||   | ||||| ||
Db         460 ACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 519

Qy         685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
               |||  |||| || |  ||||||||| |||||||||||||  | || |||||||  ||  |
Db         520 ATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGC 579

Qy         745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
               ||| || ||  || || | |  ||      ||| |||||||| ||||||||||| ||
Db         580 CAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCAC 639

Qy         805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
                ||  ||||| ||||| | |  |  | | ||   |||| | | |   ||||  | |||||
Db         640 TATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGA 699

Qy         865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
                ||||| ||||| ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db         700 GGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 756

Qy         925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
                 |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db         757 TAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 816

Qy         985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
                ||| ||||  |  |||| || |||||||| || |||||  |||||||||||||   |||
Db         817 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCAC 876

Qy        1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
               |||||||||| |  | || ||  | || ||  | || || |
Db         877 CAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 917


RESULT 9
US-09-135-080-1
; Sequence 1, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  2...976
;      OTHER INFORMATION:
US-09-135-080-1

  Query Match             20.3%;  Score 340.6;  DB 3;  Length 977;
  Best Local Similarity   63.3%;  Pred. No. 3.8e-83;
  Matches  558;  Conservative    0;  Mismatches  314;  Indels    9;  Gaps    2;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
              |||   |  |||| |||| || |||||||  |||      ||   |  ||  | ||||||
Db         46 TCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 99

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
              | | || ||  ||||||||||| |  |||| ||||||||||  | | ||  ||  |  | |
Db        100 CATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTC 159

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
                 |||||||||| | |||||      |||| | | ||||||  ||||||||||||  ||
Db        160 AAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCT 219

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
              ||| || || || |  ||   ||    |        | | |||||| ||   ||||||||
Db        220 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAA 279

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
               |||||||| ||||| |||||  | ||||| ||||| || |||||| |  |  | || ||
Db        280 GGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAA 339

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
              ||||||    ||  || | || || |||||  | || || ||     | || || || ||
Db        340 GACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGA 399

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
              | || |  | ||||| || | |||  | |  ||   |||||| || | |||  | || ||
Db        400 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGA 459

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
               |||    | || ||||||||| |  | || |  |     |  ||||   | ||||| ||
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Db        460 ACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 519

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
              |||  |||| || |  ||||||||| |||||||||||||  | || |||||||  ||  |
Db        520 ATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGC 579

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
              ||| || ||  || || | |  ||      ||| |||||||| ||||||||||| ||
Db        580 CAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCAC 639

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
               ||  ||||| ||||| | |  |  | | ||   |||| | | |   ||||  | |||||
Db        640 TATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGA 699

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
               ||||| ||||| ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db        700 GGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 756

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
                |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db        757 TAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 816

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
               ||| ||||  |  |||| || |||||||| || |||||  |||||||||||||   |||
Db        817 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCAC 876

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
              |||||||||| |  | || ||  | || ||  | || || |
Db        877 CAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 917


RESULT 10
US-08-414-657D-5
; Sequence 5, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1014 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1014
;      OTHER INFORMATION:
US-08-414-657D-5

  Query Match             20.3%;  Score 340.6;  DB 2;  Length 1014;
  Best Local Similarity   61.9%;  Pred. No. 3.9e-83;
  Matches  595;  Conservative    0;  Mismatches  354;  Indels   12;  Gaps    3;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
              |||   |  |||| ||||||| |||||||  |||      ||   |  ||  | ||||||
Db         66 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 119

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
              | | || ||  |||||||||| |  |||| |||||||||     | ||  ||  |  | |
Db        120 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 179

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
                  ||||||||| | ||||||     |||| |||  |||||  | ||||||||||  ||
Db        180 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 239

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
              ||| ||||| || |  ||   ||    |        | | |||||| ||   ||||||||
Db        240 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 299

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
               |||||||| ||||| || ||  | ||||| ||||| || |||||| |  |  | || ||
Db        300 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 359

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
              |||||||   ||  || | ||||| |||||  | || || ||     | || || || ||
Db        360 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 419

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
              | || |  | ||||| || | |||| | | |||   |||||| || | |||  | || ||
Db        420 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 479

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
               |||    | || ||||||||| |  | ||    |     |  ||||   | ||||| ||
Db        480 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 539

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
              |||  |||| || |  ||||||||| |||| ||||||||  | |  |||||||  ||  |
Db        540 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 599

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
              ||| || ||  || |  | |  ||      ||| |||||||| ||||||||||||||
Db        600 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
              |||  ||||  | ||| | |   | | | ||   |||| | | |     ||  | |||||
Db        660 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 719

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
              ||||||||| || ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db        720 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 776

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
                |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db        777 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 836

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
               ||| ||||  |  |||| || ||||| || || |||||  |||||||||| |||  |||
Db        837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 896

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 1104
              |||||||||| |  | || ||  | || ||  | || ||    |  | ||||||  |
Db        897 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAG---AGGAATCAACGGATCCAT 953
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Qy       1105 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1164
               ||   ||| |      | ||||||||| |        | ||   ||| ||   |||||
Db        954 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCCTTCTCAGCAAATG 1013

Qy       1165 T 1165
              |
Db       1014 T 1014


RESULT 11
US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1014 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1014
;      OTHER INFORMATION:
US-09-135-080-7

  Query Match             20.3%;  Score 340.6;  DB 3;  Length 1014;
  Best Local Similarity   61.9%;  Pred. No. 3.9e-83;
  Matches  595;  Conservative    0;  Mismatches  354;  Indels   12;  Gaps    3;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
              |||   |  |||| ||||||| |||||||  |||      ||   |  ||  | ||||||
Db         66 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 119

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
              | | || ||  |||||||||| |  |||| |||||||||     | ||  ||  |  | |
Db        120 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 179

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
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                  ||||||||| | ||||||     |||| |||  |||||  | ||||||||||  ||
Db        180 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 239

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
              ||| ||||| || |  ||   ||    |        | | |||||| ||   ||||||||
Db        240 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 299

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
               |||||||| ||||| || ||  | ||||| ||||| || |||||| |  |  | || ||
Db        300 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 359

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
              |||||||   ||  || | ||||| |||||  | || || ||     | || || || ||
Db        360 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 419

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
              | || |  | ||||| || | |||| | | |||   |||||| || | |||  | || ||
Db        420 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 479

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
               |||    | || |||||||||| |  | ||    |     |  ||||   | ||||| ||
Db        480 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 539

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
              |||  |||| || |  |||||||||| ||||| ||||||||  | || |||||||  ||  |
Db        540 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 599

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
              ||| || ||  || |  | |  ||      ||| |||||||| ||||||||||||||
Db        600 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
              |||  ||||  | ||| | |  |  | | ||   |||| | | |   | ||  | |||||
Db        660 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 719

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
              ||||||||| || ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db        720 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 776

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
                |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db        777 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 836

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
               ||| ||||  |  |||| || ||||| || || |||||  |||||||||| |||  |||
Db        837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 896

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 1104
              |||||||||| |  | || ||  | || ||  | || ||    |  | ||||||  |
Db        897 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAG---AGGAATCAACGGATCCAT 953

Qy       1105 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1164
               ||   ||| |      | ||||||||| |        | ||   ||| ||   |||||
Db        954 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCCTTCTCAGCAAATG 1013

Qy       1165 T 1165
              |
Db       1014 T 1014

RESULT 12
US-08-414-657D-9
; Sequence 9, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  861 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...861
;      OTHER INFORMATION:
US-08-414-657D-9

  Query Match             20.2%;  Score 338.6;  DB 2;  Length 861;
  Best Local Similarity   63.7%;  Pred. No. 1.2e-82;
  Matches  531;  Conservative    0;  Mismatches  299;  Indels    3;  Gaps    1;

Qy        253 AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGA 312
              ||  | ||||||| | || ||  |||||||||| |  |||| ||||||||||  | | ||
Db         24 AGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGA 83

Qy        313 CAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA 372
                ||  |  | |   |||||||||| | |||||      |||| | | ||||||  ||||
Db         84 AGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGA 143

Qy        373 CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT 432
              ||||||||  ||||| || || || |  ||   ||    |        | | |||||| |
Db        144 CAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCT 203

Qy        433 CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGA 492
              |   |||||||| ||||||||| ||||| |||||  | ||||| ||||| || |||||| |
Db        204 CCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACA 263

Qy        493 CAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGA 552
                |  | || ||||||||    ||  || | || || |||||  | || || ||     |
Db        264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAA 323

Qy        553 GATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAAC 612
               || || || ||| || |  | ||||| || | |||  | |  ||   ||||||| || |
Db        324 TATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAA 383

Qy        613 TGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT 672
              |||  | || || |||    | || ||||||||| |  | || |  |     |  ||||
Db        384 TGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGA 443

Qy        673 GAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGA 732
                | ||||| |||||  |||| || |  ||||||||| ||||||||||||  |    ||
Db        444 AGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGA 503
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Qy        733 GTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAA 792
              |||||  ||  |||| || ||  || || |  |  ||      ||| |||| |||| |||||
Db        504 GTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAA 563

Qy        793 CTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGAC 852
              |||||| ||    ||  ||||| ||||| |  |  |  | | ||   |||| | | |   |
Db        564 CTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTC 623

Qy        853 ACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAA 912
              |||  | |||||| ||||| |||||| ||  || | || || ||||||||  ||||||||
Db        624 ACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACAC 683

Qy        913 AAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACT 972
               ||   |||  |  |    || ||  |  |  |  | | | |       ||  ||    ||
Db        684 TAG---GATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCT 740

Qy        973 CATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAA 1032
               |   |   ||| ||| ||||  |  |||| || ||||||| || || |||||  |||||||
Db        741 GACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAA 800

Qy       1033 GCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
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Db        801 GCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 853
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RESULT 13
US-08-414-657D-6
; Sequence 6, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  912 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...912
;      OTHER INFORMATION:
US-08-414-657D-6

  Query Match             20.2%;  Score 338.6;  DB 2;  Length 912;
  Best Local Similarity   63.7%;  Pred. No. 1.3e-82;
  Matches  531;  Conservative    0;  Mismatches  299;  Indels    3;  Gaps    1;

Qy        253 AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGA 312
              ||  | |||||||| | || ||  |||||||||| |  ||||| ||||||||||  | | ||
Db         24 AGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGA 83

Qy        313 CAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA 372
                ||  |  | |   |||||||||| | ||||      ||||| | | ||||||  ||||
Db         84 AGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGA 143

Qy        373 CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT 432
              ||||||||  ||||| || || || |  ||   ||    |        | | |||||| |
Db        144 CAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCT 203

Qy        433 CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGA 492
              |   |||||||| ||||||| | ||||| |||||  | ||||| ||||| || |||||| |
Db        204 CCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACA 263

Qy        493 CAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGA 552
                |  | || ||||||||    ||  || | || || |||||  | || || ||     |
Db        264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAA 323

Qy        553 GATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAAC 612
               || || || ||| || |  | ||||| || | ||   | |  ||   ||||||| || |
Db        324 TATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAA 383

Qy        613 TGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT 672
              |||  | || || |||    | || ||||||||| |  | || |  |     |  |||| 
Db        384 TGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGA 443

Qy        673 GAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGA 732
                | ||||| |||||  |||| || |  ||||||||| ||||||||||||  | || ||
Db        444 AGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGA 503

Qy        733 GTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAA 792
              |||||  ||  |||| || ||  || || |  |  ||      ||| |||| |||| |||||
Db        504 GTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAA 563

Qy        793 CTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGAC 852
              |||||| ||    ||  ||||| ||||| |  |  |  | | ||   |||| | | |   |
Db        564 CTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTC 623

Qy        853 ACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAA 912
              |||  | |||||| ||||| |||||| ||  || | || || ||||||||  ||||||||
Db        624 ACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACAC 683

Qy        913 AAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACT 972
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Db        684 TAG---GATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCT 740

Qy        973 CATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAA 1032
               |   |   ||| ||| ||||  |  |||| || ||||||| || || |||||  |||||||
Db        741 GACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAA 800

Qy       1033 GCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
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RESULT 14
US-08-414-657D-8
; Sequence 8, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  945 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...945
;      OTHER INFORMATION:
US-08-414-657D-8

  Query Match             20.1%;  Score 337.4;  DB 2;  Length 945;
  Best Local Similarity   63.1%;  Pred. No. 2.8e-82;
  Matches  556;  Conservative    0;  Mismatches  316;  Indels    9;  Gaps    2;

Qy        205 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
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Db         66 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 119

Qy        265 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 324
              | | || ||  ||||||||||| |  |||| |||||||||     | ||  ||  |  | |
Db        120 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 179

Qy        325 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 384
                  ||||||||| | ||||||     |||| |||  |||||  | ||||||||||  ||
Db        180 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 239

Qy        385 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 444
              ||| ||||| || |  ||   ||    |        | | |||||| ||   ||||||||
Db        240 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 299

Qy        445 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 504
               |||||||| ||||| || ||  | ||||| ||||| || |||||| |  |  | || ||
Db        300 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 359

Qy        505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 564
              |||||||   ||  || | ||||| |||||  | || || ||     | || || || ||
Db        360 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 419

Qy        565 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 624
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Db        420 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 479

Qy        625 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
               |||    | || ||||||||| |  | ||    |     |  ||||   | ||||| ||
Db        480 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 539

Qy        685 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 744
              |||  |||| || |  |||||||||| ||||  ||||||||  | || |||||||  ||  |
Db        540 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 599

Qy        745 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 804
              ||| || ||  || |  | |  ||      ||| |||||||| ||||||||||||||   
Db        600 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659

Qy        805 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 864
              |||  ||||  | ||| | |  |  | | ||   |||| | | |   | ||  | |||||
Db        660 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 719

Qy        865 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 924
              ||||||||| || ||  || | ||  || ||||||||  ||||||||  ||   |||  |
Db        720 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 776

Qy        925 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 984
                |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db        777 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 836

Qy        985 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 1044
               ||| ||||  |  |||| || ||||| || || |||||  ||||||||||| |||  |||
Db        837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 896

Qy       1045 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 1085
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RESULT 15
US-08-414-657D-10
; Sequence 10, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  861 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  Coding Sequence
;       LOCATION:  1...861
;       OTHER INFORMATION:
US-08-414-657D-10

  Query Match             19.9%;  Score 333.8;  DB 2;  Length 861;
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  Matches  528;  Conservative    0;  Mismatches  302;  Indels    3;  Gaps    1;

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Qy         313 CAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA 372
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Db          84 AGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGA 143

Qy         373 CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT 432
               ||||||||  ||||| ||||| || |  ||   ||    |        | | |||||| |
Db         144 CAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCT 203

Qy         433 CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGA 492
               | . |||||||| |||||||| ||||| || ||  | ||||| ||||| || |||||| |
Db         204 CCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACA 263

Qy         493 CAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGA 552
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Db         264 GCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAA 323

Qy         553 GATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAAC 612
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Db         324 CATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAA 383

Qy         613 TGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT 672
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Qy         673 GAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGA 732
                 | ||||| |||||  |||| || |  ||||||||| |||| ||||||||  | || ||
Db         444 AGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGA 503

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Qy         793 CTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGAC 852
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Qy         853 ACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAA 912
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                        GenCore version 5.1.6
              Copyright (c) 1993 - 2005  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:         June 15, 2005, 22:05:42 ; Search time 1109.23 Seconds
                                          (without alignments)
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Perfect score:  1679
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Scoring table:  IDENTITY_NUC
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Searched:       6046767 seqs, 3099530249 residues

Total number of hits satisfying chosen parameters:      12093534

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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  No.   Score   Match Length DB  ID                      Description
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   674  1601.4    95.4   1603  15  US-10-189-940-3           Sequence 3, Appli
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   677  1438.4    85.7   3987  20  US-10-723-860-7421        Sequence 7421, Ap
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   679  1432.8    85.3   1839  17  US-10-295-027-455         Sequence 455, App
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   685   891.8    53.1   1130  14  US-10-161-572-18          Sequence 18, Appl
   686   539.2    32.1   1478  14  US-10-161-572-35          Sequence 35, Appl
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   855   272.6    16.2   4834  15  US-10-219-065-1           Sequence 1, Appli
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   916     271    16.1   2383  17  US-10-104-047-995         Sequence 995, App
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   988   269.4    16.0   2840  17  US-10-210-028-611         Sequence 611, App
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 1007   269.4   16.0   2840  21  US-10-897-359-611         Sequence 611, App
 1008   269.4   16.0   2840  21  US-10-893-802-611         Sequence 611, App
 1009   269.4   16.0   2840  21  US-10-897-360-611         Sequence 611, App
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 1016     246   14.7   1169  17  US-10-015-115-27          Sequence 27, Appl
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OM nucleic - nucleic search, using sw model

Run on:          June 15, 2005, 23:29:51 ; Search time 6080.03 Seconds
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      Pred. No. is the number of results predicted by chance to have a
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  235     178   10.6    178  6  CB118055                 CB118055 K-EST0164
  236     178   10.6    909  5  BU132565                 BU132565 603120307
c 237   176.4   10.5    448  4  BG375509                 BG375509 UI-R-CV1-
  238   176.4   10.5    496  2  BF523086                 BF523086 UI-R-C2p-
  239     176   10.5    666  5  BM951674                 BM951674 UI-M-EG0-
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  241   175.2   10.4    795  1  AU080106                 AU080106 AU080106
  242   174.6   10.4    867  7  CO543917                 CO543917 LyEST116
c 243   174.4   10.4    572  2  BF407747                 BF407747 UI-R-BJ2-
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c 250   169.6   10.1    637  6  CB528708             CB528708 UI-H-FT2-
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  252     169   10.1    470  5  BX954423             BX954423 DKFZp781K
  253   167.8   10.0    791  7  CK308721             CK308721 SB02047A2
  254   167.4   10.0    923  1  AL583491             AL583491 AL583491
  255     167    9.9    617  6  BY730405             BY730405 BY730405
c 256   166.6    9.9    458  7  CO667956             CO667956 DG33-31f8
c 257   166.6    9.9    541  5  BU735309             BU735309 UI-E-DW0-
  258   166.2    9.9    566  7  CF977262             CF977262 2-84-B04.
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c 261   165.4    9.9    544  6  CA439326             CA439326 UI-H-DT1-
c 262   165.4    9.9    580  7  CN089827             CN089827 EC2BBA32B
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  265     164    9.8    773  4  BG208674             BG208674 RST28306
  266   163.2    9.7    894  6  CB199088             CB199088 AGENCOURT
c 267   162.4    9.7    424  1  AI556916             AI556916 UI-R-C2p-
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  277   157.4    9.4    169  7  T06151               T06151 EST04040 Fe
  278   157.2    9.4    858  2  BF676478             BF676478 602086277
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  281   156.4    9.3    884  5  BU323269             BU323269 603405983
  282   156.2    9.3    464  2  BB311856             BB311856 BB311856
  283   155.8    9.3    815  1  AU079716             AU079716 AU079716
  284   155.6    9.3    533  2  BB767692             BB767692 BB767692
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c 287     153    9.1    520  7  CK618674             CK618674 mk15a07.y
c 288   152.8    9.1    436  2  BE991815             BE991815 UI-M-BZ1-
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  294     149    8.9    547  6  BY727136             BY727136 BY727136
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  297   147.4    8.8    429  5  BY272572             BY272572 BY272572
  298   146.4    8.7    600  6  CA526928             CA526928 8023-83 M
  299   146.2    8.7    862  5  BP462754             BP462754 BP462754
  300     146    8.7    411  5  BY276562             BY276562 BY276562
  301   145.8    8.7    409  6  BY607794             BY607794 BY607794
  302   145.4    8.7    386  6  CB806970             CB806970 AMGNNUC:N
  303     145    8.6    418  5  BY278505             BY278505 BY278505
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c 307     144    8.6    511  1  AI415689             AI415689 mc70a03.x
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  309   143.4    8.5    878  5  BP165624             BP165624 BP165624
  310   142.2    8.5    535  9  AY409768             AY409768 Pan trogl
c 311   141.8    8.4    470  1  AI580850             AI580850 ta33e06.x
c 312   141.4    8.4    397  2  AW046074             AW046074 UI-M-BH1-
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  314   141.2    8.4    437  1  AA219849             AA219849 mv62c03.r
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  316   140.4    8.4    478  6  CA885050             CA885050 B0115E08-
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  318   140.4    8.4    969  6  BY718203             BY718203 BY718203
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  320   139.8    8.3    380  6  BY606458             BY606458 BY606458
  321   139.4    8.3    801  5  BU357013             BU357013 603475462
  322   139.4    8.3    809  2  BF304194             BF304194 601887043
  323   138.4    8.2    402  5  BY289266             BY289266 BY289266
  324   138.2    8.2    914  5  BX843874             BX843874 BX843874
  325     138    8.2    775  4  BI199955             BI199955 602761121
  326   137.8    8.2    530  5  BY480409             BY480409 BY480409
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  328   136.4    8.1    661  6  CA452139             CA452139 UI-M-FZ0-
c 329   136.2    8.1    304  7  CR472042             CR472042 CR472042
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  331   135.4    8.1    372  6  BY768835             BY768835 BY768835
  332   134.6    8.0    386  5  BY263646             BY263646 BY263646
  333   134.4    8.0    594  5  BU400899             BU400899 603481850
  334   134.2    8.0    778  7  CK315507             CK315507 SB02026A1
  335     134    8.0    855  5  BP158085             BP158085 BP158085
  336   130.6    7.8    700  7  CN458398             CN458398 UI-M-HN0-
  337   130.6    7.8    801  7  CK303983             CK303983 SB02022A1
c 338   129.4    7.7    372  2  BE990143             BE990143 UI-M-BZ1-
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  344   127.6    7.6    421  2  BB674781             BB674781 BB674781
  345   126.6    7.5    825  5  BP464677             BP464677 BP464677
  346     125    7.4    646  6  CA334396             CA334396 NISC_ls08
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  348   124.2    7.4    868  5  BQ672092             BQ672092 AGENCOURT
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  350   123.4    7.3    562  5  BU381982             BU381982 603582664
c 351     123    7.3    463  1  AI341423             AI341423 qx91e11.x
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  367   115.4    6.9    336  5  BY134531             BY134531 BY134531
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  370   113.8    6.8    579  7  CN089828             CN089828 EC2BBA32B
c 371   113.6    6.8    514  1  AI285235             AI285235 qk59h04.x
  372   112.8    6.7    665  9  BX243020             BX243020 Danio rer
c 373   112.4    6.7    528  2  AW490008             AW490008 UI-M-BH3-
c 374   112.4    6.7    582  7  CO626674             CO626674 DG9-278a2
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c 376   111.2    6.6    446  7  CO352257             CO352257 DR_AOV_SU
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  381   110.4    6.6    417  6  CA884109             CA884109 B0107H12-
c 382   110.4    6.6    782  8  AZ731274             AZ731274 RPCI-24-1
c 383   110.2    6.6    267  7  R75390               R75390 MDB0556 Mou
c 384   110.2    6.6    451  1  AA933871             AA933871 ol91d04.s
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  386     109    6.5    283  2  BB194430             BB194430 BB194430
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    394    105.6    6.3    394  9  AY400234                  AY400234 Pan trogl
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    409    100.8    6.0    483  8  AZ457316                  AZ457316 1M0260A07
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    420     97.2    5.8    656  2  BB617916                  BB617916 BB617916
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c   481     76.8    4.6    467  4  BI134406                  BI134406 UI-M-BH3-
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c   498     72.4    4.3    378  8  AZ089779                  AZ089779 RPCI-23-2
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    512       69    4.1    191  2  BB301025                  BB301025 BB301025
    513     68.6    4.1    581  7  CO879831                  CO879831 BovGen_08
    514     68.4    4.1    221  2  BB048644                  BB048644 BB048644
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    516     68.2    4.1    313  2  AW430704                  AW430704 70599 MAR
    517       68    4.1    223  2  BB380518                  BB380518 BB380518
c   518     67.6    4.0    514  7  CK769283                  CK769283 956841 MA
    519     67.2    4.0    821  5  BU389844                  BU389844 603511165
    520       67    4.0    417  1  AV589904                  AV589904 AV589904
    521       66    3.9    226  2  BB048138                  BB048138 BB048138
    522       66    3.9    433  4  BG515406                  BG515406 dae04h10.
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    524     65.8    3.9    726  5  BU395513                  BU395513 603404749
    525     65.6    3.9    502  4  BG078950                  BG078950 H3033H12-
    526       65    3.9    259  2  BB607028                  BB607028 BB607028
c   527     64.8    3.9    702  9  CNS02PTU                  AL208443 Tetraodon
c   528     64.4    3.8    527  1  AA741334                  AA741334 ob30f08.s
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c   532     62.6    3.7    539  1  AL918370                  AL918370 AL918370
    533     61.8    3.7    201  1  AV227064                  AV227064 AV227064
c   534     61.8    3.7    247  7  CR474371                  CR474371 CR474371
    535     61.8    3.7    550  7  CR544600                  CR544600 DKFZp459F
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c 540    60.4    3.6   484  5  BX099260          BX099260 BX099260
  541    60.2    3.6  1008  9  CL093894          CL093894 ISB1-24C2
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  543    59.6    3.5   420  6  CB798880          CB798880 AMGNNUC:N
c 544    59.6    3.5   845  4  BM042630          BM042630 603615963
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  546    58.6    3.5   276  2  BB268580          BB268580 BB268580
c 547    58.6    3.5   426  7  CK776772          CK776772 968132 MA
c 548    58.6    3.5   736  8  AZ989621          AZ989621 2M0273I04
c 549    58.4    3.5   242  4  BG980478          BG980478 MR3-CN014
c 550    58.4    3.5   565  7  CO590783          CO590783 DG2-41k22
  551    58.2    3.5   369  7  CO182357          CO182357 EC22490.5
  552    58.2    3.5   376  7  CO181363          CO181363 EC14144.5
  553    58.2    3.5   421  7  CO181992          CO181992 EC18396.5
  554    58.2    3.5   504  7  CO193442          CO193442 EC35796.5
  555    58.2    3.5   531  7  CO193920          CO193920 EC36996.5
  556    57.8    3.4   831  9  CNS011FZ          AL100217 Drosophil
  557    57.4    3.4   559  7  CF123525          CF123525 UI-HF-CH0
c 558      57    3.4   643  8  AQ327238          AQ327238 nbxb0040J
  559      57    3.4   841  5  BU530009          BU530009 AGENCOURT
  560    56.8    3.4   569  5  BP377634          BP377634 BP377634
  561    56.8    3.4   574  5  BP321522          BP321522 BP321522
  562    56.8    3.4   582  5  BP208357          BP208357 BP208357
  563    56.6    3.4   324  7  CO192533          CO192533 EC33980.5
c 564    56.6    3.4   502  7  CO691339          CO691339 DG11-30f1
  565    56.6    3.4   574  7  CO184164          CO184164 EC27256.5
c 566    56.6    3.4   964  9  CNS05CLJ          AL331264 Tetraodon
  567    56.4    3.4  1389  4  BI911314          BI911314 603062429
  568    56.2    3.3   481  7  CO180995          CO180995 EC13317.5
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  570    56.2    3.3  1119  6  CD050433          CD050433 AGENCOURT
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  572      56    3.3   710  7  CO961229          CO961229 pe19c10.y
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c 574      56    3.3  1472  9  CL490510          CL490510 SAIL_539_
c 575    55.8    3.3   929  9  CNS050XX          AL316158 Tetraodon
c 576    55.8    3.3  1376  9  AG320971          AG320971 Mus muscu
c 577    55.6    3.3   861  7  CK017071          CK017071 AGENCOURT
  578    55.4    3.3   311  4  BG193769          BG193769 RST12905
  579    55.4    3.3   555  7  CO878692          CO878692 BovGen_07
c 580    55.4    3.3   626  8  AZ385580          AZ385580 1M0144G07
  581    55.4    3.3   835  5  BU554638          BU554638 AGENCOURT
  582    55.2    3.3   285  6  CB986322          CB986322 AGENCOURT
  583    55.2    3.3   518  7  CN974991          CN974991 24676_125
  584    55.2    3.3   991  4  BG435647          BG435647 602506930
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  586      55    3.3   230  7  CO885649          CO885649 BovGen_13
  587      55    3.3   647  9  AG044222          AG044222 Pan trogl
  588      55    3.3  1043  6  CD385012          CD385012 AGENCOURT
  589      55    3.3  1123  5  BU502918          BU502918 AGENCOURT
  590    54.8    3.3   262  6  CB337385          CB337385 laa33a05.
  591    54.8    3.3   400  7  CF578533          CF578533 AGENCOURT
  592    54.8    3.3   684  7  CV274449          CV274449 WS0173.B2
c 593    54.6    3.3   204  4  BG980696          BG980696 MR3-CN014
  594    54.6    3.3   246  1  AL040243          AL040243 DKFZp434I
  595    54.6    3.3   348  6  CB829769          CB829769 ri04h12.y
  596    54.6    3.3   390  1  AA490022          AA490022 ab02b04.s
  597    54.6    3.3   434  6  CA399771          CA399771 EL01N0325
  598    54.6    3.3   478  6  CB179629          CB179629 EST0729 Z
  599    54.6    3.3   842  7  CK128791          CK128791 AGENCOURT
  600    54.6    3.3   844  9  CNS0052P          AL056652 Drosophil
  601    54.6    3.3   847  7  CK400611          CK400611 AGENCOURT
  602    54.6    3.3  1049  4  BG623609          BG623609 602648818
  603    54.6    3.3  1056  4  BG032994          BG032994 602300394
  604    54.4    3.2   625  7  CF921039          CF921039 gmrhRww3-
  605    54.4    3.2   637  7  CO541834          CO541834 gm_K005.2
  606    54.2    3.2   573  7  CF977921          CF977921 FAR17G1.R
  607    54.2    3.2   736  9  CNS03WTV          AL264172 Tetraodon
  608    54.2    3.2   749  5  BU534260          BU534260 AGENCOURT

  609    54.2    3.2   806  4  BI762516          BI762516 603048638
  610    54.2    3.2   859  6  CB319037          CB319037 AGENCOURT
c 611      54    3.2   212  4  BG981747          BG981747 MR3-CN014
c 612      54    3.2   241  4  BG980534          BG980534 MR3-CN014
  613      54    3.2   365  6  CB573833          CB573833 AGENCOURT
  614      54    3.2   774  1  AJ786997          AJ786997 AJ786997
  615      54    3.2  1176  5  BM927266          BM927266 AGENCOURT
c 616    53.8    3.2   244  2  BF362751          BF362751 RC1-NN007
  617    53.8    3.2   276  7  CO181006          CO181006 EC13331.5
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  621    53.8    3.2   350  7  CO191915          CO191915 EC32401.5
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  624    53.8    3.2   385  7  CO180258          CO180258 EC01313.5
  625    53.8    3.2   395  7  CO182619          CO182619 EC23422.5
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  627    53.8    3.2   450  7  CO194401          CO194401 EC38508.5
  628    53.8    3.2   452  7  CO193143          CO193143 EC35202.5
  629    53.8    3.2   464  7  CO183541          CO183541 EC25934.5
  630    53.8    3.2   487  7  CO195262          CO195262 EC39947.5
  631    53.8    3.2   490  7  CO180558          CO180558 EC02047.5
  632    53.8    3.2   523  7  CO183076          CO183076 EC24521.5
  633    53.8    3.2   524  7  CO182642          CO182642 EC23489.5
  634    53.8    3.2   547  7  CO185170          CO185170 EC29789.5
  635    53.8    3.2   552  7  CO194609          CO194609 EC38890.5
c 636    53.8    3.2   569  8  AQ394216          AQ394216 CITBI-E1-
  637    53.8    3.2   582  4  BG219746          BG219746 RST39511
  638    53.8    3.2   759  9  CNS06QXV          AL411257 T7 end of
  639    53.8    3.2   880  6  CD522648          CD522648 AGENCOURT
  640    53.8    3.2   913  7  CK157193          CK157193 FGAS03828
  641    53.8    3.2  1511  3  BC030320          BC030320 Mus muscu
  642    53.6    3.2   271  2  BB432888          BB432888 BB432888
  643    53.6    3.2   532  6  CA354283          CA354283 625969 NC
  644    53.6    3.2   551  1  AL036240          AL036240 DKFZp564J
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c 646    53.6    3.2   754  9  AG483752          AG483752 Mus muscu
  647    53.6    3.2   772  5  BU537238          BU537238 AGENCOURT
  648    53.6    3.2   778  4  BI859188          BI859188 603385268
c 649    53.6    3.2   893  7  CK196964          CK196964 FGAS00543
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  651    53.4    3.2   226  6  CD765502          CD765502 EST00188
  652    53.4    3.2   230  4  BF968205          BF968205 602268946
  653    53.4    3.2   363  2  BF076420          BF076420 225985 MA
  654    53.4    3.2   422  7  CV525233          CV525233 Mdlv4010h
  655    53.4    3.2   582  5  BP283085          BP283085 BP283085
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  661    53.4    3.2   880  7  CN835143          CN835143 AGENCOURT
  662    53.4    3.2   884  5  BU963135          BU963135 AGENCOURT
c 663    53.4    3.2   885  9  AG566030          AG566030 Mus muscu
  664    53.4    3.2   935  5  BU960555          BU960555 AGENCOURT
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  666    53.2    3.2   195  7  CF546382          CF546382 lae72e03.
  667    53.2    3.2   422  2  AW778899          AW778899 ho16e08.x
c 668    53.2    3.2   560  6  CB339387          CB339387 CA23EI03I
  669    53.2    3.2   609  6  CA367906          CA367906 643919 NC
  670    53.2    3.2   693  7  CK463316          CK463316 934211 MA
  671    53.2    3.2   712  9  CNS04AL2          AL281999 Tetraodon
  672    53.2    3.2   808  7  CF150373          CF150373 AGENCOURT
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  674    53.2    3.2   864  7  CK395877          CK395877 AGENCOURT
  675    53.2    3.2   869  5  BU938204          BU938204 AGENCOURT
  676    53.2    3.2   871  5  BU540167          BU540167 AGENCOURT
  677    53.2    3.2   895  5  BU588665          BU588665 AGENCOURT
  678    53.2    3.2   906  5  BU531084          BU531084 AGENCOURT
c 679    53.2    3.2  1101  9  CNS00KFT          AL077924 Drosophil
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c 684     53    3.2    432  1  AV665533               AV665533 AV665533
  685     53    3.2    659  9  AG083939               AG083939 Pan trogl
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  688     53    3.2    938  5  BU960786               BU960786 AGENCOURT
  689     53    3.2    941  7  CK420653               CK420653 AUF_IpTrk
c 690     53    3.2    999  5  BU426211               BU426211 603232486
c 691     53    3.2   1015  9  CL135318               CL135318 ISB1-106F
c 692     53    3.2   1293  9  AG346949               AG346949 Mus muscu
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  694   52.8    3.1    234  1  AV349585               AV349585 AV349585
  695   52.8    3.1    250  7  CO191457               CO191457 EC30893.5
  696   52.8    3.1    279  7  CR559257               CR559257 DKFZp468M
  697   52.8    3.1    295  7  CR630157               CR630157 DKFZp469M
c 698   52.8    3.1    302  2  BF362739               BF362739 RC1-NN007
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c 700   52.8    3.1    317  7  CN537157               CN537157 UI-M-HS0-
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  702   52.8    3.1    399  4  BG113662               BG113662 602284164
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  709   52.8    3.1    866  5  BU587173               BU587173 AGENCOURT
  710   52.8    3.1    914  5  BU563375               BU563375 AGENCOURT
  711   52.8    3.1    945  5  BU851541               BU851541 AGENCOURT
  712   52.8    3.1    947  6  CB205316               CB205316 AGENCOURT
  713   52.8    3.1   1131  4  BM542918               BM542918 AGENCOURT
  714   52.8    3.1   2186  3  CR749590               CR749590 Homo sapi
  715   52.6    3.1    274  7  CV072032               CV072032 EST4193 Z
  716   52.6    3.1    304  7  CN927725               CN927725 000530AEP
c 717   52.6    3.1    350  5  BX553079               BX553079 BX553079
  718   52.6    3.1    427  6  CA778567               CA778567 MPL384_9_
  719   52.6    3.1    493  7  CK377070               CK377070 lah97h03.
  720   52.6    3.1    504  6  CB678747               CB678747 OSJNEf01F
  721   52.6    3.1    560  4  BG924474               BG924474 HNC27-1-D
  722   52.6    3.1    659  6  CD771540               CD771540 AGENCOURT
  723   52.6    3.1    731  7  CF924696               CF924696 DD005C04.
  724   52.6    3.1    778  5  BU534338               BU534338 AGENCOURT
  725   52.6    3.1    811  6  CB951950               CB951950 AGENCOURT
  726   52.6    3.1    812  9  AG031898               AG031898 Pan trogl
  727   52.6    3.1    825  5  BU850748               BU850748 AGENCOURT
  728   52.6    3.1    829  7  CK794790               CK794790 AGENCOURT
  729   52.6    3.1    856  5  BU934849               BU934849 AGENCOURT
  730   52.6    3.1   1002  6  CB206065               CB206065 AGENCOURT
c 731   52.6    3.1   1380  9  AG311242               AG311242 Mus muscu
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  735   52.4    3.1    199  4  BJ699239               BJ699239 BJ699239
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  739   52.4    3.1    432  2  AW773386               AW773386 rp06c01.y
  740   52.4    3.1    490  7  CO874828               CO874828 BovGen_03
  741   52.4    3.1    562  2  AW636413               AW636413 bl46d05.w
  742   52.4    3.1    579  7  CF752690               CF752690 om_A001.0
  743   52.4    3.1    603  7  CN004672               CN004672 ip21e12.g
  744   52.4    3.1    619  7  CO535894               CO535894 tah10e04.
c 745   52.4    3.1    648  8  AZ379719               AZ379719 1M0135K02
  746   52.4    3.1    803  6  CB318690               CB318690 AGENCOURT
  747   52.4    3.1    826  4  BM041903               BM041903 603615963
  748   52.4    3.1    870  5  BU843763               BU843763 AGENCOURT
  749   52.4    3.1    873  6  CB844849               CB844849 M2PN-0411
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  751   52.4    3.1    887  5  BU850963               BU850963 AGENCOURT
  752   52.4    3.1    949  9  CNS00ZPI               AL097968 Drosophil
  753   52.4    3.1   1010  6  CD171719               CD171719 AGENCOURT
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  758   52.4    3.1   1699  3  HSM801509              AL133640 Homo sapi
  759   52.4    3.1   1775  9  CL513862               CL513862 SAIL_880_
c 760   52.4    3.1   1924  4  BI524436               BI524436 603051712
  761   52.2    3.1    207  7  CF890463               CF890463 TcTR-1266
c 762   52.2    3.1    211  4  BG981484               BG981484 MR3-CN014
  763   52.2    3.1    214  6  CA689180               CA689180 wlm96.pk0
  764   52.2    3.1    231  4  BM529684               BM529684 fy14h03.y
  765   52.2    3.1    234  7  CO193387               CO193387 EC35693.5
  766   52.2    3.1    276  7  CK379421               CK379421 lai11d07.
  767   52.2    3.1    289  5  BU764209               BU764209 sas54a02.
  768   52.2    3.1    290  5  BQ640732               BQ640732 he32e05.y
  769   52.2    3.1    301  7  CF622338               CF622338 laf02f12.
  770   52.2    3.1    308  7  CK375298               CK375298 lai48a03.
  771   52.2    3.1    352  7  CO181785               CO181785 EC14973.5
c 772   52.2    3.1    381  9  CNS03O01               AL252730 Tetraodon
  773   52.2    3.1    387  8  AZ878524               AZ878524 RPCI-23-1
  774   52.2    3.1    400  7  CK384950               CK384950 lah56e09.
  775   52.2    3.1    405  7  CF968846               CF968846 lag73f11.
  776   52.2    3.1    428  1  AV681953               AV681953 AV681953
  777   52.2    3.1    431  6  CB524077               CB524077 UI-M-GK0-
  778   52.2    3.1    445  7  CK632450               CK632450 AM1-AP000
  779   52.2    3.1    466  7  CK421958               CK421958 AUF_IpSpn
  780   52.2    3.1    473  4  BG622466               BG622466 602647179
  781   52.2    3.1    548  7  CK983417               CK983417 re24g03.y
  782   52.2    3.1    573  7  CV223060               CV223060 taj56f08.
  783   52.2    3.1    584  4  BJ519721               BJ519721 BJ519721
  784   52.2    3.1    614  6  CD251677               CD251677 AGENCOURT
  785   52.2    3.1    635  4  BG107420               BG107420 602277525
  786   52.2    3.1    688  7  CV522032               CV522032 0089P0069
  787   52.2    3.1    710  7  CN590804               CN590804 TTE000144
c 788   52.2    3.1    712  4  BJ532300               BJ532300 BJ532300
  789   52.2    3.1    723  7  CK451264               CK451264 904423 MA
  790   52.2    3.1    743  1  AV757929               AV757929 AV757929
  791   52.2    3.1    819  5  BU534439               BU534439 AGENCOURT
  792   52.2    3.1    846  5  BU564052               BU564052 AGENCOURT
  793   52.2    3.1    906  7  CK159239               CK159239 FGAS04064
  794   52.2    3.1   1000  4  BG572421               BG572421 602593463
  795     52    3.1    169  4  BJ703874               BJ703874 BJ703874
  796     52    3.1    172  5  BX504780               BX504780 DKFZp686F
  797     52    3.1    192  1  AA276487               AA276487 vc32e10.r
  798     52    3.1    202  7  CO883666               CO883666 BovGen_11
  799     52    3.1    228  7  CK381405               CK381405 lag38a01.
  800     52    3.1    243  4  BM187410               BM187410 fw17d12.y
  801     52    3.1    266  1  AA616347               AA616347 vn65b12.r
  802     52    3.1    403  6  CA366868               CA366868 642552 NC
  803     52    3.1    425  7  CF424254               CF424254 lad27b04.
c 804     52    3.1    461  6  CB348689               CB348689 CAB2SG000
  805     52    3.1    478  7  CF779197               CF779197 tad24e10.
  806     52    3.1    500  7  CK406831               CK406831 AUF_IfLvr
c 807     52    3.1    590  9  BX240864               BX240864 Danio rer
  808     52    3.1    615  4  BG435835               BG435835 602508457
  809     52    3.1    743  5  BU108854               BU108854 603112530
  810     52    3.1    852  5  BU946451               BU946451 AGENCOURT
c 811     52    3.1    882  7  CK160127               CK160127 FGAS04167
  812     52    3.1    935  6  CD384935               CD384935 AGENCOURT
  813     52    3.1    939  7  CN310359               CN310359 170005999
  814     52    3.1   1016  9  CNS016U9               AL107211 Drosophil
  815     52    3.1   1331  5  BM904910               BM904910 AGENCOURT
  816   51.8    3.1    194  5  BU530627               BU530627 AGENCOURT
  817   51.8    3.1    218  7  CO727269               CO727269 UMC-bend_
  818   51.8    3.1    225  4  BG736457               BG736457 rk57d03.y
  819   51.8    3.1    236  2  AW657557               AW657557 110971 MA
  820   51.8    3.1    252  4  BM531343               BM531343 fx86a07.y
c 821   51.8    3.1    269  4  BG980699               BG980699 MR3-CN014
c 822   51.8    3.1    278  4  BG983803               BG983803 MR4-CN014
  823   51.8    3.1    310  4  BM154701               BM154701 fv88c10.y
  824   51.8    3.1    311  4  BM154695               BM154695 fv88c02.y
  825   51.8    3.1    320  4  BM574233               BM574233 fx60g11.y
  826   51.8    3.1    320  5  BU709836               BU709836 fs44b03.y
  827   51.8    3.1    321  4  BM154709               BM154709 fv88d07.y
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   828    51.8    3.1    323  4  BM155040                 BM155040 fv92g05.y
   829    51.8    3.1    336  5  BQ783539                 BQ783539 fab30h11.
   830    51.8    3.1    340  4  BM155408                 BM155408 fw04e06.y
   831    51.8    3.1    345  4  BM534831                 BM534831 fx71h06.y
   832    51.8    3.1    351  1  AL724883                 AL724883 AL724883
   833    51.8    3.1    354  4  BM154696                 BM154696 fv88c03.y
   834    51.8    3.1    356  4  BM155084                 BM155084 fv93c11.y
   835    51.8    3.1    358  6  CB721263                 CB721263 jnn603C06
   836    51.8    3.1    439  1  AV682218                 AV682218 AV682218
   837    51.8    3.1    463  1  AV682001                 AV682001 AV682001
c  838    51.8    3.1    503  8  B08074                   B08074 T7G24-Sp6.1
   839    51.8    3.1    540  6  CA320990                 CA320990 UI-M-FV0-
c  840    51.8    3.1    557  9  CE135710                 CE135710 tigr-gss-
   841    51.8    3.1    563  7  CF805126                 CF805126 lad62f08.
   842    51.8    3.1    599  8  B16188                   B16188 347E7.TV CI
   843    51.8    3.1    606  6  CD239409                 CD239409 FNPBUB12
   844    51.8    3.1    610  8  B17639                   B17639 347E7.TVB C
   845    51.8    3.1    632  7  CV199140                 CV199140 km36h05.y
   846    51.8    3.1    674  6  CD638408                 CD638408 AGENCOURT
   847    51.8    3.1    700  6  CD640967                 CD640967 AGENCOURT
   848    51.8    3.1    747  9  CNS011RQ                 AL100640 Drosophil
   849    51.8    3.1    748  9  AG031854                 AG031854 Pan trogl
   850    51.8    3.1    780  7  CN323584                 CN323584 AGENCOURT
   851    51.8    3.1    797  5  BU555131                 BU555131 AGENCOURT
   852    51.8    3.1    804  5  BU530964                 BU530964 AGENCOURT
   853    51.8    3.1    814  5  BU566469                 BU566469 AGENCOURT
   854    51.8    3.1    820  6  CA464889                 CA464889 AGENCOURT
c  855    51.8    3.1    872  7  CK157539                 CK157539 FGAS03867
   856    51.8    3.1    877  3  BC040855                 BC040855 Homo sapi
   857    51.8    3.1    920  5  BU563586                 BU563586 AGENCOURT
   858    51.8    3.1    973  5  BQ721625                 BQ721625 AGENCOURT
   859    51.8    3.1    982  4  BG288697                 BG288697 602385510
   860    51.8    3.1   1084  5  BU189453                 BU189453 AGENCOURT
   861    51.8    3.1   1126  6  CD523341                 CD523341 AGENCOURT
   862    51.8    3.1   1452  9  CL125503                 CL125503 ISB1-87B2
   863    51.6    3.1    191  7  CK895966                 CK895966 SGP158500
   864    51.6    3.1    216  4  BJ699031                 BJ699031 BJ699031
   865    51.6    3.1    220  2  BE014996                 BE014996 126931 MA
c  866    51.6    3.1    254  4  BG981471                 BG981471 MR3-CN014
   867    51.6    3.1    300  7  CK428349                 CK428349 laj14g03.
   868    51.6    3.1    309  4  BM186118                 BM186118 fv98b09.y
   869    51.6    3.1    335  7  CF211902                 CF211902 CGF100066
   870    51.6    3.1    347  4  BM130321                 BM130321 pb29e10.y
   871    51.6    3.1    348  7  CK379136                 CK379136 lai31b08.
   872    51.6    3.1    375  1  AL713177                 AL713177 DKFZp686L
   873    51.6    3.1    432  7  CF337277                 CF337277 JMT--07-K
   874    51.6    3.1    438  4  BJ679676                 BJ679676 BJ679676
   875    51.6    3.1    484  4  BM342763                 BM342763 fw47g02.y
   876    51.6    3.1    495  5  BM903137                 BM903137 NXLV_080_
   877    51.6    3.1    577  4  BG927541                 BG927541 HNC10-1-B
   878    51.6    3.1    602  5  BU589676                 BU589676 AGENCOURT
   879    51.6    3.1    604  4  BG927528                 BG927528 HNC10-1-C
   880    51.6    3.1    607  1  AA522011                 AA522011 vh78c09.r
   881    51.6    3.1    617  4  BI829090                 BI829090 603079182
   882    51.6    3.1    627  6  CA330151                 CA330151 haa92b01.
c  883    51.6    3.1    643  4  BI870743                 BI870743 603392853
   884    51.6    3.1    673  6  CD770749                 CD770749 AGENCOURT
   885    51.6    3.1    697  6  CB319237                 CB319237 AGENCOURT
   886    51.6    3.1    761  5  BU555158                 BU555158 AGENCOURT
   887    51.6    3.1    771  7  CN831817                 CN831817 AGENCOURT
   888    51.6    3.1    780  9  CNS04I4Z                 AL291788 Tetraodon
c  889    51.6    3.1    787  9  AG364646                 AG364646 Mus muscu
   890    51.6    3.1    818  5  BU850480                 BU850480 AGENCOURT
   891    51.6    3.1    833  5  BU850474                 BU850474 AGENCOURT
   892    51.6    3.1    853  1  AV758844                 AV758844 AV758844
   893    51.6    3.1    855  7  CN330709                 CN330709 AGENCOURT
   894    51.6    3.1    856  2  BE909150                 BE909150 601501758
   895    51.6    3.1    866  7  CF765154                 CF765154 CES002716
   896    51.6    3.1    868  5  BU530888                 BU530888 AGENCOURT
   897    51.6    3.1    869  5  BU566247                 BU566247 AGENCOURT
   898    51.6    3.1    902  2  BF575271                 BF575271 602133679
   899    51.6    3.1    926  5  BU554921                 BU554921 AGENCOURT
   900    51.6    3.1    932  3  CR648408                 CR648408 Tetraodon
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   901    51.6    3.1    963  7  CF780924                 CF780924 AGENCOURT
c  902    51.6    3.1    968  5  BX381631                 BX381631 BX381631
c  903    51.6    3.1    969  7  CK426147                 CK426147 AUF_IpTes
   904    51.6    3.1   1002  5  BU590111                 BU590111 AGENCOURT
   905    51.6    3.1   1006  5  BU530175                 BU530175 AGENCOURT
   906    51.6    3.1   1035  6  CD246704                 CD246704 AGENCOURT
   907    51.6    3.1   1093  9  CNS04C0C                 AL283845 Tetraodon
   908    51.6    3.1   1122  4  BI259611                 BI259611 602968384
c  909    51.6    3.1   1333  9  AG390651                 AG390651 Mus muscu
   910    51.6    3.1   1426  4  BG388238                 BG388238 602413232
   911    51.4    3.1    201  2  AW102260                 AW102260 sd85d10.y
   912    51.4    3.1    232  4  BM280863                 BM280863 ki06b01.y
   913    51.4    3.1    252  4  BM574901                 BM574901 fx37e09.y
   914    51.4    3.1    277  6  CD722233                 CD722233 oj07b05.y
   915    51.4    3.1    334  7  CO194571                 CO194571 EC38826.5
c  916    51.4    3.1    361  1  AI819970                 AI819970 wj88h03.x
   917    51.4    3.1    366  7  CO722305                 CO722305 Mdfr3019o
   918    51.4    3.1    371  1  AV689111                 AV689111 AV689111
   919    51.4    3.1    372  7  CF331850                 CF331850 NACL--08-
   920    51.4    3.1    401  4  BG108147                 BG108147 602280213
c  921    51.4    3.1    440  4  BG944106                 BG944106 ax46e08.x
   922    51.4    3.1    441  4  BM285111                 BM285111 kh94h02.y
   923    51.4    3.1    464  5  BQ639526                 BQ639526 he16g12.y
   924    51.4    3.1    475  5  BQ093142                 BQ093142 fy94c12.y
   925    51.4    3.1    476  6  CB721269                 CB721269 jnn603D03
   926    51.4    3.1    487  5  BQ196890                 BQ196890 NXLV106_F
   927    51.4    3.1    557  6  CA779552                 CA779552 MPL384_12
   928    51.4    3.1    557  7  CF123296                 CF123296 UI-HF-CH0
   929    51.4    3.1    578  5  BP265719                 BP265719 BP265719
   930    51.4    3.1    583  6  CB073419                 CB073419 taa32f07.
   931    51.4    3.1    591  4  BI378442                 BI378442 BFLG1_000
   932    51.4    3.1    620  6  CA321372                 CA321372 UI-M-FV0-
   933    51.4    3.1    624  4  BG622353                 BG622353 602647035
c  934    51.4    3.1    702  8  AQ256508                 AQ256508 nbxb0016M
   935    51.4    3.1    720  6  CD641235                 CD641235 AGENCOURT
   936    51.4    3.1    762  7  CK655134                 CK655134 AGENCOURT
   937    51.4    3.1    783  7  CN385817                 CN385817 LE2TR04J2
   938    51.4    3.1    789  6  CB571699                 CB571699 AGENCOURT
   939    51.4    3.1    800  5  BU843107                 BU843107 AGENCOURT
   940    51.4    3.1    859  7  CN839423                 CN839423 AGENCOURT
   941    51.4    3.1    867  5  BU843011                 BU843011 AGENCOURT
   942    51.4    3.1    871  6  CB204789                 CB204789 AGENCOURT
   943    51.4    3.1    883  7  CK865669                 CK865669 AGENCOURT
   944    51.4    3.1    935  5  BQ958308                 BQ958308 AGENCOURT
   945    51.4    3.1    939  7  CN014330                 CN014330 AGENCOURT
   946    51.4    3.1    941  6  CB195504                 CB195504 AGENCOURT
   947    51.4    3.1    973  5  BU945046                 BU945046 AGENCOURT
   948    51.4    3.1    975  5  BU963322                 BU963322 AGENCOURT
   949    51.4    3.1   1011  6  CD388840                 CD388840 AGENCOURT
   950    51.4    3.1   1014  5  BU565689                 BU565689 AGENCOURT
c  951    51.4    3.1   1074  8  BZ696936                 BZ696936 SP__Ba009
   952    51.4    3.1   1101  9  CNS00ED1                 AL068937 Drosophil
   953    51.4    3.1   1112  5  BM920193                 BM920193 AGENCOURT
   954    51.4    3.1   2777  3  BC032411                 BC032411 Homo sapi
c  955    51.2    3.0    151  7  CF203260                 CF203260 RR890915N
c  956    51.2    3.0    185  4  BG980530                 BG980530 MR3-CN014
c  957    51.2    3.0    193  7  CK615915                 CK615915 ou07c12.y
c  958    51.2    3.0    199  4  BG981500                 BG981500 MR3-CN014
   959    51.2    3.0    201  4  BM265810                 BM265810 fw36b10.y
c  960    51.2    3.0    202  4  BG983780                 BG983780 MR4-CN014
   961    51.2    3.0    210  4  BM573150                 BM573150 fx98h10.y
   962    51.2    3.0    213  4  BM155328                 BM155328 fw02b03.y
c  963    51.2    3.0    217  4  BG981736                 BG981736 MR3-CN014
   964    51.2    3.0    218  4  BM154944                 BM154944 fv91e06.y
c  965    51.2    3.0    219  1  AL714277                 AL714277 AL714277
   966    51.2    3.0    219  4  BI709326                 BI709326 fs63b09.y
   967    51.2    3.0    219  4  BM154546                 BM154546 fv86d07.y
   968    51.2    3.0    220  4  BM573836                 BM573836 fy04f07.y
   969    51.2    3.0    225  4  BM154392                 BM154392 fv84e06.y
   970    51.2    3.0    225  4  BM186096                 BM186096 fv97h07.y
   971    51.2    3.0    230  4  BM186042                 BM186042 fv96h12.y
   972    51.2    3.0    231  7  CO181733                 CO181733 EC14891.5
   973    51.2    3.0    233  5  BQ786705                 BQ786705 saq72b12.
   974    51.2    3.0    234  4  BM154438            BM154438 fv85b03.y
   975    51.2    3.0    235  7  CF317850            CF317850 HD--07-L0
   976    51.2    3.0    237  4  BJ679532            BJ679532 BJ679532
   977    51.2    3.0    247  4  BM187242            BM187242 fw13g02.y
   978    51.2    3.0    248  4  BI704970            BI704970 fr60g09.y
   979    51.2    3.0    249  4  BJ682710            BJ682710 BJ682710
   980    51.2    3.0    254  4  BI705355            BI705355 fr57g11.y
   981    51.2    3.0    274  4  BM181089            BM181089 fv94a06.y
   982    51.2    3.0    278  7  CF123167            CF123167 UI-HF-CH0
   983    51.2    3.0    283  6  CB933364            CB933364 ri29a06.y
   984    51.2    3.0    302  7  CF514461            CF514461 CAbud0006
   985    51.2    3.0    304  7  CF613058            CF613058 laf32b10.
   986    51.2    3.0    312  7  CF382308            CF382308 lac61h10.
   987    51.2    3.0    328  5  BU763409            BU763409 sas42c02.
   988    51.2    3.0    336  7  CK372384            CK372384 lai84a11.
   989    51.2    3.0    336  7  CO509976            CO509976 tag91f07.
   990    51.2    3.0    340  6  CB084036            CB084036 hq08d08.b
   991    51.2    3.0    343  7  CK375218            CK375218 lai46h07.
   992    51.2    3.0    347  5  BU532791            BU532791 AGENCOURT
   993    51.2    3.0    397  6  CB257961            CB257961 85-E01113
c  994    51.2    3.0    412  7  CV354891            CV354891 MR4-EN007
   995    51.2    3.0    428  6  CA803003            CA803003 sau45g07.
c  996    51.2    3.0    453  4  BG959797            BG959797 CM2-CT077
   997    51.2    3.0    467  7  CF980284            CF980284 re03a12.y
   998    51.2    3.0    470  4  BM187391            BM187391 fw17a01.y
   999    51.2    3.0    470  5  BQ093110            BQ093110 fy94a03.y
c1000     51.2    3.0    488  6  CA811197            CA811197 CA22LI06I
  1001    51.2    3.0    489  1  AV682229            AV682229 AV682229
  1002    51.2    3.0    527  5  BM943015            BM943015 UI-M-BZ1-
  1003    51.2    3.0    530  4  BM573742            BM573742 fy03b10.y
  1004    51.2    3.0    538  1  AL925790            AL925790 AL925790
  1005    51.2    3.0    541  7  CN840817            CN840817 AGENCOURT
  1006    51.2    3.0    566  4  BM155067            BM155067 fv93a12.y
  1007    51.2    3.0    622  4  BG106619            BG106619 602290443
  1008    51.2    3.0    649  2  BF788814            BF788814 602110522
  1009    51.2    3.0    650  6  CD767936            CD767936 AGENCOURT
  1010    51.2    3.0    657  5  BQ078813            BQ078813 fy81c06.y
  1011    51.2    3.0    769  7  CV065944            CV065944 WNEL28f8
  1012    51.2    3.0    775  7  CK787487            CK787487 AGENCOURT
  1013    51.2    3.0    776  9  CNS009BD            AL053563 Drosophil
  1014    51.2    3.0    779  4  BG539542            BG539542 602568176
  1015    51.2    3.0    786  7  CF455765            CF455765 AGENCOURT
  1016    51.2    3.0    794  4  BI695737            BI695737 603345085
c1017     51.2    3.0    798  9  CNS010HK            AL098978 Drosophil
  1018    51.2    3.0    822  7  CN168497            CN168497 AGENCOURT
  1019    51.2    3.0    823  5  BU530830            BU530830 AGENCOURT
  1020    51.2    3.0    841  2  BF342119            BF342119 602012877
  1021    51.2    3.0    847  5  BU554569            BU554569 AGENCOURT
  1022    51.2    3.0    872  7  CK022958            CK022958 AGENCOURT
  1023    51.2    3.0    891  5  BU521330            BU521330 AGENCOURT
  1024    51.2    3.0    921  5  BU564012            BU564012 AGENCOURT
  1025    51.2    3.0    930  5  BU563671            BU563671 AGENCOURT
c1026     51.2    3.0    941  8  AZ539217            AZ539217 ENTEJ48TF
  1027    51.2    3.0    961  4  BM416004            BM416004 OP21087 M
  1028    51.2    3.0   1004  4  BG252914            BG252914 602365514
  1029    51.2    3.0   1005  9  AG417297            AG417297 Mus muscu
c1030     51.2    3.0   1017  8  BH155389            BH155389 ENTQX73TF
  1031    51.2    3.0   1027  6  CB205525            CB205525 AGENCOURT
  1032    51.2    3.0   1085  4  BG027405            BG027405 602296130
  1033    51.2    3.0   1087  7  CK231437            CK231437 ILLUMIGEN
c1034     51.2    3.0   1100  9  CL145579            CL145579 ISB1-146A
c1035     51.2    3.0   1101  9  CNS00186            AL058835 Drosophil
  1036    51.2    3.0   1101  9  CNS00EU8            AL069859 Drosophil
  1037    51.2    3.0   1609  9  CL080652            CL080652 CH216-159
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c1041       51    3.0    197  7  CF314022            CF314022 HD--02-G0
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  1046      51    3.0    228  7  CO182911            CO182911 EC24271.5
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  1049      51    3.0    248  7  CR772335            CR772335 DKFZp468M
  1050      51    3.0    261  4  BJ469921            BJ469921 BJ469921
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  1074      51    3.0    840  5  BU530592            BU530592 AGENCOURT
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  1076      51    3.0    860  7  CF289324            CF289324 AGENCOURT
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  1080      51    3.0    904  5  BU940115            BU940115 AGENCOURT
  1081      51    3.0    930  5  BU589620            BU589620 AGENCOURT
  1082      51    3.0    932  4  BM416498            BM416498 OP21593 M
  1083      51    3.0    944  6  CD051079            CD051079 AGENCOURT
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  1085      51    3.0    973  5  BU589938            BU589938 AGENCOURT
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  1093      51    3.0   1782  3  CR749618            CR749618 Homo sapi
  1094      51    3.0   2172  9  CL078016            CL078016 CH216-147
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  1106    50.8    3.0    264  1  AL598482            AL598482 DKFZp313J
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  1130    50.8    3.0    707  7  CV520959          CV520959 0089P0052
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 c1147    50.8    3.0    886  7  CK161161          CK161161 FGAS04285
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  1150    50.8    3.0    908  7  CV066886          CV066886 WNEL9e5 W
  1151    50.8    3.0    909  7  CK407058          CK407058 AUF_IfLvr
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 c1157    50.8    3.0    996  9  CNS04XL6          AL311811 Tetraodon
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  1161    50.8    3.0   1098  6  CD049441          CD049441 AGENCOURT
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 c1164    50.8    3.0   1227  9  AG361182          AG361182 Mus muscu
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 c1179    50.6    3.0    252  6  CB043981          CB043981 NISC_gc01
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  1186    50.6    3.0    348  6  CB704554          CB704554 AMGNNUC:S
  1187    50.6    3.0    375  3  AY068947          AY068947 Schmidtea
  1188    50.6    3.0    377  1  AL722378          AL722378 AL722378
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  1202    50.6    3.0    434  1  AJ791630          AJ791630 AJ791630
  1203    50.6    3.0    434  1  AL719646          AL719646 AL719646
  1204    50.6    3.0    436  1  AL729450          AL729450 AL729450
  1205    50.6    3.0    437  1  AV682737          AV682737 AV682737
  1206    50.6    3.0    444  6  CD239166          CD239166 FNPBLC12
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  1224    50.6    3.0    584  7  CV053519          CV053519 BNEL100b9
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  1230    50.6    3.0    624  5  BP382214          BP382214 BP382214
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  1238    50.6    3.0    772  5  BU958222          BU958222 AGENCOURT
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  1240    50.6    3.0    803  5  BU565241          BU565241 AGENCOURT
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  1250    50.6    3.0    832  9  CNS00818          AL051195 Drosophil
  1251    50.6    3.0    833  5  BU588052          BU588052 AGENCOURT
  1252    50.6    3.0    833  6  CB963986          CB963986 AGENCOURT
  1253    50.6    3.0    844  9  AG058605          AG058605 Pan trogl
  1254    50.6    3.0    845  5  BU537023          BU537023 AGENCOURT
  1255    50.6    3.0    853  5  BU588997          BU588997 AGENCOURT
  1256    50.6    3.0    854  5  BU603992          BU603992 AGENCOURT
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  1260    50.6    3.0    876  7  CN323414          CN323414 AGENCOURT
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  1262    50.6    3.0    883  9  CL067381          CL067381 CH216-110
  1263    50.6    3.0    886  9  CNS011SM          AL100672 Drosophil
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 c1265    50.6    3.0    888  7  CK160993          CK160993 FGAS04266
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  1267    50.6    3.0    904  4  BI859386          BI859386 603388113   |    1340    50.4    3.0    771  5  BU560352          BU560352 AGENCOURT
  1268    50.6    3.0    915  4  BG518636          BG518636 602578491   |    1341    50.4    3.0    777  2  BE875022          BE875022 601487588
  1269    50.6    3.0    915  5  BQ718652          BQ718652 AGENCOURT   |   c1342    50.4    3.0    778  9  AG586300          AG586300 Mus muscu
  1270    50.6    3.0    916  5  BU588527          BU588527 AGENCOURT   |    1343    50.4    3.0    787  5  BU536254          BU536254 AGENCOURT
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  1275    50.6    3.0    955  5  BU533926          BU533926 AGENCOURT   |    1348    50.4    3.0    844  9  AG129984          AG129984 Pan trogl
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  1277    50.6    3.0    956  7  CK423987          CK423987 AUF_IpSto   |    1350    50.4    3.0    873  7  CF455006          CF455006 AGENCOURT
  1278    50.6    3.0    960  6  CB597408          CB597408 AGENCOURT   |   c1351    50.4    3.0    877  7  CK159921          CK159921 FGAS04144
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  1280    50.6    3.0    978  4  BF969662          BF969662 602272040   |    1353    50.4    3.0    895  6  CB229191          CB229191 AGENCOURT
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  1283    50.6    3.0   1063  5  BU840218          BU840218 AGENCOURT   |    1356    50.4    3.0    916  9  CNS06VOC          AL417394 T3 end of
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  1320    50.4    3.0    501  6  CA336663          CA336663 NISC_lv03   |    1393    50.2    3.0    347  6  CB705238          CB705238 AMGNNUC:Y
  1321    50.4    3.0    518  7  CK431061          CK431061 oj57d12.y   |    1394    50.2    3.0    365  4  BI941631          BI941631 sc80f10.y
  1322    50.4    3.0    531  1  AL712171          AL712171 DKFZp686D   |    1395    50.2    3.0    374  7  CO878391          CO878391 BovGen_06
  1323    50.4    3.0    538  1  AV757416          AV757416 AV757416    |    1396    50.2    3.0    377  7  CO195922          CO195922 EC43542.5
  1324    50.4    3.0    568  7  CV285468          CV285468 tak47h02.   |    1397    50.2    3.0    378  7  CF124412          CF124412 UI-HF-CH0
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  1331    50.4    3.0    641  1  AV735039          AV735039 AV735039    |    1404    50.2    3.0    444  7  CF612777          CF612777 laf06b12.
  1332    50.4    3.0    643  5  BQ747828          BQ747828 UI-M-FA0-   |    1405    50.2    3.0    449  4  BI380861          BI380861 BFLG1_002
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 1433    50.2    3.0    883  5  BU181547                BU181547 AGENCOURT
 1434    50.2    3.0    891  7  CK169028                CK169028 FGAS04363
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 1444    50.2    3.0    993  5  BU565978                BU565978 AGENCOURT
c1445    50.2    3.0    996  9  CNS06HDU                AL398872 T7 end of
 1446    50.2    3.0    999  5  BU513295                BU513295 AGENCOURT
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 1450    50.2    3.0   1065  4  BG119329                BG119329 602349008
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                              ALIGNMENTS


RESULT 1
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LOCUS       AK045973                1808 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male corpora quadrigemina cDNA, RIKEN
            full-length enriched library, clone:B230328N06 product:NEUROTRIMIN
            PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
ACCESSION   AK045973
VERSION     AK045973.1  GI:26337738
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1808)
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  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match            66.7%;  Score 1119.4;  DB 3;  Length 1808;
  Best Local Similarity  83.1%;  Pred. No. 1.8e-278;
  Matches 1417;  Conservative    0;  Mismatches  251;  Indels   37;  Gaps   11;

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Db        839 ACGAAGAGTGAAGGTCACCGTGAACTATCCACCATACATCTCAGAAGCTAAGGGCACAGG 898

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RESULT 2
AK046377
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DEFINITION  Mus musculus adult male corpora quadrigemina cDNA, RIKEN
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            PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
ACCESSION   AK046377
VERSION     AK046377.1  GI:26338018
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1808)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
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ORIGIN

  Query Match             66.7%;  Score 1119.4;  DB 3;  Length 1808;
  Best Local Similarity   83.1%;  Pred. No. 1.8e-278;
  Matches 1417;  Conservative    0;  Mismatches  251;  Indels   37;  Gaps   11;

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Db         1548 GGGTGGGCAAGGGCTCAGCCACTCTGCCCACTAAAGTGCCCCACCATGAAACATTCTGGA 1607

Qy         1538 GCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATG---AGACCTTCCGGC 1594
                | |||||||||||||||  ||| ||||||||| || | || | |     | |    | |
Db         1608 GTTGGCCATCCCAAATTTCATCGGTCCATAGACACAAGCACAGAGCAAGAAACAAGGGCC 1667

Qy         1595 CCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAAC 1654
                  |   ||| | |   |||| ||||||| | |||||  ||    ||||||||  ||||
Db         1668 TTAGATGTGCCACGAAGGGCCCTTTGGTGGGCTGTGTGACAGTCGCGTGTGTCATGAAGT 1727

Qy         1655 GTGAAATAAAAAGAGCAAAAAAAAA 1679
                |||||||    ||    ||||||||
Db         1728 GTGAAATCTGGAGGAAGAAAAAAAA 1752


RESULT 3
CR602526
LOCUS       CR602526                2512 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DN005YD20 of Adult brain of Homo sapiens
            (human).
ACCESSION   CR602526
VERSION     CR602526.1  GI:50483333
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2512)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2512)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
```

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FEATURES             Location/Qualifiers
     source          1. .2512
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DN005YD20"
                     /tissue_type="Adult brain"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             60.4%;  Score 1014.6;  DB 3;  Length 2512;
  Best Local Similarity   90.4%;  Pred. No. 2.8e-251;
  Matches 1145;  Conservative    0;  Mismatches    4;  Indels  118;  Gaps    1;

Qy        531 AAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATA 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 AAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATA 160

Qy        591 TTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCT 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCT 220

Qy        651 CTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCC 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db        221 CTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCA 280

Qy        711 GGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTAC 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 GGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTAC 340

Qy        771 GGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGTACAGGTG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 GGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGTACAGGTG 400

Qy        831 TCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAAT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 TCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAAT 460

Qy        891 TCCAGTGGTACAAGGATGACAAAA------------------------------------ 914
              ||||||||||||||||||||||||
Db        461 TCCAGTGGTACAAGGATGACAAAAGAGCTGAAATCTCATTCACAGTTTGGTTATGATGGG 520

Qy        915 ------------------------------------------------------------ 914

Db        521 AAAGCTTCCTCCCCATGGTGGACGAATGGTGTCAAAACGGCCAGTGGGATCAATCAGCCT 580

Qy        915 ----------------------GACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAAC 952
                                    ||||||||||||||||||||||||||||||||||||||
Db        581 GACTTGCTCGCAGAATCCTCCCGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAAC 640

Qy        953 AGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTAC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 AGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTAC 700

Qy       1013 ACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 ACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCA 760

Qy       1073 GGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 GGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTG 820

Qy       1133 CCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGG 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 CCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGG 880

Qy       1193 GAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        881 GAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCA 940

Qy       1253 ATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGG 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        941 ATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGG 1000

Qy       1313 AGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCT 1372
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1001 AGGGGAACAAAGAATACTTTGGGGGGAAAAAAGTTTTAAAAAAGAAATTGAAAATTGCCT 1060

Qy       1373 TGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCC 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 TGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCC 1120

Qy       1433 GGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGC 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 GGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGC 1180

Qy       1493 TCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAA 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1181 TCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAA 1240

Qy       1553 TTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1241 TTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG 1300

Qy       1613 GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAA 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1301 GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAA 1360

Qy       1673 AAAAAAA 1679
               ||| ||
Db       1361 GAAAGAA 1367


RESULT 4
AY406347
LOCUS       AY406347                 874 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406347
VERSION     AY406347.1  GI:39762321
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .874
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. .>874
                     /locus_tag="HCM2527"
ORIGIN

  Query Match             50.7%;  Score 852;  DB 9;  Length 874;
  Best Local Similarity   99.3%;  Pred. No. 2.9e-209;
  Matches  868;  Conservative    0;  Mismatches    0;  Indels    6;  Gaps    1;
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Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 60

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 120

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 180

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 240

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 300

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAA--- 657
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAACC 360

Qy        658 ---AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA 714
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA 420

Qy        715 GCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAG 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAG 480

Qy        775 AGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCC 834
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCC 540

Qy        835 CGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCA 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCA 600

Qy        895 GTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAG 954
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAG 660

Qy        955 ACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACAC 1014
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACAC 720

Qy       1015 TTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGG 1074
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGG 780

Qy       1075 CGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC 1134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC 840

Qy       1135 TCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGA 1168
              ||||||||||||||||||||||||||||||||||
Db        841 TCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGA 874


RESULT 5
AY406348
LOCUS       AY406348                 773 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Pan troglodytes HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406348
VERSION     AY406348.1  GI:39762322
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 773)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 773)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..773
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1..>773
                     /locus_tag="HCM2527"
ORIGIN

  Query Match             44.3%;  Score 743.2;  DB 9;  Length 773;
  Best Local Similarity   98.4%;  Pred. No. 4.3e-181;
  Matches  761;  Conservative    0;  Mismatches    6;  Indels    6;  Gaps    1;

Qy        301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 60

Qy        361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 120

Qy        421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 180

Qy        481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||
Db        181 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCNNNTATCTCC 240

Qy        541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
              |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Db        241 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAACGAAGGGAACAATATCAGCCTCAC 300

Qy        601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAA--- 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        301 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCCCCCAAACC 360

Qy        658 ---AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA 714
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA 420

Qy        715 GCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAG 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAG 480

Qy        775 AGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCC 834
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCC 540

Qy        835 CGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCA 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCA 600
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Qy          895 GTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAG 954
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 GTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAG 660

Qy          955 ACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACAC 1014
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 ACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACAC 720

Qy         1015 TTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTG 1067
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 TTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTG 773


RESULT 6
BM807426
LOCUS       BM807426                1033 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  AGENCOURT_6581928 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5471935
            5', mRNA sequence.
ACCESSION   BM807426
VERSION     BM807426.1  GI:19124249
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1033)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1981  row: c  column: 08
            High quality sequence stop: 639.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5471935"
                     /tissue_type="amelanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_41"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             43.7%;  Score 733.4;  DB 4;  Length 1033;
  Best Local Similarity   92.5%;  Pred. No. 1.6e-178;
  Matches  830;  Conservative    0;  Mismatches   26;  Indels   41;  Gaps    4;

Qy          663 TTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAG 722
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Db            1 TTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAG 60

Qy          723 GGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGG 782
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 GGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGG 120

Qy          783 TCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGAC 842
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 TCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGAC 180

Qy          843 AAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACA 902
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 AAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACA 240

Qy          903 AGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCC 962
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Db          241 AGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCC 300

Qy          963 TCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGG 1022
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Db          301 TCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGG 360

Qy         1023 CCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTT---------------- 1066
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Db          361 CCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGAAGTGAAAACTACAG 420

Qy         1067 -----------------GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGA 1109
                                 |||||||||||||||||||||||||||||||||||||||||||
Db          421 CCCTGACCCCTTGGAAAGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGA 480

Qy         1110 GGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGAT 1169
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Db          481 GGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGAT 540

Qy         1170 GTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGC 1229
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 GTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGC 600

Qy         1230 AATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGC 1289
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 AATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGC 660

Qy         1290 CTCATGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTT 1349
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Db          661 CTCATGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAGAGTTTT 720

Qy         1350 AAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGGTACAATGGAGTTTCTTTTCCCA 1409
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Db          721 AAAAA--GAAATTGAAAATGCCTTGCAGATATTTAGGTACAATGGAGTTTCTTTTTCCC 778

Qy         1410 AACGGGAAGAACACAGCACACCC-GGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTC 1468
                ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          779 AACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTC 838

Qy         1469 TTTGGTGCCAGTGTGGG-----CAAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCC 1520
                ||| | |      ||||        ||| ||| |   |||||||||||| || ||||
Db          839 TTTTGGGGGCCAATGGGGGGCAAGGGGTTCATCTCTTCTGCCCACAGAATGGCCCC 895


RESULT 7
BM809227
LOCUS       BM809227                1083 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  AGENCOURT_6582414 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5468221
            5', mRNA sequence.
ACCESSION   BM809227
VERSION     BM809227.1  GI:19126050
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1083)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
```

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                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLCM1971  row: h  column: 14
                High quality sequence stop: 656.
FEATURES             Location/Qualifiers
     source          1. .1083
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5468221"
                     /tissue_type="amelanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_41"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             42.9%;  Score 720.2;  DB 4;  Length 1083;
  Best Local Similarity   91.7%;  Pred. No. 4.3e-175;
  Matches  853;  Conservative    0;  Mismatches   34;  Indels   43;  Gaps    7;

Qy          663 TTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAG 722
                |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db            1 TTGGCTTTGTGAGTGATGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAG 60

Qy          723 GGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGG 782
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Db           61 GGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGG 120

Qy          783 TCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGAC 842
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 TCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGAC 180

Qy          843 AAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACA 902
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 AAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACA 240

Qy          903 AGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCC 962
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy          963 TCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGG 1022
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Qy         1023 CCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTT---------------- 1066
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Db          361 CCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGAAGTGAAAACTACAG 420

Qy         1067 -----------------GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGA 1109
                                 |||||||||||||||||||||||||||||||||||||||||||
Db          421 CCCTGACCCCTTGGAAAGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGA 480

Qy         1110 GGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGAT 1169
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 GGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGAT 540

Qy         1170 GTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGC 1229
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 GTGAGTGCCACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGC 600

Qy         1230 AATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGC 1289
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Db          601 AATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGC 660

Qy         1290 CTCATGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTT-GGGGGGAAAAGAGTTT 1348
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Db          661 CTCATGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGGAAAAGAGTTT 720

Qy         1349 TAAAAAAGAAATTGAAAATTG-CCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCC 1407
                ||||||||||||||||||||| ||||||| |||||||||||||||||||||||  ||
Db          721 TAAAAAAGAAATTGAAAATTGCCCTTGCACATATTTAGGTACAATGGAGTTTTTCTTATT 780

Qy         1408 CAAACGGGAAGAACACAGCA----CACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCA 1463
                | ||   | | ||  || ||      || ||||||||||||||||||||||||||||||
Db          781 CCAAAACGGAAAAANCACCAGCACACCCGGGCTTGGACCCACTGCAAGCTGCATCGTGCC 840

Qy         1464 ACCTCTTTGGTGCCAGTGTGGG-CAAGGGCTCAGCC-TCTCTGCCCACAGAGTGCCCCCA 1521
                |||   |||||||||||||||| ||||||||||||| |||||||||||||| || |||||
Db          841 ACCCTCTTGGTGCCAGTGTGGGCCAAGGGCTCAGCCTTCTCTGCCCACAGAATGGCCCCA 900

Qy         1522 --CGTGGAACATTCTGGAGCTGGCCATCCC 1549
                     | ||||||||||| |||| |   ||
Db          901 ACGTGGAAACATTCTGGAACTGGGCCATCC 930


RESULT 8
AY406349
LOCUS       AY406349                 874 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406349
VERSION     AY406349.1  GI:39762323
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .874
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
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ORIGIN

  Query Match             42.3%;  Score 709.6;  DB 9;  Length 874;
  Best Local Similarity   89.1%;  Pred. No. 2.3e-172;
  Matches  779;  Conservative    0;  Mismatches   89;  Indels    6;  Gaps    1;

Qy          301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Db            1 GTGCACAATTGACAACCGAGTCACCCGGGTGGCCTGGCTAAACCGCAGTACCATCCTCTA 60

Qy          361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
                |||||| ||||||||||||||||| |||||||| |||||||| ||||| |||||||| ||
Db           61 TGCTGGAAATGACAAGTGGTGCCTAGATCCTCGTGTGGTCCTCCTGAGTAACACCCAGAC 120

Qy          421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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                ||||||||||| ||||||||||| ||||||||||| || ||||||||||| ||||||||
Db         121 CCAGTACAGCATTGAGATCCAGAATGTGGATGTGTACGATGAGGGCCCTTATACCTGCTC 180

Qy         481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
               ||| ||||||||||||||||| |||||||| ||||||||||||||||| |||||||||||
Db         181 GGTACAGACAGACAACCACCCTAAGACCTCCAGGGTCCACCTCATTGTACAAGTATCTCC 240

Qy         541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
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Db         241 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAACATCAGCCTCAC 300

Qy         601 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAA--- 657
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Db         301 TTGCATAGCCACAGGTAGACCGGAGCCTACAGTAACCTGGAGACATATTTCTCCCAAGCC 360

Qy         658 ---AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA 714
                  ||| ||||||||||||||||| || || ||| |||| || ||||||||||| |||||
Db         361 CGCAGCCGTTGGCTTTGTGAGTGAGGATGAGTACCTGGAGATCCAGGGCATCACTCGGGA 420

Qy         715 GCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAG 774
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Db         421 ACAGTCAGGCGAGTACGAGTGCAGCGCCTCCAACGACGTGGCGGCACCAGTGGTACGAAG 480

Qy         775 AGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCC 834
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Db         481 AGTGAAGGTCACCGTGAACTATCCACCATACATCTCAGAAGCTAAGGGCACAGGTGTCCC 540

Qy         835 CGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCA 894
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Db         541 CGTGGGGCAGAAGGGGACTCTGCAGTGTGAAGCTTCCGCAGTCCCTTCAGCAGAATTTCA 600

Qy         895 GTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAG 954
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Db         601 ATGGTTCAAGGATGACAAAAGACTGGTCGAAGGAAAGAAGGGAGTCAAAGTGGAAAACAG 660

Qy         955 ACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACAC 1014
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Db         661 ACCTTTCCTTTCAAAACTCACCTTTTTCAACGTCTCTGAACATGACTATGGGAACTACAC 720

Qy        1015 TTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGG 1074
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Db         721 ATGTGTGGCCTCCAACAAGCTGGGTCACACCAACGCCAGCATCATGCTATTTGGTCCCGG 780

Qy        1075 CGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC 1134
                || ||||| ||||| | ||| || || || ||||||||||||||| | ||||| || ||
Db         781 TGCTGTCAGTGAGGTCAACAATGGGACATCAAGGAGGGCAGGCTGCATTTGGCTCCTCCC 840

Qy        1135 TCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGA 1168
               |||||||||||| |||||||| ||||||||||||
Db         841 TCTTCTGGTCTTACACCTGCTCCTCAAATTTTGA 874


RESULT 9
BI666583
LOCUS       BI666583                 865 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603291469F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310833 5',
            mRNA sequence.
ACCESSION   BI666583
VERSION     BI666583.1  GI:15580816
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 865)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
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             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11787  row: j  column: 18
            High quality sequence stop: 742.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5310833"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length  clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

  Query Match             40.1%;  Score 674;  DB 4;  Length 865;
  Best Local Similarity   99.9%;  Pred. No. 3.8e-163;
  Matches  685;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy           1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
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Db          50 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 109

Qy          61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         110 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAG 169

Qy         121 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         170 AAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT 229

Qy         181 CTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC 240
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Qy         241 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG 300
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Qy         301 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 360
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Qy         361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 420
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Qy         421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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Db         470 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 529

Qy         481 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
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Qy         541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC-AATATTAGCCTCA 599
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Qy         660 CGGTTGGCTTTGTGAGTGAAGACGAA 685
                 ||||||||||||||||||||||||||
Db         710 CGGTTGGCTTTGTGAGTGAAGACGAA 735


RESULT 10
CR736885
LOCUS       CR736885                 673 bp    mRNA    linear   EST 27-AUG-2004
DEFINITION  CR736885 Homo sapiens library (Ebert L) Homo sapiens cDNA clone
            IMAGp971B1852 ; IMAGE:789137 5', mRNA sequence.
ACCESSION   CR736885
VERSION     CR736885.1  GI:51585450
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 673)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E.,
            Peters,M., Radelof,U. and Schneider,D.
  TITLE     I.M.A.G.E. cDNA Clone Collection
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Email: www.rzpd.de
            RZPD; IMAGp971B1852.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .673
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp971B1852 ; IMAGE:789137"
                     /clone_lib="Homo sapiens library (Ebert L)"
ORIGIN

  Query Match            39.9%;  Score 669.8;  DB 7;  Length 673;
  Best Local Similarity  99.7%;  Pred. No. 4.4e-162;
  Matches  671;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         945 TGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATG 1004
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 TGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATG 60

Qy        1005 GGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTAT 1064
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTAT 120

Qy        1065 TTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCT 1124
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCT 180

Qy        1125 GGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCC 1184
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCC 240

Qy        1185 CCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGAC 1244
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGAC 300

Qy        1245 AGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGACAGAAA 1304
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 AGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGACAGAAA 360

Qy        1305 TTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA 1364
                 ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         361 TTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAAAGTTTTAAAAAAGAAATTGAA 420

Qy        1365 AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACA 1424
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACA 480

Qy        1425 GCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGG 1484
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGG 540

Qy        1485 GCAAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCC 1544
                 ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         541 GCAAGGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCATGTGGAACATTCTGGAGCTGGCC 600

Qy        1545 ATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGG 1604
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 ATCCCAAATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGG 660

Qy        1605 CGCTGCGGGCACT 1617
                 |||||||||||||
Db         661 CGCTGCGGGCACT 673


RESULT 11
BU155617
LOCUS       BU155617                 856 bp    mRNA    linear   EST 03-SEP-2002
DEFINITION  AGENCOURT_7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839
            5', mRNA sequence.
ACCESSION   BU155617
VERSION     BU155617.1  GI:22669149
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13527  row: m  column: 16
            High quality sequence stop: 593.
FEATURES             Location/Qualifiers
     source          1. .856
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6166839"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match            39.6%;  Score 664.8;  DB 5;  Length 856;
  Best Local Similarity  97.6%;  Pred. No. 9.2e-161;
  Matches  728;  Conservative    0;  Mismatches   12;  Indels    6;  Gaps    5;

Qy        214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 153

Qy        274 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 213

Qy        334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 273

Qy        394 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 333

Qy        454 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 393

Qy        514 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 453

Qy        574 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 633
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 513

Qy        634 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 573

Qy        694 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 633

Qy        754 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 693

Qy        814 AGCCAAGGGTACAGGTGT-CCCCGTGGGACAAAAGGGGACACTGCAG-TGTGAAGCCTCA 871
              |||||||||||||||||| |||||||||||||||||||||||||||| |||||| |||||
Db        694 AGCCAAGGGTACAGGTGTCCCCCGTGGGACAAAAGGGGACACTGCAGTTGTGAAACCTCA 753

Qy        872 GCAGTCCCCTCAGCAG-AATTCCAGTGGTACAAGGATG-ACAAAAGACTGATT--GAAGG 927
              |||||||||||||||| ||||||||||||||| ||||| || |||||||||||   | ||
Db        754 GCAGTCCCCTCAGCAGAAATTCCAGTGGTACAGGGATGAACCAAAGACTGATTTGAAGGG 813

Qy        928 AAAGAAAGGGGTGAAAGTGGAAAACA 953
              ||| ||||||||| ||  ||  || |
Db        814 AAAAAAAGGGGTGGAAAGGGGGAAAA 839


RESULT 12
AL533026
LOCUS       AL533026                1027 bp    mRNA    linear   EST 24-MAR-2004
DEFINITION  AL533026 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
            CS0DN005YD20 5-PRIME, mRNA sequence.
ACCESSION   AL533026
VERSION     AL533026.3  GI:45707932
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1027)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:31070858.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 6387.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DN005DB10QP1&c=6387.f.
FEATURES             Location/Qualifiers
     source          1. .1027
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DN005YD20"
                     /tissue_type="ADULT BRAIN"
                     /dev_stage="adult"
                     /clone_lib="Homo sapiens ADULT BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN

  Query Match             38.4%;  Score 645;  DB 1;  Length 1027;
  Best Local Similarity   86.8%;  Pred. No. 1.3e-155;
  Matches  806;  Conservative    1;  Mismatches    1;  Indels  121;  Gaps    4;

Qy        531 AAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATA 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 AAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATA 161

Qy        591 TTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCT 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 TTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCT 221

Qy        651 CTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCC 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 CTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCC 281

Qy        711 GGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTAC 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTAC 341

Qy        771 GGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 GGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTG 401

Qy        831 TCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAAT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 TCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAAT 461

Qy        891 TCCAGTGGTACAAGGATGACAAAA------------------------------------ 914
              ||||||||||||||||||||||||
Db        462 TCCAGTGGTACAAGGATGACAAAAGAGCTGAAATCTCATTCACAGTTTGGTTATGATGGG 521

Qy        915 ------------------------------------------------------------ 914

Db        522 AAAGCTTCCTCCCCATGGTGGACGAATGGTGTCAAAACGGCCAGTGGGATCAATCAGCCT 581

Qy        915 ----------------------GACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAAC 952
                                    ||||||||||||||||||||||||||||||||||||||
Db        582 GACTTGCTCGCAGAATCCTCCCGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAAC 641

Qy        953 AGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGAACTAC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 AGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGAACTAC 701

Qy       1013 ACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         702 ACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCA 761

Qy        1073 GGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTG 1132
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         762 GGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTG 821

Qy        1133 CCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGG 1192
               ||||||||||||||||||||||||||||||||||||||||||| :|||||||||||||||
Db         822 CCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGT-SCACTTCCCCACCCGG 880

Qy        1193 GAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCA 1252
               ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         881 GAAAGGCTGCCGCCACCACCACCACCAACACAACAGC-ATGGCAACACCGACAGCAACCA 939

Qy        1253 ATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGG 1312
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         940 ATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGG 999

Qy        1313 AGGGGAACAAAGAATACTTTGGGGGGAAA 1341
               ||||| ||||||||||||||||||| |||
Db        1000 AGGGG-ACAAAGAATACTTTGGGGGAAAA 1027


RESULT 13
BI551784
LOCUS       BI551784                 732 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603197479F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277115 5',
            mRNA sequence.
ACCESSION   BI551784
VERSION     BI551784.1  GI:15439096
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 732)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11699  row: m  column: 20
            High quality sequence stop: 732.
FEATURES             Location/Qualifiers
     source          1..732
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5277115"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.5 kb and normalized to ROT 5. This is a
                     primary library enriched for  full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health).  Note: this
                     is a NIH_MGC Library."
ORIGIN

  Query Match             38.3%;  Score 643;  DB 4;  Length 732;
  Best Local Similarity   99.4%;  Pred. No. 3.9e-155;
  Matches  676;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy           1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          54 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACAC 113

Qy          61 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAA-AAAGAA 119
               ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         114 AATCTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAACAAAGAA 173

Qy         120 GAAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAA 179
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         174 GAAGAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAA 233

Qy         180 TCTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATG 239
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         234 TCTTCACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATG 293

Qy         240 CCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCA 299
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         294 CCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCA 353

Qy         300 GGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCT 359
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         354 GGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCT 413

Qy         360 ATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAA 419
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 ATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAA 473

Qy         420 CGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCT 479
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 CGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCT 533

Qy         480 CGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTC 539
               |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db         534 CGGTGCAGACAGACAANCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTC 593

Qy         540 CCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCA 599
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         594 CCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCA 653

Qy         600 CCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGG-AGACACATCTCTCCCAAA 658
               ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         654 CCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAAGACACATCTCTCCCAAA 713

Qy         659 GCGGTTGGCTTTGTGAGTGA 678
               |||| |||||||||||||||
Db         714 GCGG-TGGCTTTGTGAGTGA 732


RESULT 14
CN362539
LOCUS       CN362539                 748 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000470517655 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN362539
VERSION     CN362539.1  GI:47362473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 748)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 748   Std Error: 0.00.
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                     H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                     conditions."
ORIGIN

  Query Match             38.1%;  Score 640;  DB 7;  Length 748;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-154;
  Matches  640;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        214 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 273
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Db        109 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 168

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Qy        334 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 393
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Qy        514 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 573
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BE798585
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DEFINITION  601581610F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935955 5',
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ACCESSION   BE798585
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KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1039)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM779  row: d  column: 04
            High quality sequence stop: 849.
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                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
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                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match             37.8%;  Score 635.2;  DB 2;  Length 1039;
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Job time : 6280.03 secs
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          June 16, 2005, 02:42:13 ; Search time 4692.58 Seconds
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Perfect score:   1035
Sequence:        1 atgaaaaccatccagccaaa..........acctgcttctcaaattttga 1035

Scoring table:   IDENTITY_NUC
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Searched:        4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:      9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

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      Pred. No. is the number of results predicted by chance to have a
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    34     539   52.1   3069 10  RATCALMA                   M88709 Rattus norv
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    48   356.4   34.4   1158  5  GGLAMPG19                 Z94720 G.gallus mR
    49   354.8   34.3   2050  5  GGE19SPRO                 Y08171 Gallus gall
    50   348.4   33.7   1194  5  GGLAMPG11                 Z94719 G.gallus mR
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    54   340.6   32.9    924  6  AR030579                  AR030579 Sequence
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    67   331.8   32.1   1276 10  AY326256                   AY326256 Rattus no
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    87     271   26.2   2383  6  AX747470                  AX747470 Sequence
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   103   207.2   20.0  168745  2  AC119552              AC119552 Rattus no
   104   207.2   20.0  248329  2  AC109989              AC109989 Rattus no
c  105   205.6   19.9  110000  2  AC102028_1            Continuation (2 of
   106   193.6   18.7     352  6  AX886912              AX886912 Sequence
   107   193.6   18.7     352  6  BD026522              BD026522 Sequence
   108   180.4   17.4    5666  6  AX740565              AX740565 Sequence
   109   176.6   17.1     540  6  AX665354              AX665354 Sequence
   110   176.6   17.1  116069  2  AP000784              AP000784 Homo sapi
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   112   176.6   17.1  176676  2  AC012234              AC012234 Homo sapi
   113   176.6   17.1  177102  2  AP002808              AP002808 Homo sapi
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c  128   135.2   13.1  110000  2  AC102028_0            AC102028 Mus muscu
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c  132     121   11.7  152686  2  AC018913              AC018913 Homo sapi
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c  137   110.4   10.7  213331  2  AC125960              AC125960 Rattus no
   138   109.6   10.6  175963  2  AC148913              AC148913 Sus scrof
   139   109.4   10.6  134184  2  AC150028              AC150028 Canis fam
   140   108.8   10.5  186110  2  AC102204              AC102204 Mus muscu
   141     108   10.4  168861  2  AC130786              AC130786 Papio anu
   142     108   10.4  172146  2  AC130272              AC130272 Papio anu
c  143   107.8   10.4  169206 10   AC123550              AC123550 Mus muscu
c  144   107.8   10.4  277603  2  AC079543              AC079543 Mus muscu
   145   106.2   10.3  229330  2  AC137057              AC137057 Rattus no
   146   106.2   10.3  238070  2  AC134313              AC134313 Rattus no
c  147   106.2   10.3  242260  2  AC094567              AC094567 Rattus no
c  148   106.2   10.3  255120  2  AC127219              AC127219 Rattus no
c  149     106   10.2  142000  9  AC078813              AC078813 Homo sapi
   150   105.6   10.2     913  6  AR542162              AR542162 Sequence
   151   104.4   10.1  237376  2  AC124949              AC124949 Rattus no
c  152   104.4   10.1  277228  2  AC106911              AC106911 Rattus no
   153   102.2    9.9  131490 10   AC122207              AC122207 Mus muscu
   154   102.2    9.9  177251 10   AC124565              AC124565 Mus muscu
   155     102    9.9  187203  2  AP000832              AP000832 Homo sapi
c  156     102    9.9  202505  2  AP000912              AP000912 Homo sapi
   157     100    9.7     219  6  AR030583              AR030583 Sequence
   158      99    9.6  219713  2  AC112456              AC112456 Rattus no
   159      99    9.6  234283  2  AC114113              AC114113 Rattus no
c  160      99    9.6  250355  2  AC127766              AC127766 Rattus no
   161      99    9.6  263661  2  AC106603              AC106603 Rattus no
c  162      99    9.6  319104  2  AC106602              AC106602 Rattus no
   163    98.4    9.5     411  6  CQ731080              CQ731080 Sequence
   164    96.8    9.4  187746  2  AC087123              AC087123 Mus muscu
   165    95.2    9.2     219  6  AR030584              AR030584 Sequence
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c  166    92.6    8.9  214942 10   AC125214              AC125214 Mus muscu
   167    89.8    8.7  114269  2  AP002341              AP002341 Homo sapi
   168    89.8    8.7  152797  2  AC012134              AC012134 Homo sapi
c  169    89.8    8.7  159520  9  AC113009              AC113009 Homo sapi
   170    89.8    8.7  172128  2  AP000762              AP000762 Homo sapi
   171    89.8    8.7  190104  2  AP002831              AP002831 Homo sapi
   172    89.8    8.7  199079  9  AP000844              AP000844 Homo sapi
c  173      89    8.6     987  6  CQ734933              CQ734933 Sequence
c  174      89    8.6  170006  9  AP005122              AP005122 Homo sapi
   175      88    8.5     882  6  CQ732721              CQ732721 Sequence
c  176    87.2    8.4  163120  5  BX296535              BX296535 Zebrafish
c  177    87.2    8.4  180842  2  CR536619              CR536619 Danio rer
c  178    86.6    8.4  169582  2  AC102190              AC102190 Mus muscu
c  179    86.2    8.3   74368  9  AL391239              AL391239 Human DNA
c  180    86.2    8.3  131457  9  AL356600              AL356600 Human DNA
c  181    86.2    8.3  153852  2  AC009694              AC009694 Homo sapi
   182    86.2    8.3  315761  2  AL158079              AL158079 Homo sapi
   183    85.8    8.3  162247  2  AC102328              AC102328 Mus muscu
   184    85.4    8.3     295  6  CQ732164              CQ732164 Sequence
   185    84.4    8.2   36000  9  AP003166              AP003166 Homo sapi
   186    84.4    8.2  189323  2  AC150620              AC150620 Callithri
   187    84.4    8.2  191545  2  AC151029              AC151029 Callithri
   188    84.2    8.1  246900  2  AC128465              AC128465 Rattus no
   189      84    8.1  189037  2  AC150026              AC150026 Papio anu
c  190    83.4    8.1  162717 10   AC127259              AC127259 Mus muscu
   191    83.4    8.1  258847  2  AC112746              AC112746 Rattus no
   192    83.4    8.1  285603  2  AC104926              AC104926 Mus muscu
   193    81.8    7.9  110000  2  AC110642_3            Continuation (4 of
c  194    79.6    7.7  168191  2  AC151813              AC151813 Dasypus n
c  195    79.6    7.7  215743  2  AC148958              AC148958 Otolemur
   196    78.6    7.6     420  6  AX665356              AX665356 Sequence
c  197    78.6    7.6  113063  2  AC010946              AC010946 Homo sapi
c  198    78.6    7.6  191204  9  AP000843              AP000843 Homo sapi
   199    78.6    7.6  202505  2  AP000912              AP000912 Homo sapi
c  200    78.2    7.6  150308 10   AC098294              AC098294 Rattus no
   201    78.2    7.6  225433  2  AC106484              AC106484 Rattus no
   202    78.2    7.6  237199 10   AC094830              AC094830 Rattus no
   203      78    7.5  133989  2  AC149777              AC149777 Bos tauru
c  204      78    7.5  205738  4  AC150499              AC150499 Bos tauru
   205    77.8    7.5     177  6  AR030585              AR030585 Sequence
   206    77.8    7.5     177  6  AR030586              AR030586 Sequence
   207    76.8    7.4     479  6  AX665358              AX665358 Sequence
   208    76.6    7.4  259743  2  AC113965              AC113965 Mus muscu
   209    71.4    6.9     480  6  AX665357              AX665357 Sequence
   210    69.2    6.7   62350  9  AC067725              AC067725 Homo sapi
   211      69    6.7  146352  2  CR548641              CR548641 Danio rer
   212      69    6.7  186279  5  BX950870              BX950870 Zebrafish
c  213      69    6.7  191779  2  CR376789              CR376789 Danio rer
   214      67    6.5  176744  2  AC027631              AC027631 Homo sapi
   215    65.6    6.3     198  6  AR030587              AR030587 Sequence
c  216      65    6.3  195956  2  AC127626              AC127626 Rattus no
c  217      65    6.3  249701  2  AC106525              AC106525 Rattus no
   218    63.4    6.1     198  6  AR030588              AR030588 Sequence
   219    61.6    6.0     270  6  AX665353              AX665353 Sequence
c  220    60.8    5.9  117951  9  AL359821              AL359821 Human DNA
   221    60.8    5.9  199301  2  AC119938              AC119938 Mus muscu
   222    58.6    5.7    2000  6  AX655393              AX655393 Sequence
   223    58.6    5.7  166417 10   AC127685              AC127685 Mus muscu
   224    57.6    5.6     420  6  AX665355              AX665355 Sequence
c  225    57.6    5.6  142882  9  AP003029              AP003029 Homo sapi
c  226      56    5.4  193180  2  AC112588              AC112588 Rattus no
   227    55.4    5.4   34930  2  AC099999              AC099999 Mus muscu
   228    53.8    5.2  134609  2  AC021416              AC021416 Homo sapi
   229    53.8    5.2  150407  2  AC093228              AC093228 Homo sapi
   230    53.8    5.2  163538  9  AC012598              AC012598 Homo sapi
   231    52.2    5.0    2010  6  CQ586755              CQ586755 Sequence
   232    52.2    5.0    3927  3  DMU78177              U78177 Drosophila
   233    52.2    5.0    4052  3  AY060363              AY060363 Drosophil
c  234    52.2    5.0  189627 10   AC122934              AC122934 Mus muscu
   235      52    5.0    4807  9  HSM808173             BX648027 Homo sapi
   236      52    5.0  180842  2  CR536619              CR536619 Danio rer
   237      50    4.8    3806  5  AJ720876              AJ720876 Gallus ga
c  238    49.8    4.8    2000  6  AX655393              AX655393 Sequence
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   239    48.4    4.7   4073  6  AX269342             AX269342 Sequence
   240    48.4    4.7   8546  6  AX828406             AX828406 Sequence
   241    48.4    4.7   8546  9  HSA306906            AJ306906 Homo sapi
   242    48.4    4.7  18207  6  AX828384             AX828384 Sequence
   243    48.4    4.7  18207  9  AF156100             AF156100 Homo sapi
   244    47.6    4.6  63585  2  AC026983             AC026983 Homo sapi
c  245    47.6    4.6  84492  2  AC021676             AC021676 Homo sapi
   246      47    4.5 157263  2  BX957285             BX957285 Danio rer
   247    46.8    4.5   2229  6  CQ729908             CQ729908 Sequence
   248    46.6    4.5 172407  2  AC148515             AC148515 Sus scrof
   249    46.4    4.5   6267 10   AF315558             AF315558 Mus muscu
   250    46.4    4.5   6829 10   AY005483             AY005483 Mus muscu
c  251    46.2    4.5  68409  2  AC119994             AC119994 Mus muscu
   252      46    4.4   4641 10   RNU68726             U68726 Rattus norv
c  253    45.4    4.4   7218  6  I66494               I66494 Sequence 14
   254      45    4.3   4784  5  GDU07644             U07644 Gallus gall
   255      45    4.3  41219  9  AL135797             AL135797 Human DNA
   256      44    4.3   3498 10   RNU81035             U81035 Rattus norv
   257      44    4.3   3651 10   RNU81036             U81036 Rattus norv
   258      44    4.3   3752 10   AY061639             AY061639 Rattus no
   259      44    4.3   4465 10   MMU543322            AJ543322 Mus muscu
   260      44    4.3   4496  6  CQ715482             CQ715482 Sequence
   261      44    4.3   5071 10   AK129207             AK129207 Mus muscu
   262      44    4.3   5822 10   RATANKBIND           L11002 Rat ankyrin
   263      44    4.3 171637  2  AC116691             AC116691 Mus muscu
   264      44    4.3 228647  2  AC134289             AC134289 Rattus no
c  265      44    4.3 229948  2  AC126070             AC126070 Rattus no
c  266      44    4.3 262363  2  AC105703             AC105703 Rattus no
   267    43.8    4.2   4041  5  GGNEUFASC            X65224 G.gallus mR
   268    43.8    4.2 143045  9  AC008750             AC008750 Homo sapi
   269    43.2    4.2 195958  2  BX957263             BX957263 Danio rer
   270      43    4.2 157282  2  AC136089             AC136089 Rattus no
   271    42.6    4.1   1565 10   AF314149             AF314149 Mus muscu
   272    42.4    4.1   3588  6  CQ870412             CQ870412 Sequence
   273    42.4    4.1   4306  9  AK124736             AK124736 Homo sapi
   274    42.4    4.1   4479  9  HSTAG1               X68274 Homo sapien
   275    42.4    4.1   4548  6  AR453309             AR453309 Sequence
   276    42.4    4.1   4548  6  AX305052             AX305052 Sequence
   277    42.4    4.1   4548  9  HSTAG1A              X67734 H.sapiens m
   278    42.4    4.1   6137  6  CQ870414             CQ870414 Sequence
c  279    41.8    4.0 131042 10   AC110166             AC110166 Mus muscu
c  280    41.8    4.0 181463 10   AC122452             AC122452 Mus muscu
   281    41.8    4.0 268912  2  AC094291             AC094291 Rattus no
   282    41.6    4.0   1912  3  SAREGA1PT            X93601 S.americana
   283    41.6    4.0   5374  9  AF289030             AF289030 Homo sapi
   284    41.6    4.0   5387  6  CQ731799             CQ731799 Sequence
   285    41.6    4.0   6110  9  AF023449             AF023449 Homo sapi
   286    41.6    4.0   6413  9  AF023450             AF023450 Homo sapi
   287    41.6    4.0   6649  9  AF217525             AF217525 Homo sapi
c  288    41.6    4.0  79444  2  AC150153             AC150153 Gallus ga
   289    41.6    4.0 125020  9  AF429315             AF429315 Homo sapi
c  290    41.6    4.0 143178  2  AC150117             AC150117 Gallus ga
   291    41.6    4.0 166863  2  AC150140             AC150140 Gallus ga
c  292    41.6    4.0 199942  2  AC150038             AC150038 Gallus ga
   293    41.6    4.0 208621  2  AC150078             AC150078 Gallus ga
   294    41.4    4.0   2753 10   BC060263             BC060263 Mus muscu
   295    41.4    4.0 110000  1  BX571965_07          Continuation (8 of
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c  297    41.4    4.0 201324  2  AC149607             AC149607 Mus muscu
c  298    41.4    4.0 215601  2  AC073806             AC073806 Mus muscu
   299    41.4    4.0 223121  2  AC073726             AC073726 Mus muscu
   300    41.2    4.0   2083  6  AX590224             AX590224 Sequence
   301    41.2    4.0   2142  6  AX275019             AX275019 Sequence
   302    41.2    4.0   2397  6  AX392995             AX392995 Sequence
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   305    41.2    4.0   2633  6  AR380405             AR380405 Sequence
   306    41.2    4.0   2633  9  HSU63041             U63041 Human neura
   307    41.2    4.0   2756  6  AX590252             AX590252 Sequence
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   309    41.2    4.0   2960  6  AX658287             AX658287 Sequence
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   312    41.2    4.0   3266  6  CQ728451             CQ728451 Sequence
   313    41.2    4.0   3309  6  AX714869             AX714869 Sequence
   314    41.2    4.0   3309  9  AK057509             AK057509 Homo sapi
   315    41.2    4.0   4050  9  BC047244             BC047244 Homo sapi
   316    41.2    4.0   4290  9  BC014205             BC014205 Homo sapi
   317    41.2    4.0   5807  6  AR447664             AR447664 Sequence
   318    41.2    4.0   8513  6  AX207284             AX207284 Sequence
c  319    41.2    4.0 168144  2  CR792456             CR792456 Danio rer
c  320    41.2    4.0 192097  9  AC008743             AC008743 Homo sapi
   321      41    4.0   1140 10   BC034209             BC034209 Mus muscu
   322      41    4.0   2547 10   BC037721             BC037721 Mus muscu
   323      41    4.0   3470 10   BC045197             BC045197 Mus muscu
   324      41    4.0   3486 10   AY237727             AY237727 Mus muscu
   325      41    4.0   6021 10   AY237726             AY237726 Mus muscu
   326      41    4.0 249562 10   AL627327             AL627327 Mouse DNA
c  327    40.8    3.9 262336  2  AC006786             AC006786 Caenorhab
c  328    40.6    3.9 163399  2  AC079860             AC079860 Homo sapi
c  329    40.6    3.9 180569  9  AL354949             AL354949 Human DNA
c  330    40.6    3.9 186759  9  AL645608             AL645608 Human DNA
c  331    40.6    3.9 187746  2  AC087123             AC087123 Mus muscu
c  332    40.6    3.9 200491  2  AB107102             AB107102 Homo sapi
c  333    40.6    3.9 327883  2  BX571684             BX571684 Homo sapi
c  334    40.4    3.9  53661  2  AC134672             AC134672 Homo sapi
   335    40.4    3.9  82019  2  AC139567             AC139567 Homo sapi
   336    40.4    3.9 216161  9  AC087749             AC087749 Homo sapi
   337    40.2    3.9   2019 10   BC025840             BC025840 Mus muscu
   338    40.2    3.9   2811 10   AF487347             AF487347 Mus muscu
   339    40.2    3.9   4631  9  HSU72391             U72391 Human neoge
   340    40.2    3.9   5021  6  CQ729613             CQ729613 Sequence
   341    40.2    3.9   5292 10   AB093285             AB093285 Mus muscu
   342    40.2    3.9   5297  6  AX587800             AX587800 Sequence
   343    40.2    3.9   5297  6  AX771417             AX771417 Sequence
   344    40.2    3.9   5297  9  HSU61262             U61262 Human neoge
   345    40.2    3.9   5506  6  AR447897             AR447897 Sequence
   346    40.2    3.9  11850  4  AY136513             AY136513 Canis fam
   347    40.2    3.9  16799  2  AC020355             AC020355 Drosophil
   348    40.2    3.9  68727  3  AC004516             AC004516 Drosophil
c  349    40.2    3.9  71023  2  AC004426             AC004426 Drosophil
   350    40.2    3.9 193262  3  AC007579             AC007579 Drosophil
c  351    40.2    3.9 260367  3  AE003808             AE003808 Drosophil
   352      40    3.9 173062  9  AL445587             AL445587 Human DNA
   353    39.8    3.8   1623  6  AX298209             AX298209 Sequence
   354    39.8    3.8   3788  5  CHKKLGG              M63437 Chicken KLG
   355    39.8    3.8   5040 10  RATTAG1               M31725 Rat axonal
   356    39.8    3.8  18848  4  OCY14852             Y14852 Oryctolagus
   357    39.8    3.8 110000  2  BX255276_05          Continuation (6 of
   358    39.8    3.8 162208  9  AC073321             AC073321 Homo sapi
   359    39.8    3.8 225416 10   AC131744             AC131744 Mus muscu
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   361    39.6    3.8 124281 10   AL645976             AL645976 Mouse DNA
   362    39.4    3.8    741  6  AX756349             AX756349 Sequence
   363    39.4    3.8   2650  6  CQ882042             CQ882042 Sequence
   364    39.4    3.8   5992 10   BC058610             BC058610 Mus muscu
   365    39.4    3.8 234447  2  AC111017             AC111017 Mus muscu
   366    39.2    3.8    579 11   BV103163             BV103163 MARC 1613
   367    39.2    3.8    611 11   BV103131             BV103131 MARC 2423
c  368    39.2    3.8  63585  2  AC026983             AC026983 Homo sapi
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c  370      39    3.8    518  6  CQ782392             CQ782392 Sequence
c  371      39    3.8    518  6  BD125813             BD125813 Primer fo
c  372      39    3.8    518  6  BD127101             BD127101 Primer fo
   373      39    3.8   1883  6  CQ598923             CQ598923 Sequence
   374      39    3.8   2040  3  AY118318             AY118318 Drosophil
   375      39    3.8   2742  6  CQ782949             CQ782949 Sequence
   376      39    3.8   2742  6  BD127395             BD127395 Primer fo
   377      39    3.8   2742  9  AK074976             AK074976 Homo sapi
   378      39    3.8   3974  3  AY051554             AY051554 Drosophil
c  379      39    3.8   4012  6  CQ598922             CQ598922 Sequence
c  380      39    3.8   4057  6  CQ598919             CQ598919 Sequence
   381      39    3.8 148432  3  AC004642             AC004642 Drosophil
c  382      39    3.8 154840  3  AC099018             AC099018 Drosophil
   383      39    3.8 157851  2  AC020509             AC020509 Drosophil
c  384      39    3.8 160252  2  AC119373             AC119373 Rattus no
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c 385      39     3.8 163322  9  AC138389                  AC138389 Homo sapi
c 386      39     3.8 186241  9  AC103560                  AC103560 Homo sapi
  387      39     3.8 265053  2  AC098057                  AC098057 Rattus no
c 388      39     3.8 303823  3  AE003462                  AE003462 Drosophil
c 389    38.8     3.7   4285  6  CQ607487                  CQ607487 Sequence
  390    38.8     3.7   5913  6  CQ869760                  CQ869760 Sequence
  391    38.8     3.7   6656  10  AF334385                  AF334385 Rattus no
  392    38.8     3.7  13654  1  AE005754                  AE005754 Caulobact
c 393    38.8     3.7  48870  2  AC017807                  AC017807 Drosophil
  394    38.8     3.7  70712  2  AC135970                  AC135970 Homo sapi
c 395    38.8     3.7 155666  3  AC007854                  AC007854 Drosophil
c 396    38.8     3.7 168471  3  AC006170                  AC006170 Drosophil
  397    38.8     3.7 170056  2  AC087643                  AC087643 Homo sapi
c 398    38.8     3.7 188948  2  AC132884                  AC132884 Homo sapi
c 399    38.8     3.7 231562  3  AE003767                  AE003767 Drosophil
  400    38.6     3.7    607  3  AF254364                  AF254364 Drosophil
  401    38.6     3.7   2303  5  GGNEU9                    Y14344 Gallus gall
  402    38.6     3.7   2313  9  AK097802                  AK097802 Homo sapi
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  404    38.6     3.7   2462  9  AK090639                  AK090639 Homo sapi
  405    38.6     3.7   3525  6  CQ715490                  CQ715490 Sequence
  406    38.6     3.7   4398  5  D85084                    D85084 Cynops pyrr
  407    38.6     3.7   4955  9  AB018299                  AB018299 Homo sapi
  408    38.6     3.7 115292  9  AL391822                  AL391822 Human DNA
  409    38.6     3.7 161034  2  AL359927                  AL359927 Homo sapi
c 410    38.6     3.7 176522  2  AC018373                  AC018373 Homo sapi
c 411    38.6     3.7 182666  5  AL929172                  AL929172 Zebrafish
  412    38.6     3.7 349028  1  BX640413                  BX640413 Bordetell
  413    38.4     3.7    366  6  AR393998                  AR393998 Sequence
  414    38.4     3.7    591  6  AR393996                  AR393996 Sequence
  415    38.4     3.7    984  6  BD173702                  BD173702 Novel cel
  416    38.4     3.7   1062  6  CQ738382                  CQ738382 Sequence
  417    38.4     3.7   1523  6  BD173703                  BD173703 Novel cel
  418    38.4     3.7   1523  9  AK172835                  AK172835 Homo sapi
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   702     36    3.5 182573  2  AC120353          AC120353 Mus muscu
   703     36    3.5 190575  2  AC135024          AC135024 Rattus no
 c 704     36    3.5 192213  2  CR847542          CR847542 Danio rer
   705     36    3.5 194328  2  AC139902          AC139902 Rattus no
   706     36    3.5 199175  2  AC113055          AC113055 Mus muscu
   707     36    3.5 200673 10   AC131676          AC131676 Mus muscu
 c 708     36    3.5 235086  2  AC097672          AC097672 Rattus no
 c 709     36    3.5 310550  1  SCO939113         AL939113 Streptomy
   710   35.8    3.5    444  9  HSNRCAM           AJ001054 Homo sapi
   711   35.8    3.5    975  6  BD179599          BD179599 Highly th
   712   35.8    3.5   1731  6  AX433258          AX433258 Sequence
 c 713   35.8    3.5   1774  9  AF016029          AF016029 Homo sapi
   714   35.8    3.5   2734  6  AX954539          AX954539 Sequence
   715   35.8    3.5   3170 10   RNNCAM14          X06564 Rat mRNA fo
 c 716   35.8    3.5   3531  9  AF030112          AF030112 Homo sapi
   717   35.8    3.5   3574  4  BTADCYC           X16451 Bovine mRNA
   718   35.8    3.5   3900  9  HSC7NRCAM         AJ001057 Homo sapi
   719   35.8    3.5   3997  6  A87637            A87637 Sequence 1
   720   35.8    3.5   4134  9  HSU55258          U55258 Human hBRAV
   721   35.8    3.5   6218  9  AB002341          AB002341 Homo sapi
   722   35.8    3.5   6219  6  CQ716062          CQ716062 Sequence
   723   35.8    3.5   6240  9  HSM806153         BX538010 Homo sapi
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   725   35.8    3.5   6254  6  AX099489          AX099489 Sequence
   726   35.8    3.5   6384  6  AR448063          AR448063 Sequence
 c 727   35.8    3.5   6384  6  AR531706          AR531706 Sequence
 c 728   35.8    3.5  11085  1  AE004450          AE004450 Pseudomon
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 c 731   35.8    3.5  59339  9  AF287967          AF287967 Homo sapi
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 c 738   35.8    3.5 150151  9  AL356115          AL356115 Human DNA
   739   35.8    3.5 159246  9  AL590235          AL590235 Human DNA
 c 740   35.8    3.5 168215  9  AC009789          AC009789 Homo sapi
 c 741   35.8    3.5 168656  9  AC009108          AC009108 Homo sapi
   742   35.8    3.5 177203  9  AC074321          AC074321 Homo sapi
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 c 744   35.8    3.5 187386  9  AC103702          AC103702 Homo sapi
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   754   35.6    3.4   1932  6  AX078612          AX078612 Sequence
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   757   35.6    3.4  15597  3  AF074901          AF074901 Caenorhab
   758   35.6    3.4  41345  3  CEF15G9           Z47068 Caenorhabdi
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 c 767   35.6    3.4 185967  2  BX640499          BX640499 Danio rer
   768   35.6    3.4 187131  2  AP001535          AP001535 Homo sapi
 c 769   35.6    3.4 204548  5  AC145960          AC145960 Gallus ga
 c 770   35.6    3.4 209071  3  AC005285          AC005285 Drosophil
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   772   35.6    3.4 230267  5  BX324146          BX324146 Zebrafish
 c 773   35.6    3.4 280096  3  AE003613          AE003613 Drosophil
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 c 782   35.4    3.4   6741  6  E32987            E32987 Gene encodi
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 c 784   35.4    3.4  16524  3  AF369890S1        AF369890 Branchios
   785   35.4    3.4  37941  1  AOPCZA361         AJ223998 Amycolato
   786   35.4    3.4  58645  9  AC002068          AC002068 Homo sapi
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   788   35.4    3.4 110000  1  AE017180_12       Continuation (13 o
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   792   35.4    3.4 141988  2  AC109703          AC109703 Rattus no
   793   35.4    3.4 155628  1  AE016876          AE016876 Pseudomon
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 c 797   35.4    3.4 232240  2  AC150191          AC150191 Gallus ga
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 c 800   35.4    3.4 300425  1  AP005044          AP005044 Streptomy
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   803   35.2    3.4   2868  5  GGTRKC            X59669 G.gallus tr
   804   35.2    3.4   3157  5  S74248            S74248 trkC=tyrosi
   805   35.2    3.4   3606 10   AB107882          AB107882 Mus muscu
   806   35.2    3.4   4500  1  HMA277440         AJ277440 Haloarcul
   807   35.2    3.4  10242  6  CQ600663          CQ600663 Sequence
   808   35.2    3.4  11087  1  HMA429077         AJ429077 Haloarcul
 c 809   35.2    3.4  20978  6  CQ600662          CQ600662 Sequence
 c 810   35.2    3.4  23759  1  AE008802          AE008802 Salmonell
   811   35.2    3.4  27060  3  AB055927          AB055927 Procambar
   812   35.2    3.4  39115  2  AC019792          AC019792 Drosophil
   813   35.2    3.4  70398  3  DME271740         AJ271740 Drosophil
 c 814   35.2    3.4  83495  3  AC087076          AC087076 Caenorhab
   815   35.2    3.4 107595 10   BX571734          BX571734 Mouse DNA
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 c 819   35.2    3.4 136884  2  AC013397          AC013397 Homo sapi
 c 820   35.2    3.4 144056  3  AC091222          AC091222 Drosophil
 c 821   35.2    3.4 167281  2  AP001147          AP001147 Homo sapi
   822   35.2    3.4 173572  2  AC135112          AC135112 Mus muscu
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c 823    35.2    3.4 179661  2  AC134788          AC134788 Mus muscu
  824    35.2    3.4 184794  2  AP000849          AP000849 Homo sapi
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c 826    35.2    3.4 215434  2  AC019214          AC019214 Homo sapi
  827    35.2    3.4 233861  2  AC148064          AC148064 Bos tauru
  828    35.2    3.4 300550  1  AP005021          AP005021 Streptomy
c 829    35.2    3.4 315108  3  AE003473          AE003473 Drosophil
  830    35      3.4    879  6  E09376            E09376 Nucleotide
  831    35      3.4   1251  6  BD179636          BD179636 Highly th
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  833    35      3.4   1749  6  AR388820          AR388820 Sequence
c 834    35      3.4   2116  9  AK094031          AK094031 Homo sapi
  835    35      3.4   2771  9  HSCYP216          X58906 H.sapiens C
  836    35      3.4   2989  1  AF262989          AF262989 Klebsiell
  837    35      3.4   2989  1  AF262990          AF262990 Klebsiell
  838    35      3.4   3000  1  AY193871          AY193871 Thermus t
  839    35      3.4   3324  1  KPNASTAB          M31938 K.aerogenes
  840    35      3.4   3832  1  KPN131525         AJ131525 Klebsiell
  841    35      3.4   4044  9  BC002377          BC002377 Homo sapi
  842    35      3.4   4044  9  BC014626          BC014626 Homo sapi
  843    35      3.4   7447  1  AF012100          AF012100 Pseudomon
  844    35      3.4  11558  1  AE004652          AE004652 Pseudomon
c 845    35      3.4  41630  3  U97592            U97592 Caenorhabdi
  846    35      3.4  59030  9  AC067959          AC067959 Homo sapi
  847    35      3.4  63882  7  AY349011          AY349011 Burkholde
  848    35      3.4  72165  10  AL844574          AL844574 Mouse DNA
c 849    35      3.4  79405  10  AL928721          AL928721 Mouse DNA
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  853    35      3.4 110542  10  AC087042          AC087042 Rattus no
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  855    35      3.4 150797  2  AC026817          AC026817 Homo sapi
c 856    35      3.4 157463  8  AC136377          AC136377 Oryza sat
  857    35      3.4 159875  9  AC148692          AC148692 Macaca mu
  858    35      3.4 164176  2  AC080147          AC080147 Homo sapi
  859    35      3.4 164396  2  AC024961          AC024961 Homo sapi
c 860    35      3.4 165866  2  AC073202          AC073202 Homo sapi
c 861    35      3.4 170665  5  BX072563          BX072563 Zebrafish
c 862    35      3.4 174149  2  AC009688          AC009688 Homo sapi
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  865    35      3.4 176129  9  AP003061          AP003061 Homo sapi
c 866    35      3.4 177623  2  CR394571          CR394571 Danio rer
c 867    35      3.4 196137  10  AC097257          AC097257 Rattus no
c 868    35      3.4 199446  10  AC125069          AC125069 Mus muscu
c 869    35      3.4 229065  2  BX284665          BX284665 Danio rer
c 870    35      3.4 231332  10  AC096070          AC096070 Rattus no
  871    35      3.4 270418  1  AE017303          AE017303 Thermus t
c 872    35      3.4 296300  1  AP005035          AP005035 Streptomy
c 873    35      3.4 315041  2  AC106711          AC106711 Homo sapi
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  875    34.8    3.4   1563  3  AY051911          AY051911 Drosophil
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  879    34.8    3.4   3496  1  RLE427840         AJ427840 Rhizobium
  880    34.8    3.4   3718  1  AF005842          AF005842 Rhodobact
  881    34.8    3.4   4640  3  DMDTRK            X63453 D.melanogas
  882    34.8    3.4   4645  6  CQ591393          CQ591393 Sequence
  883    34.8    3.4   4645  6  CQ847776          CQ847776 Sequence
  884    34.8    3.4   4775  3  BT015249          BT015249 Drosophil
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  887    34.8    3.4  20348  6  CQ591392          CQ591392 Sequence
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  890    34.8    3.4  84246  3  AC002512          AC002512 Drosophil
  891    34.8    3.4  98816  10  AL928861          AL928861 Mouse DNA
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c 894    34.8    3.4 133079  8  AC146581          AC146581 Oryza sat
c 895    34.8    3.4 147205  8  AC146702          AC146702 Genomic s

c 896    34.8    3.4 153950  8  AC104429          AC104429 Oryza sat
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  901    34.8    3.4 178137  9  AC011302          AC011302 Homo sapi
  902    34.8    3.4 179937  9  CNS05TCV          AL355840 Human chr
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c 904    34.8    3.4 184393  9  AC018665          AC018665 Homo sapi
c 905    34.8    3.4 185351  9  AC015801          AC015801 Homo sapi
c 906    34.8    3.4 187733  2  AC151388          AC151388 Callithri
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c 919    34.8    3.4 266099  2  AC094795          AC094795 Rattus no
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  972    34.4    3.3   1179  6  BD167330           BD167330 Method of
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  974    34.4    3.3   1181  6  E51166             E51166 Method for
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ALIGNMENTS

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ACCESSION   CQ768055
VERSION     CQ768055.1  GI:45108887
KEYWORDS    .
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REFERENCE   1
  AUTHORS   Wood,W.I., Goddard,A., Gurney,A., Yuan,J., Baker,K.P. and Chen,J.
  TITLE     Human neurotrimin homologue
  JOURNAL   Patent: EP 1386931-A 522 04-FEB-2004;
            Genentech, Inc. (US)
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ORIGIN

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Qy        181 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 240
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy        241 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 300
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433
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Qy        301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        481 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960
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Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy       1021 CTTCTCAAATTTTGA 1035
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Db       1154 CTTCTCAAATTTTGA 1168

RESULT 2
AR528639
LOCUS       AR528639                1679 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 375 from patent US 6725730.
ACCESSION   AR528639
VERSION     AR528639.1  GI:53916717
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Bollinger,C.L. Jr.
  TITLE     Crane test weight assembly and method
  JOURNAL   Patent: US 6725730-A 375 27-APR-2004;
FEATURES             Location/Qualifiers
     source          1..1679
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1035;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-284;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         61 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy        121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy        181 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 240
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy        241 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 300
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        481 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 540
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960
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Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy       1021 CTTCTCAAATTTTGA 1035
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Db          1154 CTTCTCAAATTTTGA 1168


RESULT 3
AX358872
LOCUS       AX358872                1679 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 125 from Patent WO0193983.
ACCESSION   AX358872
VERSION     AX358872.1  GI:18675337
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0193983-A 125 13-DEC-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1679
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1035;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-284;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy             1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60
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Db           134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy            61 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
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Db           194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy           121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180
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Qy           181 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 240
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Qy           241 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 300
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Db           374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy           301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy           361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy           421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
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Db           554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy           481 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 540
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Db           614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy           541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
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Db           674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy           601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
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Db           734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy           661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720
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Db           794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy           721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780
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Db           854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy           781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
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Qy           841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900
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Db           974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy           901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960
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Db          1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy           961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy          1021 CTTCTCAAATTTTGA 1035
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Db          1154 CTTCTCAAATTTTGA 1168


RESULT 4
AX362365
LOCUS       AX362365                1679 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 125 from Patent WO0208288.
ACCESSION   AX362365
VERSION     AX362365.1  GI:18694640
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0208288-A 125 31-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1679
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ORIGIN

  Query Match             100.0%;  Score 1035;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-284;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy             1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60
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Db           134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy            61 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy           121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180
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Qy        181 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 240
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy        241 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 300
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        481 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 540
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780
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Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960
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Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy       1021 CTTCTCAAATTTTGA 1035
              |||||||||||||||
Db       1154 CTTCTCAAATTTTGA 1168


RESULT 5
AX403748
LOCUS       AX403748                1679 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 103 from Patent WO0077037.
ACCESSION   AX403748
VERSION     AX403748.1  GI:21437184
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A., Baker,K., Botstein,D., Desnoyers,L., Eaton,D.L.,
            Ferrara,N., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
            Goddard,A., Godowski,P., Gurney,A., Kljavin,I.J., Mather,J.,
            Napier,M., Pan,J., Paoni,N., Roy,M., Tumas,D., Watanabe,C.,
            Williams,P.M., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0077037-A 103 21-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1679
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1035;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-284;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         61 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
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Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy        121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

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Qy        481 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 540
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Qy        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780
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Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy       1021 CTTCTCAAATTTTGA 1035
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Db       1154 CTTCTCAAATTTTGA 1168


RESULT 6
AX454470
LOCUS       AX454470                1679 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 55 from Patent WO0208284.
ACCESSION   AX454470
VERSION     AX454470.1  GI:21713859
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0208284-A 55 31-JAN-2002;
            Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
            (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
            Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
            Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
            ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
            Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
            I. (US)
FEATURES             Location/Qualifiers
     source          1..1679
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1035;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-284;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

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Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
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RESULT 7
AX464242
LOCUS       AX464242                1679 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 375 from Patent WO0140466.
ACCESSION   AX464242
VERSION     AX464242.1  GI:21899137
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
            Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Wood,W.L. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            same
  JOURNAL   Patent: WO 0140466-A 375 07-JUN-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
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ORIGIN

  Query Match             100.0%;  Score 1035;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-284;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60
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Qy        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
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Qy        661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720
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Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
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Db       1154 CTTCTCAAATTTTGA 1168


RESULT 8
AX490948
LOCUS       AX490948                1679 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 55 from Patent WO0200690.
ACCESSION   AX490948
VERSION     AX490948.1  GI:22323811
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0200690-A 55 03-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
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ORIGIN

  Query Match             100.0%;  Score 1035;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-284;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60
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Qy        361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960
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Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy       1021 CTTCTCAAATTTTGA 1035
              |||||||||||||||
Db       1154 CTTCTCAAATTTTGA 1168


RESULT 9
AY358331
LOCUS       AY358331                1679 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA43316 HNT (UNQ297) mRNA, complete cds.
ACCESSION   AY358331
VERSION     AY358331.1  GI:37181786
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1679)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1..1679
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DNA43316"
     gene            1..1679
                     /locus_tag="UNQ297"
     CDS             134..1168
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                     /note="PRO337"
                     /codon_start=1
                     /product="HNT"
                     /protein_id="AAQ88697.1"
                     /db_xref="GI:37181787"
                     /translation="MKTIQPKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDN
                     VTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEI
                     QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIAT
                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVT
                     VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPF
                     LSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLP
                     LLVLHLLLKF"
ORIGIN

  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-284;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         61 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy        121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy        181 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy        241 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 300
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420
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Qy        421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
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Qy        481 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 540
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy       1021 CTTCTCAAATTTTGA 1035
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Db       1154 CTTCTCAAATTTTGA 1168


RESULT 10
AR439649
LOCUS       AR439649                1693 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 2 from patent US 6664383.
ACCESSION   AR439649
VERSION     AR439649.1  GI:42665573
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1693)
  AUTHORS   Fukushima,D., Shibayama,S. and Tada,H.
  TITLE     Polypeptides, cDNA encoding the same and utilization thereof
  JOURNAL   Patent: US 6664383-A 2 16-DEC-2003;
FEATURES             Location/Qualifiers
     source          1..1693
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1035;  DB 6;  Length 1693;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-284;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60
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Db        130 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 189

Qy         61 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 249

Qy        121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180
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Db        250 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 309

Qy        181 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 369

Qy        241 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 300
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Db        370 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 429

Qy        301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
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Db        430 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 489

Qy        361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420
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Db        490 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 549

Qy        421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
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Qy        541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
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Qy        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
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Db        730 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 789

Qy        661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720
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Db        790 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 849

Qy        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780
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Db        850 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 909

Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
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Db        910 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 969

Qy        841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900
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Qy        901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960
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Db       1030 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1089

Qy        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020
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Db       1090 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1149

Qy       1021 CTTCTCAAATTTTGA 1035
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Db       1150 CTTCTCAAATTTTGA 1164


RESULT 11
AR439648
LOCUS       AR439648                1032 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 1 from patent US 6664383.
ACCESSION   AR439648
VERSION     AR439648.1  GI:42665572
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1032)
  AUTHORS   Fukushima,D., Shibayama,S. and Tada,H.
  TITLE     Polypeptides, cDNA encoding the same and utilization thereof
  JOURNAL   Patent: US 6664383-A 1 16-DEC-2003;
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ORIGIN

  Query Match             99.7%;  Score 1032;  DB 6;  Length 1032;
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  Matches 1032;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGCAATCTTCACGGGGCTG 60

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Qy        121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180
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Db        121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180

Qy        181 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 240
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Qy        241 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 300
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Db        241 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 300

Qy        301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
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Db        301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360

Qy        361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420

Qy        421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480

Qy        481 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 540
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Qy        541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
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Db        541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600

Qy        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660

Qy        661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720
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Qy        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780
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Db        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780

Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840

Qy        841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900

Qy        901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960

Qy        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020

Qy       1021 CTTCTCAAATTT 1032
              ||||||||||||
Db       1021 CTTCTCAAATTT 1032


RESULT 12
AX665342
LOCUS       AX665342                1839 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 100 from Patent WO03002765.
ACCESSION   AX665342
VERSION     AX665342.1  GI:29290464
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sellar,G.C. and Gabra,H.
  TITLE     Cancer
  JOURNAL   Patent: WO 03002765-A 100 09-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .1839
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             92.1%;  Score 953.4;  DB 6;  Length 1839;
  Best Local Similarity   99.9%;  Pred. No. 1.3e-260;
  Matches  954;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         81 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 140
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Db        345 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 404

Qy        141 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 464

Qy        201 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 260
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Db        465 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 524

Qy        261 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 320
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Db        525 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 584

Qy        321 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 644

Qy        381 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 440
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Db        645 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 704

Qy        441 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 500
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Db        705 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 764

Qy        501 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 560
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Db        765 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 824

Qy        561 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 620
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Db        825 AATTCAGGGCATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 884
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Qy        621 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 680
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Db        885 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 944

Qy        681 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 740
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Db        945 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 1004

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Db       1005 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 1064

Qy        801 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 860
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Db       1065 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 1124

Qy        861 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 920
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Db       1185 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 1244

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Db       1245 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGA 1299


RESULT 13
AF126426
LOCUS       AF126426                1839 bp    mRNA    linear   PRI 10-JUN-2002
DEFINITION  Homo sapiens neurotrimin (HNT) mRNA, complete cds.
ACCESSION   AF126426
VERSION     AF126426.1  GI:7158997
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1839)
  AUTHORS   Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
  TITLE     Cloning and identification of human neurotrimin full length cDNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1839)
  AUTHORS   Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical
            Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
FEATURES             Location/Qualifiers
     source          1. .1839
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
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     CDS             265. .1299
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                     /codon_start=1
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                     /protein_id="AAF37591.1"
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                     QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIAT
                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVT
                     VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPF
                     LSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLP
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ORIGIN

  Query Match             92.1%;  Score 953.4;  DB 9;  Length 1839;
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  Best Local Similarity   99.9%;  Pred. No. 1.3e-260;
  Matches  954;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         81 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 404

Qy        141 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 464

Qy        201 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 524

Qy        261 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 320
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Db        525 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 584

Qy        321 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 380
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Db        585 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 644

Qy        381 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 440
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Db        645 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 704

Qy        441 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 500
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Db        705 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 764

Qy        501 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 560
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Db        765 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 824

Qy        561 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 620
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        825 AATTCAGGGCATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 884

Qy        621 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 680
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Qy        681 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 740
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Db        945 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGC 1004

Qy        741 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 800
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Db       1005 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 1064

Qy        801 AGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGA 860
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Qy        861 ACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAG 920
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Qy        921 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 980
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Db       1185 CATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGC 1244

Qy        981 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGA 1035
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Db       1245 AGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGA 1299


RESULT 14
AR439650
LOCUS       AR439650                 939 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 5 from patent US 6664383.
ACCESSION   AR439650
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VERSION     AR439650.1  GI:42665574
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   Fukushima,D., Shibayama,S. and Tada,H.
  TITLE     Polypeptides, cDNA encoding the same and utilization thereof
  JOURNAL   Patent: US 6664383-A 5 16-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .939
                     /organism="unknown"
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ORIGIN

  Query Match             90.7%;  Score 939;  DB 6;  Length 939;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-256;
  Matches  939;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         154 AGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGC 213
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGC 120

Qy         214 AGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTG 273
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 AGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTG 180

Qy         274 AGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGC 333
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 AGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGC 240

Qy         334 CCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATT 393
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATT 300

Qy         394 GTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC 453
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC 360

Qy         454 AATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACAC 513
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Db         361 AATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACAC 420

Qy         514 ATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATC 573
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Db         421 ATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATC 480

Qy         574 ACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTG 633
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Qy         634 GTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACA 693
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Qy         694 GGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCA 753
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Qy         814 GAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGG 873
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Db         721 GAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGG 780

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Qy         994 CTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 1032
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RESULT 15
AX665344
LOCUS       AX665344                1068 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 102 from Patent WO03002765.
ACCESSION   AX665344
VERSION     AX665344.1  GI:29290465
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sellar,G.C. and Gabra,H.
  TITLE     Cancer
  JOURNAL   Patent: WO 03002765-A 102 09-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             88.0%;  Score 910.4;  DB 6;  Length 1068;
  Best Local Similarity   96.6%;  Pred. No. 2.2e-248;
  Matches  954;  Conservative    0;  Mismatches    1;  Indels   33;  Gaps    1;

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Qy         141 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 200
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Qy         201 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 260
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Db         261 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 320

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Qy         381 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 440
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Db         381 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 440

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Db         441 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 500

Qy         501 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         501 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 560

Qy         561 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 620
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Db         561 AATTCAGGGCATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 620
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Qy        621 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 680
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Qy        741 AGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAA 800
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Qy        921 CATCATGCTATTT---------------------------------GGTCCAGGCGCCGT 947
              |||||||||||||                                 ||||||||||||||
Db        921 CATCATGCTATTTGAAGTGAAAACTACAGCCCTGACCCCTTGGAAAGGTCCAGGCGCCGT 980

Qy        948 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT 1007
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Qy       1008 GGTCTTGCACCTGCTTCTCAAATTTTGA 1035
              ||||||||||||||||||||||||||||
Db       1041 GGTCTTGCACCTGCTTCTCAAATTTTGA 1068

Search completed: June 16, 2005, 10:22:55
Job time : 4832.58 secs
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                          GenCore version 5.1.6
Run on:          June 15, 2005, 23:29:46 ; Search time 605.593 Seconds
                                          (without alignments)
                                          10117.241 Million cell updates/sec
Title:           US-10-017-084A-522_COPY_134_1168
Perfect score:   1035
Sequence:        1 atgaaaaccatccagccaaa..........acctgcttctcaaattttga 1035
Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched:        4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters:      8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries
Database :       N_Geneseq_16Dec04:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002as:*
                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10:  geneseqn2003cs:*
                 11:  geneseqn2003ds:*
                 12:  geneseqn2004as:*
                 13:  geneseqn2004bs:*
      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
                                    SUMMARIES
   No.   Score  Match Length DB  ID                       Description
RESULT 1
ID   AAZ34324 standard; cDNA; 1679 BP.
DE   Human PRO337 nucleotide sequence.
PN   WO9946281-A2.
PD   16-SEP-1999.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 2;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 2
ID   AAC78590 standard; cDNA; 1679 BP.
DE   Human PRO337 nucleotide sequence SEQ ID NO:522.
PN   WO200053756-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 3;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 3
ID   AAC87037 standard; cDNA; 1679 BP.
DE   Nucleotide sequence of human polypeptide PRO337.
PN   WO200077037-A2.
PD   21-DEC-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 4;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 4
ID   AAS21431 standard; cDNA; 1679 BP.
DE   Human cDNA sequence encoding for PRO337 polypeptide.
PN   WO200140466-A2.
PD   07-JUN-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 4;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 5
ID   ABK33598 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO protein, Seq ID No 125.
PN   WO200208288-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
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  Query Match             100.0%;  Score 1035;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 6
ID   ABL88099 standard; cDNA; 1679 BP.
DE   Human PRO337 cDNA sequence SEQ ID NO:55.
PN   WO200200690-A2.
PD   03-JAN-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 7
ID   ABL95588 standard; cDNA; 1679 BP.
DE   Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.
PN   WO200208284-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             100.0%;  Score 1035;  DB 6;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 8
ID   ACA63892 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2002192706-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 9
ID   ACA03790 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003036180-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 10
ID   ACA04996 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003032063-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 11
ID   ACA72056 standard; cDNA; 1679 BP.
DE   Human secreted and transmembrane PRO polypeptide #37 cDNA.
PN   US2002177553-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 12
ID   ABX89328 standard; cDNA; 1679 BP.
DE   DNA encoding novel secreted and transmembrane protein PRO337.
PN   US2003017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
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RESULT 13
ID   ABX92696 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO337 polypeptide.
PN   US2002169284-A1.
PD   14-NOV-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 14
ID   ACD41982 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #188.
PN   US2003036179-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 15
ID   ACA60526 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2002177165-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 16
ID   ACA04516 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 DNA.
PN   US2003032062-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 17
ID   ACA66437 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO337.
PN   US2003004102-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 18
ID   ACA68559 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088063-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 19
ID   ACA04211 standard; cDNA; 1679 BP.
DE   Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 8;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 20
ID   ACA65657 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO337.
PN   US2003032057-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 21
ID   ADA45894 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 22
ID   ADA76325 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 23
ID   ABT44288 standard; cDNA; 1679 BP.
DE   Human PRO337 cDNA.
PN   US2003050448-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 24
ID   ADA18975 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003054517-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 25
ID   ADA61598 standard; cDNA; 1679 BP.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 26
ID   ADB19383 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 27
ID   ADB27924 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 28
ID   ADA86403 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 29
ID   ADB15967 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 30
ID   ADA47753 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 31
ID   ADA67548 standard; cDNA; 1679 BP.
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DE   Human PRO polynucleotide #188.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 32
ID   ADB30555 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003068794-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 33
ID   ADA85851 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082693-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 34
ID   ADA97063 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082705-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 35
ID   ADA79367 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082763-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 36
ID   ADA87506 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087345-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 37
ID   ADB16708 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087349-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 38
ID   ADA91800 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082694-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 39
ID   ADB14863 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087351-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 40
ID   ADA25061 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
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PN   US2003050241-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 41
ID   ADA47275 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
PN   US2003044844-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 42
ID   ADB18824 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073211-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 43
ID   ADA94039 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077722-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 44
ID   ADB19935 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082691-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 45
ID   ADB13247 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082710-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 46
ID   ACD98611 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003044945-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 47
ID   ACD30038 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003050240-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 48
ID   ADA12722 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO337.
PN   US2003055216-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 49
ID   ADA74501 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003068798-A1.
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PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 50
ID   ADB24734 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077713-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 51
ID   ADA82258 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082701-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 52
ID   ADA75221 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003073216-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 53
ID   ADA85299 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082695-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 54
ID   ADA84747 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 55
ID   ADB30003 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 56
ID   ADA80531 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 57
ID   ADA75773 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082703-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 58
ID   ADA46998 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003073210-A1.
PD   17-APR-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 59
ID   ADB25294 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 60
ID   ADA93470 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077721-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 61
ID   ADB26820 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 62
ID   ADB31107 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 63
ID   ABT44571 standard; cDNA; 1679 BP.
DE   Human PRO337 cDNA.
PN   US2003027988-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 64
ID   ADA61035 standard; cDNA; 1679 BP.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 65
ID   ADB24182 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 66
ID   ADA96511 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082690-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 67
ID   ADA81083 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082702-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 68
ID   ADA95959 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 69
ID   ADB26268 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 70
ID   ADB21753 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 71
ID   ACD82238 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO 337 cDNA.
PN   US2003044934-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 72
ID   ACD29453 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane polypeptide cDNA #133.
PN   US2003049633-A1.
PD   13-MAR-2003.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 73
ID   ADA77532 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003068797-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 74
ID   ADB18272 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003077710-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 75
ID   ADA86955 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082709-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 76
ID   ADA88058 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082700-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 77
ID   ADA46446 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003054516-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 78
ID   ADB28476 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082699-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 79
ID   ADB29028 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082706-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 80
ID   ADA76980 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003059909-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 81
ID   ADA88610 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073213-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 82
ID   ADA97615 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082686-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 83
ID   ADB27372 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003022239-A1.
PD   30-JAN-2003.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 84
ID   ADB22305 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087344-A1.
PD   08-MAY-2003.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 85
ID   ACD30273 standard; cDNA; 1679 BP.
DE   Human cDNA encoding Pro337.
PN   US2003044902-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 86
ID   ABT43944 standard; cDNA; 1679 BP.
DE   Human membrane bound receptor/protein PRO337 cDNA sequence.
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PN   US2003065147-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 87
ID   ADA66996 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003068793-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 88
ID   ADB22857 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077711-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 89
ID   ADB23630 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077712-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 90
ID   ADA92352 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082712-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 91
ID   ADB15415 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087352-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 92
ID   ADB83615 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 93
ID   ADB80721 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088068-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 94
ID   ADB73262 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096968-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 95
ID   ADB38667 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082766-A1.
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PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 96
ID   ADB78344 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092889-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 97
ID   ADB38115 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087347-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 98
ID   ADB66587 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082689-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 9;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 99
ID   ADB84992 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003073817-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 100
ID   ADB89667 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082698-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 101
ID   ADB90399 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082762-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 102
ID   ADB39500 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082764-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 103
ID   ADB78098 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092886-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 104
ID   ADB74028 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide sequence #133.
PN   US2003045462-A1.
PD   06-MAR-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 105
ID   ADB87164 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003088067-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 106
ID   ADB84746 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003092890-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 107
ID   ADB47123 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082687-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 108
ID   ADB83861 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003069397-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 109
ID   ADB86730 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082697-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 110
ID   ADB73016 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092887-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 111
ID   ADB76744 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide sequence #133.
PN   US2003083248-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 112
ID   ADB77335 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082696-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 113
ID   ADB34492 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077717-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 114
ID   ADB35596 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 115
ID   ADB33940 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077716-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 116
ID   ADB35044 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 117
ID   ADB36148 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077720-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 118
ID   ADB46543 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082692-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 119
ID   ADC44170 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003054986-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 120
ID   ADC61930 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003049684-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 121
ID   ADC63894 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003054405-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 122
ID   ADC66994 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003060406-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 123
ID   ADC69118 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003064407-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 124
ID   ADC63178 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003068648-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 125
ID   ADC68243 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003069178-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 126
ID   ADC41563 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003072745-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 127
ID   ADC67618 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003073131-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 128
ID   ADC62554 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003073624-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 129
ID   ADC36854 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003088065-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 130
ID   ADC42187 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003104998-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 131
ID   ADC21844 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
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RESULT 132
ID   ADC50416 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092106-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 133
ID   ADC71963 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 134
ID   ADC59942 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 135
ID   ADC49875 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088064-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 136
ID   ADC49074 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088070-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 137
ID   ADC49591 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088071-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 138
ID   ADC47452 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088072-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 139
ID   ADC52949 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087365-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 140
ID   ADC57303 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087366-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 141
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ID   ADC60494 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 142
ID   ADC50969 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 143
ID   ADC65496 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 144
ID   ADC54594 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 145
ID   ADC53555 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087364-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 146
ID   ADC59078 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087359-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 147
ID   ADC55956 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087360-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 148
ID   ADC58526 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087346-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 149
ID   ADC47197 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105288-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 150
ID   ADD03200 standard; cDNA; 1679 BP.
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DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092104-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 151
ID   ADC90192 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087348-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 152
ID   ADC69611 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194770-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 153
ID   ADC48500 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194773-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 154
ID   ADD10029 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 155
ID   ADC78072 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096972-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 156
ID   ADD04604 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 157
ID   ADD06307 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073816-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 158
ID   ADC80560 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 159
ID   ADD11067 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
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PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 160
ID   ADD10344 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003105011-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 161
ID   ADC47948 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 162
ID   ADC77826 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088066-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 163
ID   ADC80008 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 164
ID   ADD11304 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 165
ID   ADD09477 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 166
ID   ADD50789 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105291-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 167
ID   ADD41190 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 168
ID   ADD52329 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 169
ID   ADD51035 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 170
ID   ADD53069 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 171
ID   ADD53621 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003203437-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 172
ID   ADD37097 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 173
ID   ADD51777 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 174
ID   ADD02576 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203431-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 175
ID   ADD50516 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096971-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 176
ID   ADD02010 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203430-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 177
ID   ADD54192 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003203432-A1.
PD   30-OCT-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 178
ID   ADD50270 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096970-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 179
ID   ADD51281 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105289-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 180
ID   ADE49556 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003096744-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 181
ID   ADD92509 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199030-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 182
ID   ADD91405 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199055-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 183
ID   ADE04019 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199057-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 184
ID   ADE32316 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194765-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 185
ID   ADE22248 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199056-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 186
ID   ADD79472 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003203428-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 187
ID   ADE35610 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203434-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 188
ID   ADE16724 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203435-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 189
ID   ADD73339 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203436-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 190
ID   ADE42008 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194772-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 191
ID   ADE17825 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199023-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 192
ID   ADD91957 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199053-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 193
ID   ADE33420 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194767-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 194
ID   ADE33972 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194791-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 195
ID   ADD80024 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207417-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 196
ID   ADD93061 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194768-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 197
ID   ADD72697 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003194781-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 198
ID   ADE19481 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199025-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 199
ID   ADE18929 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199026-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 200
ID   ADE43125 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 201
ID   ADD95914 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199059-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 202
ID   ADE22800 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 203
ID   ADD78918 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 204
ID   ADE32868 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
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RESULT 205
ID   ADE42560 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 206
ID   ADE17348 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203433-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 207
ID   ADD80576 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 208
ID   ADD89604 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 209
ID   ADE40888 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 210
ID   ADE04687 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 211
ID   ADE92816 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194777-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 212
ID   ADF47362 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195333-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 213
ID   ADG21525 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 214
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ID   ADG23166 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 215
ID   ADF97501 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 216
ID   ADG80565 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 217
ID   ADG53119 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003216561-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 218
ID   ADG60439 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003206915-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 219
ID   ADG80013 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 220
ID   ADG63784 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
PN   US2003170721-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 221
ID   ADH55305 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207381-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 222
ID   ADH55857 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207379-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 223
ID   ADI61199 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003077700-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 224
ID   ADI64076 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207385-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 225
ID   ADI65025 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207386-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 226
ID   ADI63524 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207387-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 227
ID   ADH81938 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207388-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 228
ID   ADH81386 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207377-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 229
ID   ACD24040 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003032156-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 230
ID   ACA66903 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #63.
PN   US2003036635-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 231
ID   ACD42387 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003040014-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 232
ID   ACD42857 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
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PN   US2003050239-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 233
ID   ACD68655 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003045687-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 234
ID   ACA67181 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003004311-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 10;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 235
ID   ADM82555 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087355-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 11;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 236
ID   ADN15954 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087353-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 11;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 237
ID   ADN16583 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087385-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 11;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 238
ID   ADN15402 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087356-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 11;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 239
ID   ADN14850 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087357-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 11;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 240
ID   ADC48828 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092888-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 241
ID   ADC81112 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092115-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 242
ID   ADE20999 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100735-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 243
ID   ADE05843 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100728-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 244
ID   ADD76560 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003100087-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 245
ID   ADD75072 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100712-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 246
ID   ADD75818 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100717-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 247
ID   ADD85050 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100722-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 248
ID   ADD86876 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100738-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 249
ID   ADE20753 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100734-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 250
ID   ADE39050 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096362-A1.
PD   22-MAY-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 251
ID   ADD87924 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003092113-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 252
ID   ADD86328 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203440-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 253
ID   ADE05597 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100727-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 254
ID   ADD73582 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100711-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 255
ID   ADE75776 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003211571-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 256
ID   ADE48856 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003104536-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 257
ID   ADD78422 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100737-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 258
ID   ADE41305 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 259
ID   ADE23352 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092108-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 260
ID   ADE21245 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100736-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 261
ID   ADD77360 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100732-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 262
ID   ADE20507 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100733-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 263
ID   ADD75572 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100064-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 264
ID   ADD74088 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100708-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 265
ID   ADD74334 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100709-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 266
ID   ADD76064 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100718-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 267
ID   ADD85556 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100721-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 268
ID   ADE23904 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092110-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 269
ID   ADE24547 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092111-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 270
ID   ADD87372 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 271
ID   ADE05105 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100726-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 272
ID   ADD75318 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 273
ID   ADD76862 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 274
ID   ADD86630 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 275
ID   ADE89238 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 276
ID   ADE41198 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
PN   US2003104558-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 277
ID   ADD78098 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 278
ID   ADE18377 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194794-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 279
ID   ADE88686 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 280
ID   ADE89957 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003130181-A1.
PD   10-JUL-2003.
PA   (ASHK/) ASHKENAZI A J.
PA   (BAKE/) BAKER K P.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GIRM/) GIRMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (KUOS/) KUO S S.
PA   (NAPI/) NAPIER M A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (SHEL/) SHELTON D L.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 281
ID   ADD77606 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 282
ID   ADD77852 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100730-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 283
ID   ADD85310 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100725-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 284
ID   ADD73842 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 285
ID   ADD74580 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 286
ID   ADD77108 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100716-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 287
ID   ADD85802 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100720-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 288
ID   ADE05351 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100723-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 289
ID   ADD74826 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100724-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 290
ID   ADF61597 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195345-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 291
ID   ADF40289 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003198994-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 292
ID   ADF46085 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195148-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
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RESULT 293
ID   ADE94706 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199027-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 294
ID   ADE91117 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 295
ID   ADE95258 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 296
ID   ADE93368 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 297
ID   ADF24481 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003204055-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 298
ID   ADF40913 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199021-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 299
ID   ADF23857 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203402-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 300
ID   ADF33840 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003194780-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 301
ID   ADF34949 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199029-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 302
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ID   ADF27307 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199436-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 303
ID   ADF27943 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199437-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 304
ID   ADE92264 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 305
ID   ADE90565 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 306
ID   ADF41537 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199435-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 307
ID   ADF33216 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003211091-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 308
ID   ADF25582 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003211092-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 309
ID   ADF26683 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199674-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 310
ID   ADF34472 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003194410-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 311
ID   ADF46709 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195344-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 312
ID   ADE91712 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 313
ID   ADG05638 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096959-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 314
ID   ADG27192 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096962-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 315
ID   ADG02291 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 316
ID   ADG22077 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 317
ID   ADG20147 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 318
ID   ADF98053 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 319
ID   ADG24270 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207426-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 320
ID   ADF98624 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
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PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 321
ID   ADG03455 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 322
ID   ADF99176 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 323
ID   ADG16761 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 324
ID   ADG05220 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 325
ID   ADG19487 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 326
ID   ADG11255 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 327
ID   ADG13324 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 328
ID   ADG08381 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 329
ID   ADG15551 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 330
ID   ADG12034 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 331
ID   ADF96949 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 332
ID   ADG06134 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 333
ID   ADG23718 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 334
ID   ADG04007 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 335
ID   ADG24908 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 336
ID   ADF94591 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 337
ID   ADG07205 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 338
ID   ADG07757 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207356-A1.
PD   06-NOV-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 339
ID   ADG06687 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096966-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 340
ID   ADG55252 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 341
ID   ADG60916 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 342
ID   ADG62020 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 343
ID   ADG82221 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 344
ID   ADG57460 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 345
ID   ADG56908 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 346
ID   ADG55804 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 347
ID   ADG58564 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 348
ID   ADG70930 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 349
ID   ADH39031 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096965-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 350
ID   ADG58012 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 351
ID   ADG53596 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 352
ID   ADG71482 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 353
ID   ADG50695 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003207803-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 354
ID   ADG81669 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207805-A1.
PD   06-NOV-2003.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 355
ID   ADH30631 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 356
ID   ADG63633 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
PN   US2003180796-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
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RESULT 357
ID   ADH11998 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 358
ID   ADG50071 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003215905-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 359
ID   ADG51943 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003215908-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 360
ID   ADG52420 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 361
ID   ADG54148 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 362
ID   ADG49447 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003216305-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 363
ID   ADG81117 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 364
ID   ADG56356 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 365
ID   ADH12622 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 366
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ID   ADG48823 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003216560-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 367
ID   ADG61468 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 368
ID   ADH28555 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 369
ID   ADG54700 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 370
ID   ADG59740 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 371
ID   ADG51319 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004005312-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 372
ID   ADH43488 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #28.
PN   US2003224984-A1.
PD   04-DEC-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 373
ID   ADG59263 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004005657-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 374
ID   ADG34121 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004006206-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 375
ID   ADG62719 standard; cDNA; 1679 BP.
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DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004006219-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 376
ID   ADI81164 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207361-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 377
ID   ADI33591 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096960-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 378
ID   ADH69685 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2004019183-A1.
PD   29-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 379
ID   ADH25744 standard; cDNA; 1679 BP.
DE   Human PRO337 encoding cDNA SEQ ID NO:522.
PN   EP1386931-A1.
PD   04-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 380
ID   ADG09907 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004009548-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 381
ID   ADI15378 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207382-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 382
ID   ADG09255 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004009547-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 383
ID   ADI14710 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207383-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 384
ID   ADI29846 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
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PN   US2003096961-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 385
ID   ADI18305 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207349-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 386
ID   ADM27243 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004044179-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 387
ID   ADJ63586 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 388
ID   ADJ77481 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2004038336-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 389
ID   ADK82833 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #28.
PN   US2004043927-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 390
ID   ADK66601 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2004044180-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 391
ID   ADJ65603 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004038335-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 392
ID   ADM27739 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004048333-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-309;
RESULT 393
ID   ADM17521 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004048332-A1.
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PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 394
ID   ADL07355 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004063921-A1.
PD   01-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 395
ID   ADM42463 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004058424-A1.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 396
ID   ADM28325 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004077064-A1.
PD   22-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 12;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 397
ID   ADI95807 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 13;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 398
ID   ADI96359 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207354-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              100.0%;  Score 1035;  DB 13;  Length 1679;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 399
ID   AAZ47893 standard; cDNA; 1693 BP.
DE   Human protein encoding cDNA SEQ ID NO:3.
PN   WO9958668-A1.
PD   18-NOV-1999.
PA   (ONOY ) ONO PHARM CO LTD.
  Query Match              100.0%;  Score 1035;  DB 3;  Length 1693;
  Best Local Similarity    100.0%;  Pred. No. 1.4e-309;
RESULT 400
ID   AAA88790 standard; cDNA; 1603 BP.
DE   Human SECX cDNA Clone 11753149.0.6.
PN   WO200061754-A2.
PD   19-OCT-2000.
PA   (CURA-) CURAGEN CORP.
  Query Match              99.8%;  Score 1033.4;  DB 3;  Length 1603;
  Best Local Similarity    99.9%;  Pred. No. 4.4e-309;
RESULT 401
ID   ADD18288 standard; DNA; 1603 BP.
DE   Human molecule (MOL) protein MOL10 DNA sequence.
PN   WO2003003984-A2.
PD   16-JAN-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match              99.8%;  Score 1033.4;  DB 10;  Length 1603;
  Best Local Similarity    99.9%;  Pred. No. 4.4e-309;
RESULT 402
ID   AAA88791 standard; cDNA; 2012 BP.
DE   Human SECX cDNA Clone 11753149.0.37.
PN   WO200061754-A2.
PD   19-OCT-2000.
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PA   (CURA-) CURAGEN CORP.
  Query Match              99.8%;  Score 1033.4;  DB 3;  Length 2012;
  Best Local Similarity    99.9%;  Pred. No. 5e-309;
RESULT 403
ID   ADD18290 standard; DNA; 2012 BP.
DE   Human molecule (MOL) protein MOL11 DNA sequence.
PN   WO2003003984-A2.
PD   16-JAN-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match              99.8%;  Score 1033.4;  DB 10;  Length 2012;
  Best Local Similarity    99.9%;  Pred. No. 5e-309;
RESULT 404
ID   AAZ47892 standard; cDNA; 1032 BP.
DE   Human protein encoding cDNA SEQ ID NO:2.
PN   WO9958668-A1.
PD   18-NOV-1999.
PA   (ONOY ) ONO PHARM CO LTD.
  Query Match              99.7%;  Score 1032;  DB 3;  Length 1032;
  Best Local Similarity    100.0%;  Pred. No. 9.3e-309;
RESULT 405
ID   AAI59655 standard; cDNA; 1690 BP.
DE   Human polynucleotide SEQ ID NO 3644.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              96.7%;  Score 1001;  DB 4;  Length 1690;
  Best Local Similarity    99.7%;  Pred. No. 5e-299;
RESULT 406
ID   ADI21360 standard; cDNA; 1690 BP.
DE   Novel human expressed sequence tag, EST #59.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match              96.7%;  Score 1001;  DB 10;  Length 1690;
  Best Local Similarity    99.7%;  Pred. No. 5e-299;
RESULT 407
ID   ABT17393 standard; DNA; 1061 BP.
DE   Human IG gene related nucleic acid SEQ ID No 19.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match              92.3%;  Score 955;  DB 8;  Length 1061;
  Best Local Similarity    100.0%;  Pred. No. 7e-285;
RESULT 408
ID   AAI57869 standard; cDNA; 1678 BP.
DE   Human polynucleotide SEQ ID NO 72.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              92.3%;  Score 955;  DB 4;  Length 1678;
  Best Local Similarity    100.0%;  Pred. No. 9e-285;
RESULT 409
ID   ADI21817 standard; cDNA; 2884 BP.
DE   Novel human protein cDNA #76.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match              92.3%;  Score 955;  DB 10;  Length 2884;
  Best Local Similarity    100.0%;  Pred. No. 1.2e-284;
RESULT 410
ID   ABT17390 standard; DNA; 1839 BP.
DE   Human IG gene related nucleic acid SEQ ID No 16.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match              92.1%;  Score 953.4;  DB 8;  Length 1839;
  Best Local Similarity    99.9%;  Pred. No. 3e-284;
RESULT 411
ID   ABX76448 standard; DNA; 1839 BP.
DE   Lung cancer-associated polynucleotide #312.
PN   WO200286443-A2.
PD   31-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
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  Query Match             92.1%;  Score 953.4;  DB 8;  Length 1839;
  Best Local Similarity   99.9%;  Pred. No. 3e-284;
RESULT 412
ID   ADG63208 standard; DNA; 1839 BP.
DE   Human neurotrimin DNA.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             92.1%;  Score 953.4;  DB 10;  Length 1839;
  Best Local Similarity   99.9%;  Pred. No. 3e-284;
RESULT 413
ID   ADN39137 standard; cDNA; 1839 BP.
DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:455.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
  Query Match             92.1%;  Score 953.4;  DB 11;  Length 1839;
  Best Local Similarity   99.9%;  Pred. No. 3e-284;
RESULT 414
ID   ADQ22984 standard; DNA; 3987 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5804.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             92.1%;  Score 953.4;  DB 12;  Length 3987;
  Best Local Similarity   99.9%;  Pred. No. 4.6e-284;
RESULT 415
ID   ADQ24601 standard; DNA; 3987 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7421.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             92.1%;  Score 953.4;  DB 12;  Length 3987;
  Best Local Similarity   99.9%;  Pred. No. 4.6e-284;
RESULT 416
ID   ABK49272 standard; cDNA; 1873 BP.
DE   Human Kruppel associated DNA binding protein 42 cDNA.
PN   WO200183541-A1.
PD   08-NOV-2001.
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
  Query Match             91.1%;  Score 943;  DB 6;  Length 1873;
  Best Local Similarity   99.9%;  Pred. No. 5e-281;
RESULT 417
ID   AAZ47894 standard; cDNA; 939 BP.
DE   Human protein encoding cDNA SEQ ID NO:5.
PN   WO9958668-A1.
PD   18-NOV-1999.
PA   (ONOY ) ONO PHARM CO LTD.
  Query Match             90.7%;  Score 939;  DB 3;  Length 939;
  Best Local Similarity   100.0%;  Pred. No. 6e-280;
RESULT 418
ID   ABT17391 standard; DNA; 1094 BP.
DE   Human IG gene related nucleic acid SEQ ID No 17.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             88.1%;  Score 912;  DB 8;  Length 1094;
  Best Local Similarity   96.7%;  Pred. No. 1.5e-271;
RESULT 419
ID   ADG63210 standard; DNA; 1068 BP.
DE   Human neurotrimin DNA +33bp isoform.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             88.0%;  Score 910.4;  DB 10;  Length 1068;
  Best Local Similarity   96.6%;  Pred. No. 4.7e-271;
RESULT 420
ID   ADI35771 standard; DNA; 2129 BP.
DE   Human neurotrimin DNA.
PN   US2003100485-A1.
PD   29-MAY-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             88.0%;  Score 910.4;  DB 10;  Length 2129;
  Best Local Similarity   96.6%;  Pred. No. 6.9e-271;
RESULT 421
ID   ADG63212 standard; DNA; 1104 BP.
DE   Human neurotrimin DNA +69bp isoform.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             84.5%;  Score 874.4;  DB 10;  Length 1104;
  Best Local Similarity   93.2%;  Pred. No. 7e-260;
RESULT 422
ID   ABT17392 standard; DNA; 1130 BP.
DE   Human IG gene related nucleic acid SEQ ID No 18.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             84.3%;  Score 872.8;  DB 8;  Length 1130;
  Best Local Similarity   93.1%;  Pred. No. 2.2e-259;
RESULT 423
ID   ADG63214 standard; DNA; 1140 BP.
DE   Human neurotrimin DNA +108bp isoform.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             82.3%;  Score 851.8;  DB 10;  Length 1140;
  Best Local Similarity   99.8%;  Pred. No. 7.2e-253;
RESULT 424
ID   AAA44536 standard; cDNA; 832 BP.
DE   Human secreted expressed sequence tag SEQ ID NO:1111.
PN   WO200021991-A1.
PD   20-APR-2000.
PA   (GEMY ) GENETICS INST INC.
  Query Match             64.8%;  Score 670.8;  DB 3;  Length 832;
  Best Local Similarity   99.7%;  Pred. No. 7.8e-197;
RESULT 425
ID   ADE07017 standard; DNA; 3298 BP.
DE   Novel coding sequence (useful for identifying genetic disorders) #83.
PN   WO2003054152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match             54.1%;  Score 559.8;  DB 10;  Length 3298;
  Best Local Similarity   72.5%;  Pred. No. 4.3e-162;
RESULT 426
ID   AAQ51015 standard; cDNA; 3069 BP.
DE   Rat opioid receptor gene.
PN   WO9321309-A1.
PD   28-OCT-1993.
PA   (LEEN/) LEE N M.
PA   (LOHH/) LOH H H.
PA   (LIPP/) LIPPMAN D.
  Query Match             52.1%;  Score 539;  DB 2;  Length 3069;
  Best Local Similarity   71.2%;  Pred. No. 1.2e-155;
RESULT 427
ID   ABT17409 standard; DNA; 1478 BP.
DE   Human IG gene related nucleic acid SEQ ID No 35.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             51.9%;  Score 537.2;  DB 8;  Length 1478;
  Best Local Similarity   73.3%;  Pred. No. 2.8e-155;
RESULT 428
ID   ABT17406 standard; DNA; 3110 BP.
DE   Human IG gene related nucleic acid SEQ ID No 32.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             51.9%;  Score 537.2;  DB 8;  Length 3110;
  Best Local Similarity   73.3%;  Pred. No. 4.3e-155;
RESULT 429
ID   ADG63206 standard; DNA; 3110 BP.
DE   Opioid-binding protein/cell adhesion molecule-like DNA.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
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  Query Match             51.9%;  Score 537.2;  DB 10;  Length 3110;
  Best Local Similarity   73.3%;  Pred. No. 4.3e-155;
RESULT 430
ID   ABT17408 standard; DNA; 1071 BP.
DE   Human IG gene related nucleic acid SEQ ID No 34.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             51.7%;  Score 535.6;  DB 8;  Length 1071;
  Best Local Similarity   73.2%;  Pred. No. 7.4e-155;
RESULT 431
ID   ABT17407 standard; DNA; 1080 BP.
DE   Human IG gene related nucleic acid SEQ ID No 33.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             51.7%;  Score 535.6;  DB 8;  Length 1080;
  Best Local Similarity   73.2%;  Pred. No. 7.4e-155;
RESULT 432
ID   AAQ51017 standard; cDNA; 2179 BP.
DE   Rat opioid receptor gene.
PN   WO9321309-A1.
PD   28-OCT-1993.
PA   (LEEN/) LEE N M.
PA   (LOHH/) LOH H H.
PA   (LIPP/) LIPPMAN D.
  Query Match             50.4%;  Score 521.2;  DB 2;  Length 2179;
  Best Local Similarity   72.2%;  Pred. No. 3.2e-150;
RESULT 433
ID   AAQ51016 standard; cDNA; 2337 BP.
DE   Rat opioid receptor gene.
PN   WO9321309-A1.
PD   28-OCT-1993.
PA   (LEEN/) LEE N M.
PA   (LOHH/) LOH H H.
PA   (LIPP/) LIPPMAN D.
  Query Match             50.4%;  Score 521.2;  DB 2;  Length 2337;
  Best Local Similarity   72.2%;  Pred. No. 3.3e-150;
RESULT 434
ID   AAZ34325 standard; DNA; 503 BP.
DE   Human EST DNA42301.
PN   WO9946281-A2.
PD   16-SEP-1999.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 2;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 435
ID   AAC78591 standard; cDNA; 503 BP.
DE   Human EST DNA42301 nucleotide sequence SEQ ID NO:524.
PN   WO200053756-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 3;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 436
ID   ACA63893 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein DNA42301.
PN   US2002192706-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 8;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 437
ID   ACA72057 standard; DNA; 503 BP.
DE   Human PRO polypeptide associated oligonucleotide SEQ ID NO 524.
PN   US2002177553-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 8;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 438
ID   ABX92697 standard; cDNA; 503 BP.
DE   Human PRO337 EST polynucleotide sequence.
PN   US2002169284-A1.
PD   14-NOV-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 8;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 439
ID   ACA66438 standard; cDNA; 503 BP.
DE   Human secreted/transmembrane protein EST DNA42301.
PN   US2003004102-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 8;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 440
ID   ADA25063 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein EST DNA42301.
PN   US2003050241-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 9;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 441
ID   ACD30039 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein EST DNA42301.
PN   US2003050240-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 9;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 442
ID   ADA12724 standard; cDNA; 503 BP.
DE   Human secreted/transmembrane polypeptide PRO337 EST.
PN   US2003055216-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 9;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 443
ID   ACD29454 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane polypeptide cDNA #134.
PN   US2003049633-A1.
PD   13-MAR-2003.
  Query Match             47.5%;  Score 492;  DB 9;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 444
ID   ADB74030 standard; cDNA; 503 BP.
DE   Human PRO polynucleotide sequence #134.
PN   US2003045462-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 445
ID   ADB76746 standard; cDNA; 503 BP.
DE   Human PRO polynucleotide sequence #134.
PN   US2003083248-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 446
ID   ADC44172 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003054986-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 447
ID   ADC61932 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003049684-A1.
PD   13-MAR-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 448
ID   ADC63896 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003054405-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 449
ID   ADC66996 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003060406-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 450
ID   ADC69120 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003064407-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 451
ID   ADC63180 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003068648-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 452
ID   ADC68245 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003069178-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 453
ID   ADC41565 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003072745-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 454
ID   ADC67620 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003073131-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 455
ID   ADC62556 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003073624-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 456
ID   ADC42189 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003104998-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 457
ID   ADE49558 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003096744-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 458
ID   ADE35612 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203434-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 459
ID   ADE16726 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203435-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 460
ID   ADD73341 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203436-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 461
ID   ADD72699 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003194781-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 462
ID   ADE17350 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203433-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 463
ID   ADF47364 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195333-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 464
ID   ADG53121 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003216561-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 465
ID   ADG60441 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003206915-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 466
ID   ADI61201 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003077700-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 467
ID   ACD42858 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein EST DNA42301.
PN   US2003050239-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 10;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 468
ID   ADE48858 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003104536-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 469
ID   ADE89959 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003130181-A1.
PD   10-JUL-2003.
PA   (ASHK/) ASHKENAZI A J.
PA   (BAKE/) BAKER K P.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GIRM/) GIRMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (KUOS/) KUO S S.
PA   (NAPI/) NAPIER M A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (SHEL/) SHELTON D L.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 470
ID   ADF61599 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195345-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 471
ID   ADF40291 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003198994-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 472
ID   ADF46087 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195148-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 473
ID   ADF24483 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003204055-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 474
ID   ADF40915 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199021-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 475
ID   ADF23859 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203402-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 476
ID   ADF33842 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003194780-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 477
ID   ADF27309 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199436-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 478
ID   ADF27945 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199437-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 479
ID   ADF41539 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199435-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 480
ID   ADF33218 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003211091-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 481
ID   ADF25584 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003211092-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 482
ID   ADF26685 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199674-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 483
ID   ADF34474 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003194410-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 484
ID   ADF46711 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195344-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 485
ID   ADG50697 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003207803-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 486
ID   ADG50073 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003215905-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 487
ID   ADG51945 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003215908-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 488
ID   ADG49449 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003216305-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 489
ID   ADG48825 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003216560-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
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RESULT 490
ID   ADG51321 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004005312-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 491
ID   ADG59265 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004005657-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 492
ID   ADG62721 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004006219-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 493
ID   ADH25746 standard; cDNA; 503 BP.
DE   Human DNA42301 expressed sequence tag (EST) SEQ ID NO:524.
PN   EP1386931-A1.
PD   04-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 494
ID   ADM17523 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004048332-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 495
ID   ADL07357 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004063921-A1.
PD   01-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             47.5%;  Score 492;  DB 12;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-141;
RESULT 496
ID   ADM47274 standard; DNA; 617 BP.
DE   Oestrogen regulated protein like NOVX 25b gene.
PN   WO2003083039-A2.
PD   09-OCT-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             43.4%;  Score 449.4;  DB 11;  Length 617;
  Best Local Similarity   97.6%;  Pred. No. 2.9e-128;
RESULT 497
ID   ACH15238 standard; cDNA; 437 BP.
DE   Human adult brain cDNA #2450.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             39.0%;  Score 404;  DB 9;  Length 437;
  Best Local Similarity   97.4%;  Pred. No. 2.8e-114;
RESULT 498
ID   AAC91321 standard; cDNA; 537 BP.
DE   Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 21.
PN   WO200073509-A2.
PD   07-DEC-2000.
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PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             35.0%;  Score 362.2;  DB 4;  Length 537;
  Best Local Similarity   99.2%;  Pred. No. 2.9e-101;
RESULT 499
ID   AAS78035 standard; cDNA; 484 BP.
DE   DNA encoding novel human diagnostic protein #13839.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             34.3%;  Score 355.4;  DB 5;  Length 484;
  Best Local Similarity   92.3%;  Pred. No. 3.5e-99;
RESULT 500
ID   ACH46276 standard; cDNA; 409 BP.
DE   Human infant brain cDNA #339.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             34.2%;  Score 353.8;  DB 9;  Length 409;
  Best Local Similarity   98.1%;  Pred. No. 1e-98;
RESULT 501
ID   AAL50356 standard; cDNA; 1411 BP.
DE   Human limbic system associated membrane protein 36-85 coding sequence.
PN   CN1345756-A.
PD   24-APR-2002.
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
  Query Match             33.1%;  Score 343;  DB 6;  Length 1411;
  Best Local Similarity   63.6%;  Pred. No. 4.4e-95;
RESULT 502
ID   AAT42080 standard; cDNA to mRNA; 1238 BP.
DE   Rat LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             33.0%;  Score 342;  DB 2;  Length 1238;
  Best Local Similarity   61.9%;  Pred. No. 8.4e-95;
RESULT 503
ID   AAT42084 standard; cDNA to mRNA; 924 BP.
DE   Human LAMP residues 8-315 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             32.9%;  Score 340.6;  DB 2;  Length 924;
  Best Local Similarity   63.3%;  Pred. No. 1.9e-94;
RESULT 504
ID   AAT42079 standard; cDNA to mRNA; 977 BP.
DE   Human LAMP residues 8-332 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             32.9%;  Score 340.6;  DB 2;  Length 977;
  Best Local Similarity   63.3%;  Pred. No. 2e-94;
RESULT 505
ID   AAT42081 standard; cDNA to mRNA; 1014 BP.
DE   Rat LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             32.9%;  Score 340.6;  DB 2;  Length 1014;
  Best Local Similarity   61.9%;  Pred. No. 2e-94;
RESULT 506
ID   ABT17402 standard; DNA; 1017 BP.
DE   Human IG gene related nucleic acid SEQ ID No 28.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             32.9%;  Score 340.6;  DB 8;  Length 1017;
  Best Local Similarity   63.3%;  Pred. No. 2e-94;
RESULT 507
ID   ABT17404 standard; DNA; 1017 BP.
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DE   Human IG gene related nucleic acid SEQ ID No 30.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             32.9%;  Score 340.6;  DB 8;  Length 1017;
  Best Local Similarity   63.3%;  Pred. No. 2e-94;
RESULT 508
ID   ABX63560 standard; cDNA; 1195 BP.
DE   Human cDNA #560 differentially expressed in activated vascular tissue.
PN   US2002137081-A1.
PD   26-SEP-2002.
PA   (BAND/) BANDMAN O.
  Query Match             32.9%;  Score 340.6;  DB 8;  Length 1195;
  Best Local Similarity   63.3%;  Pred. No. 2.2e-94;
RESULT 509
ID   ADL12674 standard; cDNA; 1195 BP.
DE   Human steroid-induced C3A liver cell cDNA #403.
PN   US6673549-B1.
PD   06-JAN-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             32.9%;  Score 340.6;  DB 12;  Length 1195;
  Best Local Similarity   63.3%;  Pred. No. 2.2e-94;
RESULT 510
ID   AAT42086 standard; cDNA to mRNA; 861 BP.
DE   Human LAMP residues 29-315 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             32.7%;  Score 338.6;  DB 2;  Length 861;
  Best Local Similarity   63.7%;  Pred. No. 7.8e-94;
RESULT 511
ID   AAT42082 standard; cDNA to mRNA; 912 BP.
DE   Human mature LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             32.7%;  Score 338.6;  DB 2;  Length 912;
  Best Local Similarity   63.7%;  Pred. No. 8e-94;
RESULT 512
ID   AAT42085 standard; cDNA to mRNA; 945 BP.
DE   Rat LAMP residues 1-315 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             32.6%;  Score 337.4;  DB 2;  Length 945;
  Best Local Similarity   63.1%;  Pred. No. 1.9e-93;
RESULT 513
ID   ABZ76264 standard; cDNA; 1757 BP.
DE   Human GENSET cDNA clone name SLAMP.
PN   WO2003014151-A2.
PD   20-FEB-2003.
PA   (GEST ) GENSET SA.
  Query Match             32.6%;  Score 337.4;  DB 8;  Length 1757;
  Best Local Similarity   63.8%;  Pred. No: 2.7e-93;
RESULT 514
ID   AAT42083 standard; cDNA to mRNA; 930 BP.
DE   Rat mature LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             32.6%;  Score 337;  DB 2;  Length 930;
  Best Local Similarity   62.1%;  Pred. No. 2.5e-93;
RESULT 515
ID   ABT17403 standard; DNA; 1075 BP.
DE   Human IG gene related nucleic acid SEQ ID No 29.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             32.4%;  Score 335;  DB 8;  Length 1075;
  Best Local Similarity   63.5%;  Pred. No. 1.1e-92;
RESULT 516
ID   AAT42087 standard; cDNA to mRNA; 861 BP.
DE   Rat LAMP residues 29-315 coding sequence.
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PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             32.3%;  Score 333.8;  DB 2;  Length 861;
  Best Local Similarity   63.4%;  Pred. No. 2.4e-92;
RESULT 517
ID   AAT42116 standard; cDNA to mRNA; 1307 BP.
DE   Rat LAMP clone 6c coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             32.1%;  Score 331.8;  DB 2;  Length 1307;
  Best Local Similarity   63.3%;  Pred. No. 1.3e-91;
RESULT 518
ID   AAF93346 standard; cDNA; 452 BP.
DE   Spinal cord tissue cDNA encoding SRT protein SEQ ID 167.
PN   WO200107611-A2.
PD   01-FEB-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             31.9%;  Score 330;  DB 5;  Length 452;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-91;
RESULT 519
ID   AAH34425 standard; cDNA; 1153 BP.
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:1507.
PN   WO200122920-A2.
PD   05-APR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             31.4%;  Score 325.2;  DB 4;  Length 1153;
  Best Local Similarity   62.7%;  Pred. No. 1.3e-89;
RESULT 520
ID   AAC19214 standard; cDNA; 333 BP.
DE   Human secreted protein 5' EST, SEQ ID NO: 23289.
PN   EP1033401-A2.
PD   06-SEP-2000.
PA   (GEST ) GENSET.
  Query Match             30.6%;  Score 316.2;  DB 3;  Length 333;
  Best Local Similarity   97.0%;  Pred. No. 4e-87;
RESULT 521
ID   ABT17405 standard; DNA; 898 BP.
DE   Human IG gene related nucleic acid SEQ ID No 31.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             30.3%;  Score 313.8;  DB 8;  Length 898;
  Best Local Similarity   63.2%;  Pred. No. 3.9e-86;
RESULT 522
ID   AAT42094 standard; cDNA to mRNA; 756 BP.
DE   Human LAMP residues 46-294 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             29.3%;  Score 303.6;  DB 2;  Length 756;
  Best Local Similarity   63.5%;  Pred. No. 5.1e-83;
RESULT 523
ID   AAT42095 standard; cDNA to mRNA; 756 BP.
DE   Rat LAMP residues 46-294 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             28.8%;  Score 298.2;  DB 2;  Length 756;
  Best Local Similarity   63.0%;  Pred. No. 2.4e-81;
RESULT 524
ID   AAS78034 standard; cDNA; 443 BP.
DE   DNA encoding novel human diagnostic protein #13838.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             28.5%;  Score 295.4;  DB 5;  Length 443;
  Best Local Similarity   89.8%;  Pred. No. 1.3e-80;
RESULT 525
ID   ABT17401 standard; DNA; 1809 BP.
DE   Human IG gene related nucleic acid SEQ ID No 27.
PN   WO200299040-A2.
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PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             27.0%;  Score 279;  DB 8;  Length 1809;
  Best Local Similarity   57.8%;  Pred. No. 3.5e-75;
RESULT 526
ID   ADS82049 standard; DNA; 4891 BP.
DE   Human cancer-associated protein coding sequence #5.
PN   WO2004035789-A1.
PD   29-APR-2004.
PA   (GLDS ) LG LIFE SCI LTD.
  Query Match             26.5%;  Score 274.2;  DB 13;  Length 4891;
  Best Local Similarity   58.6%;  Pred. No. 1.9e-73;
RESULT 527
ID   ABQ82338 standard; cDNA; 1165 BP.
DE   Human NOV12b encoding cDNA SEQ ID NO:25.
PN   WO200262999-A2.
PD   15-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             26.3%;  Score 272.6;  DB 6;  Length 1165;
  Best Local Similarity   58.4%;  Pred. No. 2.7e-73;
RESULT 528
ID   ADI28059 standard; cDNA; 1327 BP.
DE   ECMCAD gene clone 7087904CB1.
PN   WO200202634-A2.
PD   10-JAN-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             26.3%;  Score 272.6;  DB 6;  Length 1327;
  Best Local Similarity   58.4%;  Pred. No. 2.9e-73;
RESULT 529
ID   AAC87055 standard; cDNA; 4834 BP.
DE   Nucleotide sequence of human polypeptide PRO6004.
PN   WO200077037-A2.
PD   21-DEC-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 4;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 530
ID   ABK33536 standard; cDNA; 4834 BP.
DE   cDNA encoding human PRO protein, Seq ID No 1.
PN   WO200208288-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 6;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 531
ID   ACA05014 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003032063-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 8;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 532
ID   ACA60544 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2002177165-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 8;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 533
ID   ACA04534 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 DNA.
PN   US2003032062-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 8;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 534
ID   ACA68497 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088063-A1.
PD   08-MAY-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 8;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 535
ID   ACA65675 standard; cDNA; 4834 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO6004.
PN   US2003032057-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 536
ID   ABT44226 standard; cDNA; 4834 BP.
DE   Human PRO6004 cDNA.
PN   US2003050448-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 537
ID   ADA47301 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003044844-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 538
ID   ABT44509 standard; cDNA; 4834 BP.
DE   Human PRO6004 cDNA.
PN   US2003027988-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 539
ID   ACD82176 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO 6004 cDNA.
PN   US2003044934-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 540
ID   ACD30291 standard; cDNA; 4834 BP.
DE   Human cDNA encoding Pro6004.
PN   US2003044902-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 541
ID   ABT43882 standard; cDNA; 4834 BP.
DE   Human membrane bound receptor/protein PRO6004 cDNA sequence.
PN   US2003065147-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 542
ID   ADB83491 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 543
ID   ADB80597 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088068-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             26.3%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 544
ID   ADB73138 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096968-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 545
ID   ADB78220 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092889-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 9;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 546
ID   ADB84868 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003073817-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 547
ID   ADB77974 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092886-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 548
ID   ADB87040 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003088067-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 549
ID   ADB84622 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003092890-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 550
ID   ADB83737 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003069397-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 551
ID   ADB72892 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092887-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 552
ID   ADC36730 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003088065-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 553
ID   ADC21720 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 554
ID   ADC49751 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088064-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 555
ID   ADC48950 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088070-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 556
ID   ADC49467 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088071-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 557
ID   ADC47328 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088072-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 558
ID   ADC47073 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105288-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 559
ID   ADC77948 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096972-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 560
ID   ADD06183 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003073816-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 561
ID   ADC77702 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088066-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
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RESULT 562
ID   ADD50665 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105291-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 563
ID   ADD50911 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 564
ID   ADD50392 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096971-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 565
ID   ADD50146 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096970-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 566
ID   ADD51157 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105289-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 567
ID   ADG63810 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003170721-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 568
ID   ACA66841 standard; cDNA; 4834 BP.
DE   cDNA encoding human PRO polypeptide #1.
PN   US2003036635-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 569
ID   ACD42405 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003040014-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 570
ID   ACD68593 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003045687-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 10;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 571
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ID   ADC48704 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092888-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 572
ID   ADE20875 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100735-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 573
ID   ADE05719 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100728-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 574
ID   ADD74948 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100712-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 575
ID   ADD75694 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100717-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 576
ID   ADD84926 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100722-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 577
ID   ADD86752 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100738-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 578
ID   ADE20629 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100734-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 579
ID   ADE38926 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096362-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 580
ID   ADE05473 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100727-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 581
ID   ADD73458 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100711-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 582
ID   ADD78298 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100737-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 583
ID   ADE21121 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100736-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 584
ID   ADD77236 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100732-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 585
ID   ADE20383 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100733-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 586
ID   ADD75448 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100064-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 587
ID   ADD73964 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100708-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 588
ID   ADD74210 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100709-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 589
ID   ADD75940 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
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PN   US2003100718-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 590
ID   ADD85432 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100721-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 591
ID   ADE04981 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100726-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 592
ID   ADD75194 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 593
ID   ADD76738 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 594
ID   ADD86506 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 595
ID   ADE41224 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003104558-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 596
ID   ADD77974 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 597
ID   ADD77482 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 598
ID   ADD77728 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100730-A1.
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PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 599
ID   ADD85186 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100725-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 600
ID   ADD73718 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 601
ID   ADD74456 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 602
ID   ADD76984 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100716-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 603
ID   ADD85678 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100720-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 604
ID   ADE05227 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100723-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 605
ID   ADD74702 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100724-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 606
ID   ADG05514 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096959-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity   58.4%;  Pred. No. 5.8e-73;
RESULT 607
ID   ADG27068 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096962-A1.
PD   22-MAY-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 608
ID   ADG11131 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 609
ID   ADG11910 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 610
ID   ADF94467 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 611
ID   ADG06563 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096966-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 612
ID   ADH38907 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096965-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 613
ID   ADG63658 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003180796-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 614
ID   ADG33997 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2004006206-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 615
ID   ADI33467 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096960-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 616
ID   ADH69561 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2004019183-A1.
PD   29-JAN-2004.
PA   (GETH ) GENENTECH INC.
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  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 617
ID   ADI29722 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096961-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 618
ID   ADM27119 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2004044179-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 619
ID   ADK66477 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2004044180-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match              26.3%;  Score 272.6;  DB 12;  Length 4834;
  Best Local Similarity    58.4%;  Pred. No. 5.8e-73;
RESULT 620
ID   ABQ82337 standard; cDNA; 1196 BP.
DE   Human NOV12a encoding cDNA SEQ ID NO:23.
PN   WO200262999-A2.
PD   15-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match              26.3%;  Score 272.2;  DB 6;  Length 1196;
  Best Local Similarity    58.3%;  Pred. No. 3.6e-73;
RESULT 621
ID   ABN85384 standard; DNA; 1119 BP.
DE   Human NOV6, KILON-like protein, coding sequence.
PN   WO200255704-A2.
PD   18-JUL-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match              26.2%;  Score 271;  DB 6;  Length 1119;
  Best Local Similarity    58.3%;  Pred. No. 8.1e-73;
RESULT 622
ID   ADB62841 standard; cDNA; 2383 BP.
DE   Human cDNA encoding clone OCBBF20110210.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match              26.2%;  Score 271;  DB 10;  Length 2383;
  Best Local Similarity    58.3%;  Pred. No. 1.2e-72;
RESULT 623
ID   AAC78596 standard; cDNA; 2840 BP.
DE   Human PRO4993 nucleotide sequence SEQ ID NO:611.
PN   WO200053756-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
  Query Match              26.0%;  Score 269.4;  DB 3;  Length 2840;
  Best Local Similarity    58.2%;  Pred. No. 4.3e-72;
RESULT 624
ID   ACA63979 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
PN   US2002192706-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match              26.0%;  Score 269.4;  DB 8;  Length 2840;
  Best Local Similarity    58.2%;  Pred. No. 4.3e-72;
RESULT 625
ID   ACA72143 standard; cDNA; 2840 BP.
DE   Human secreted and transmembrane PRO polypeptide #39 cDNA.
PN   US2002177553-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
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  Query Match             26.0%;  Score 269.4;  DB 8;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 626
ID   ABX92783 standard; cDNA; 2840 BP.
DE   cDNA encoding human PRO4993 polypeptide.
PN   US2002169284-A1.
PD   14-NOV-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 8;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 627
ID   ACA66524 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO4993.
PN   US2003004102-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 8;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 628
ID   ADA25149 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
PN   US2003050241-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 9;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 629
ID   ACD30125 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
PN   US2003050240-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 9;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 630
ID   ADA12811 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO4993.
PN   US2003055216-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 9;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 631
ID   ACD29540 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane polypeptide cDNA #139.
PN   US2003049633-A1.
PD   13-MAR-2003.
  Query Match             26.0%;  Score 269.4;  DB 9;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 632
ID   ADB74117 standard; cDNA; 2840 BP.
DE   Human PRO polynucleotide sequence #139.
PN   US2003045462-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 633
ID   ADB76833 standard; cDNA; 2840 BP.
DE   Human PRO polynucleotide sequence #139.
PN   US2003083248-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 634
ID   ADC44259 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003054986-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 635
ID   ADC62019 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003049684-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 636
ID   ADC63983 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003054405-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 637
ID   ADC67083 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003060406-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 638
ID   ADC69207 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003064407-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 639
ID   ADC63267 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003068648-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 640
ID   ADC68332 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003069178-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 641
ID   ADC41652 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003072745-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 642
ID   ADC67707 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003073131-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 643
ID   ADC62643 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003073624-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 644
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ID   ADC42276 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003104998-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 645
ID   ADE49645 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003096744-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 646
ID   ADE35699 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203434-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 647
ID   ADE16813 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203435-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 648
ID   ADD73428 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203436-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 649
ID   ADD72786 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003194781-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 650
ID   ADE17437 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203433-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 651
ID   ADP47451 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195333-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 652
ID   ADG53208 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003216561-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 653
ID   ADG60528 standard; cDNA; 2840 BP.
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DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003206915-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 654
ID   ADI61288 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003077700-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 655
ID   ACD42944 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
PN   US2003050239-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 10;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 656
ID   ADE48945 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003104536-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 657
ID   ADE90046 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003130181-A1.
PD   10-JUL-2003.
PA   (ASHK/) ASHKENAZI A J.
PA   (BAKE/) BAKER K P.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GIRM/) GIRMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (KUOS/) KUO S S.
PA   (NAPI/) NAPIER M A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (SHEL/) SHELTON D L.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 658
ID   ADF61686 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195345-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 659
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ID   ADF40378 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003198994-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 660
ID   ADF46174 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195148-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 661
ID   ADF24570 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003204055-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 662
ID   ADF41002 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199021-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 663
ID   ADF23946 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203402-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 664
ID   ADF33929 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003194780-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 665
ID   ADF27396 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199436-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 666
ID   ADF28032 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199437-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 667
ID   ADF41626 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199435-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 668
ID   ADF33305 standard; cDNA; 2840 BP.
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DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003211091-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 669
ID   ADF25671 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003211092-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 670
ID   ADF26772 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199674-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 671
ID   ADF34561 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003194410-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 672
ID   ADF46798 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195344-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 673
ID   ADG50784 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003207803-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 674
ID   ADG50160 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003215905-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 675
ID   ADG52032 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003215908-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 676
ID   ADG49536 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003216305-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 677
ID   ADG48912 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
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PN   US2003216560-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 678
ID   ADG51408 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004005312-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 679
ID   ADG59352 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004005657-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 680
ID   ADG62808 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004006219-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 681
ID   ADM17610 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004048332-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 682
ID   ADL07444 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004063921-A1.
PD   01-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             26.0%;  Score 269.4;  DB 12;  Length 2840;
  Best Local Similarity   58.2%;  Pred. No. 4.3e-72;
RESULT 683
ID   ADP28685 standard; DNA; 834 BP.
DE   Human secreted protein encoding sequence SEQ ID #683.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 834;
  Best Local Similarity   59.5%;  Pred. No. 1.3e-69;
RESULT 684
ID   ADH71401 standard; DNA; 926 BP.
DE   Human gene of the invention NOV11i SEQ ID NO:297.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 926;
  Best Local Similarity   59.5%;  Pred. No. 1.4e-69;
RESULT 685
ID   ADH71405 standard; DNA; 927 BP.
DE   Human gene of the invention NOV11k SEQ ID NO:301.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 927;
  Best Local Similarity   59.5%;  Pred. No. 1.4e-69;
RESULT 686
ID   ADH71409 standard; DNA; 946 BP.
DE   Human gene of the invention NOV11m SEQ ID NO:305.
PN   WO2003102155-A2.
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PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 946;
  Best Local Similarity   59.5%;  Pred. No. 1.4e-69;
RESULT 687
ID   ADH71393 standard; DNA; 946 BP.
DE   Human gene of the invention NOV11e SEQ ID NO:289.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 946;
  Best Local Similarity   59.5%;  Pred. No. 1.4e-69;
RESULT 688
ID   ADH71395 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11f SEQ ID NO:291.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 976;
  Best Local Similarity   59.5%;  Pred. No. 1.5e-69;
RESULT 689
ID   ADH71415 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11p SEQ ID NO:311.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 976;
  Best Local Similarity   59.5%;  Pred. No. 1.5e-69;
RESULT 690
ID   ADH71389 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11c SEQ ID NO:285.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 976;
  Best Local Similarity   59.5%;  Pred. No. 1.5e-69;
RESULT 691
ID   ADH71397 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11g SEQ ID NO:293.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 976;
  Best Local Similarity   59.5%;  Pred. No. 1.5e-69;
RESULT 692
ID   ABS71699 standard; DNA; 1017 BP.
DE   DNA encoding human NOV5b protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 6;  Length 1017;
  Best Local Similarity   59.5%;  Pred. No. 1.5e-69;
RESULT 693
ID   ADL35978 standard; cDNA; 1017 BP.
DE   Human NOVX cDNA #12.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
  Query Match             25.2%;  Score 260.4;  DB 11;  Length 1017;
  Best Local Similarity   59.5%;  Pred. No. 1.5e-69;
RESULT 694
ID   ADH71417 standard; DNA; 1030 BP.
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DE   Human gene of the invention NOV11q SEQ ID NO:313.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 1030;
  Best Local Similarity   59.5%;  Pred. No. 1.5e-69;
RESULT 695
ID   ADH71411 standard; DNA; 1033 BP.
DE   Human gene of the invention NOV11n SEQ ID NO:307.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 1033;
  Best Local Similarity   59.5%;  Pred. No. 1.5e-69;
RESULT 696
ID   ADH71387 standard; DNA; 1033 BP.
DE   Human gene of the invention NOV11b SEQ ID NO:283.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 1033;
  Best Local Similarity   59.5%;  Pred. No. 1.5e-69;
RESULT 697
ID   ADH71413 standard; DNA; 1035 BP.
DE   Human gene of the invention NOV11o SEQ ID NO:309.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.2%;  Score 260.4;  DB 12;  Length 1035;
  Best Local Similarity   59.5%;  Pred. No. 1.5e-69;
RESULT 698
ID   ABS76364 standard; DNA; 1427 BP.
DE   DNA encoding human immunoglobulin superfamily protein IGSFP-9.
PN   WO200272794-A2.
PD   19-SEP-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             25.2%;  Score 260.4;  DB 6;  Length 1427;
  Best Local Similarity   59.5%;  Pred. No. 1.8e-69;
RESULT 699
ID   AAD47371 standard; DNA; 2653 BP.
DE   Human LP289 DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
  Query Match             25.2%;  Score 260.4;  DB 8;  Length 2653;
  Best Local Similarity   59.5%;  Pred. No. 2.5e-69;
RESULT 700
ID   ABS71698 standard; DNA; 1018 BP.
DE   DNA encoding human NOV5a protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.0%;  Score 258.8;  DB 6;  Length 1018;
  Best Local Similarity   59.4%;  Pred. No. 4.7e-69;
RESULT 701
ID   ADL35976 standard; cDNA; 1018 BP.
DE   Human NOVX cDNA #11.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
  Query Match             25.0%;  Score 258.8;  DB 11;  Length 1018;
  Best Local Similarity   59.4%;  Pred. No. 4.7e-69;
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RESULT 702
ID   ADH71399 standard; DNA; 1018 BP.
DE   Human gene of the invention NOV11h SEQ ID NO:295.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             25.0%;  Score 258.8;  DB 12;  Length 1018;
  Best Local Similarity   59.4%;  Pred. No. 4.7e-69;
RESULT 703
ID   ABS71700 standard; DNA; 1136 BP.
DE   DNA encoding human NOV5c protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             24.9%;  Score 257.2;  DB 6;  Length 1136;
  Best Local Similarity   59.3%;  Pred. No. 1.6e-68;
RESULT 704
ID   ADH71403 standard; DNA; 1171 BP.
DE   Human gene of the invention NOV11j SEQ ID NO:299.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             24.9%;  Score 257.2;  DB 12;  Length 1171;
  Best Local Similarity   59.3%;  Pred. No. 1.6e-68;
RESULT 705
ID   ADH71385 standard; DNA; 1271 BP.
DE   Human gene of the invention NOV11a SEQ ID NO:281.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             24.9%;  Score 257.2;  DB 12;  Length 1271;
  Best Local Similarity   59.3%;  Pred. No. 1.7e-68;
RESULT 706
ID   ADH71421 standard; DNA; 1271 BP.
DE   Human gene of the invention NOV11s SEQ ID NO:317.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             24.9%;  Score 257.2;  DB 12;  Length 1271;
  Best Local Similarity   59.3%;  Pred. No. 1.7e-68;
RESULT 707
ID   ADH71419 standard; DNA; 1271 BP.
DE   Human gene of the invention NOV11r SEQ ID NO:315.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             24.7%;  Score 255.6;  DB 12;  Length 1271;
  Best Local Similarity   59.1%;  Pred. No. 5.2e-68;
RESULT 708
ID   ABK35606 standard; DNA; 1011 BP.
DE   Gene encoding novel human secreted or membrane-associated protein #25.
PN   WO200204600-A2.
PD   17-JAN-2002.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
  Query Match             23.8%;  Score 246;  DB 6;  Length 1011;
  Best Local Similarity   58.4%;  Pred. No. 4.3e-65;
RESULT 709
ID   ABS71701 standard; DNA; 1169 BP.
DE   DNA encoding human NOV5d protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             23.8%;  Score 246;  DB 6;  Length 1169;
  Best Local Similarity   58.4%;  Pred. No. 4.7e-65;
RESULT 710
ID   ADH71407 standard; DNA; 1169 BP.
DE   Human gene of the invention NOV11l SEQ ID NO:303.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             23.8%;  Score 246;  DB 12;  Length 1169;
  Best Local Similarity   58.4%;  Pred. No. 4.7e-65;
RESULT 711
ID   ABA06475 standard; cDNA; 2813 BP.
DE   Human cDNA SEQ ID NO: 141.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             23.3%;  Score 240.8;  DB 4;  Length 2813;
  Best Local Similarity   58.3%;  Pred. No. 3.1e-63;
RESULT 712
ID   ABV83812 standard; cDNA; 2813 BP.
DE   Human polynucleotide SEQ ID NO 141.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match             23.3%;  Score 240.8;  DB 6;  Length 2813;
  Best Local Similarity   58.3%;  Pred. No. 3.1e-63;
RESULT 713
ID   ADH71391 standard; DNA; 760 BP.
DE   Human gene of the invention NOV11d SEQ ID NO:287.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             22.9%;  Score 236.6;  DB 12;  Length 760;
  Best Local Similarity   59.9%;  Pred. No. 3e-62;
RESULT 714
ID   AAD47374 standard; DNA; 2601 BP.
DE   Human LP319b DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
  Query Match             22.6%;  Score 234;  DB 8;  Length 2601;
  Best Local Similarity   58.3%;  Pred. No. 3.8e-61;
RESULT 715
ID   ABK35605 standard; DNA; 1056 BP.
DE   Gene encoding novel human secreted or membrane-associated protein #24.
PN   WO200204600-A2.
PD   17-JAN-2002.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
  Query Match             22.4%;  Score 232;  DB 6;  Length 1056;
  Best Local Similarity   58.1%;  Pred. No. 9.7e-61;
RESULT 716
ID   ADL35982 standard; cDNA; 1168 BP.
DE   Human NOVX cDNA #14.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
  Query Match             22.3%;  Score 231.2;  DB 11;  Length 1168;
  Best Local Similarity   58.1%;  Pred. No. 1.8e-60;
RESULT 717
ID   ADL35980 standard; cDNA; 1133 BP.
DE   Human NOVX cDNA #13.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
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PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
  Query Match             21.7%;  Score 224.8;  DB 11;  Length 1133;
  Best Local Similarity   59.3%;  Pred. No. 1.7e-58;
RESULT 718
ID   AAS28811 standard; cDNA; 4656 BP.
DE   Human immunoglobulin encoding cDNA SEQ ID No 57.
PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             21.3%;  Score 220.6;  DB 4;  Length 4656;
  Best Local Similarity   57.5%;  Pred. No. 7.5e-57;
RESULT 719
ID   ADB31536 standard; cDNA; 4656 BP.
DE   Human cDNA encoding a novel protein SEQ ID NO 57.
PN   US2003077606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             21.3%;  Score 220.6;  DB 10;  Length 4656;
  Best Local Similarity   57.5%;  Pred. No. 7.5e-57;
RESULT 720
ID   AAS78003 standard; cDNA; 2883 BP.
DE   DNA encoding novel human diagnostic protein #13807.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             21.0%;  Score 217.8;  DB 5;  Length 2883;
  Best Local Similarity   71.1%;  Pred. No. 4.3e-56;
RESULT 721
ID   ADE08816 standard; DNA; 2883 BP.
DE   Novel DNA-related contig nucleotide sequence #60.
PN   WO2003054152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match             21.0%;  Score 217.8;  DB 10;  Length 2883;
  Best Local Similarity   71.1%;  Pred. No. 4.3e-56;
RESULT 722
ID   AAD47372 standard; DNA; 754 BP.
DE   Human LP289 splice variant (LP343) DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
  Query Match             20.4%;  Score 211.4;  DB 8;  Length 754;
  Best Local Similarity   61.1%;  Pred. No. 2e-54;
RESULT 723
ID   ADP28686 standard; DNA; 666 BP.
DE   Human secreted protein encoding sequence SEQ ID #684.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
  Query Match             20.3%;  Score 210;  DB 12;  Length 666;
  Best Local Similarity   60.2%;  Pred. No. 5e-54;
RESULT 724
ID   AAD47373 standard; DNA; 2597 BP.
DE   Human LP319a DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
  Query Match             20.2%;  Score 208.6;  DB 8;  Length 2597;
  Best Local Similarity   58.1%;  Pred. No. 2.9e-53;
RESULT 725
ID   AAC02777 standard; cDNA; 352 BP.
DE   Human secreted protein 5' EST, SEQ ID NO: 2775.
PN   EP1033401-A2.
PD   06-SEP-2000.
PA   (GEST ) GENSET.
  Query Match             18.7%;  Score 193.6;  DB 3;  Length 352;
  Best Local Similarity   82.5%;  Pred. No. 4.2e-49;
RESULT 726
ID   ABL99899 standard; cDNA; 5666 BP.
DE   Human secretory polynucleotide (sptm) 154.
PN   WO200220756-A2.
PD   14-MAR-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             17.4%;  Score 180.4;  DB 6;  Length 5666;
  Best Local Similarity   56.1%;  Pred. No. 2.4e-44;
RESULT 727
ID   ADG63283 standard; DNA; 540 BP.
DE   Human OBCAM gene exon 2.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             17.1%;  Score 176.6;  DB 10;  Length 540;
  Best Local Similarity   74.9%;  Pred. No. 1e-43;
RESULT 728
ID   ADQ83739 standard; cDNA; 919 BP.
DE   Human tumour-associated antigenic target (TAT) cDNA sequence #553.
PN   WO2004060270-A2.
PD   22-JUL-2004.
PA   (GETH ) GENENTECH INC.
PA   (WUTD/) WU T D.
PA   (ZHOU/) ZHOU Y.
  Query Match             16.9%;  Score 175;  DB 12;  Length 919;
  Best Local Similarity   58.0%;  Pred. No. 4.2e-43;
RESULT 729
ID   AAF93597 standard; cDNA; 585 BP.
DE   Umbilical vein endothelial cell cDNA encoding SRT protein SEQ ID 418.
PN   WO200107611-A2.
PD   01-FEB-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             15.8%;  Score 163.2;  DB 5;  Length 585;
  Best Local Similarity   62.0%;  Pred. No. 1.5e-39;
RESULT 730
ID   ABS52769 standard; cDNA; 408 BP.
DE   Murine tuberous sclerosis complex 8 (TSC8) DNA.
PN   WO200246475-A2.
PD   13-JUN-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             15.5%;  Score 160;  DB 6;  Length 408;
  Best Local Similarity   63.7%;  Pred. No. 1.2e-38;
RESULT 731
ID   ADQ21981 standard; DNA; 125 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 4801.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             10.7%;  Score 110.8;  DB 12;  Length 125;
  Best Local Similarity   97.6%;  Pred. No. 1.1e-23;
RESULT 732
ID   AAS78037 standard; cDNA; 767 BP.
DE   DNA encoding novel human diagnostic protein #13841.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             10.3%;  Score 106.8;  DB 5;  Length 767;
  Best Local Similarity   94.1%;  Pred. No. 5.3e-22;
RESULT 733
ID   ABX71182 standard; cDNA; 913 BP.
DE   Novel human cDNA sequence #407.
PN   WO200281731-A2.
PD   17-OCT-2002.
PA   (HYSE-) HYSEQ INC.
PA   (GOOD/) GOODRICH R W.
  Query Match             10.2%;  Score 105.6;  DB 8;  Length 913;
  Best Local Similarity   61.1%;  Pred. No. 1.4e-21;
RESULT 734
ID   ADQ54463 standard; DNA; 351 BP.
DE   Novel canine microarray-related DNA sequence SeqID5765.
PN   WO2004063324-A2.
PD   29-JUL-2004.
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PA   (GENE-) GENE LOGIC INC.
PA   (PFIZ ) PFIZER PROD INC.
  Query Match             10.1%;  Score 104.6;  DB 13;  Length 351;
  Best Local Similarity   60.8%;  Pred. No. 1.7e-21;
RESULT 735
ID   AAS78038 standard; cDNA; 693 BP.
DE   DNA encoding novel human diagnostic protein #13842.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              9.9%;  Score 102;  DB 5;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-20;
RESULT 736
ID   AAS78592 standard; cDNA; 1275 BP.
DE   DNA encoding novel human diagnostic protein #14396.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              9.9%;  Score 102;  DB 5;  Length 1275;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-20;
RESULT 737
ID   AAS71904 standard; cDNA; 1275 BP.
DE   DNA encoding novel human diagnostic protein #7708.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              9.9%;  Score 102;  DB 5;  Length 1275;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-20;
RESULT 738
ID   AAS78036 standard; cDNA; 1275 BP.
DE   DNA encoding novel human diagnostic protein #13840.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              9.9%;  Score 102;  DB 5;  Length 1275;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-20;
RESULT 739
ID   AAT42088 standard; cDNA to mRNA; 219 BP.
DE   Human LAMP residues 46-118 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match              9.7%;  Score 100;  DB 2;  Length 219;
  Best Local Similarity   67.0%;  Pred. No. 3.4e-20;
RESULT 740
ID   AAT42089 standard; cDNA to mRNA; 219 BP.
DE   Rat LAMP residues 46-118 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match              9.2%;  Score 95.2;  DB 2;  Length 219;
  Best Local Similarity   65.6%;  Pred. No. 1e-18;
RESULT 741
ID   AAS67246 standard; cDNA; 2678 BP.
DE   DNA encoding novel human diagnostic protein #3050.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              9.1%;  Score 94.4;  DB 5;  Length 2678;
  Best Local Similarity   57.1%;  Pred. No. 7.4e-18;
RESULT 742
ID   AAS71723 standard; cDNA; 2678 BP.
DE   DNA encoding novel human diagnostic protein #7527.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              9.1%;  Score 94.4;  DB 5;  Length 2678;
  Best Local Similarity   57.1%;  Pred. No. 7.4e-18;
RESULT 743
ID   AAS64445 standard; cDNA; 3131 BP.
DE   DNA encoding novel human diagnostic protein #249.
PN   WO200175067-A2.
PD   11-OCT-2001.
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PA   (HYSE-) HYSEQ INC.
  Query Match             9.1%;  Score 94.4;  DB 5;  Length 3131;
  Best Local Similarity   57.1%;  Pred. No. 8.1e-18;
RESULT 744
ID   AAS64798 standard; cDNA; 3131 BP.
DE   DNA encoding novel human diagnostic protein #602.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             9.1%;  Score 94.4;  DB 5;  Length 3131;
  Best Local Similarity   57.1%;  Pred. No. 8.1e-18;
RESULT 745
ID   ADM18382 standard; DNA; 2026 BP.
DE   Human chromosome 11qtel subtelomeric DNA probe SEQ ID NO:6.
PN   WO2004029283-A2.
PD   08-APR-2004.
PA   (CHIL-) CHILDREN'S MERCY HOSPITAL.
  Query Match             8.6%;  Score 89;  DB 12;  Length 2026;
  Best Local Similarity   100.0%;  Pred. No. 3e-16;
RESULT 746
ID   ADG63285 standard; DNA; 420 BP.
DE   Human OBCAM gene exon 4.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             7.6%;  Score 78.6;  DB 10;  Length 420;
  Best Local Similarity   70.5%;  Pred. No. 2.1e-13;
RESULT 747
ID   AAT42090 standard; cDNA to mRNA; 177 BP.
DE   Human LAMP residues 156-204 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             7.5%;  Score 77.8;  DB 2;  Length 177;
  Best Local Similarity   65.0%;  Pred. No. 2.3e-13;
RESULT 748
ID   AAT42091 standard; cDNA to mRNA; 177 BP.
DE   Rat LAMP residues 156-204 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             7.5%;  Score 77.8;  DB 2;  Length 177;
  Best Local Similarity   65.0%;  Pred. No. 2.3e-13;
RESULT 749
ID   ADG63287 standard; DNA; 480 BP.
DE   Human OBCAM gene exon 6.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             7.4%;  Score 76.8;  DB 10;  Length 480;
  Best Local Similarity   70.8%;  Pred. No. 8.2e-13;
RESULT 750
ID   AAS28866 standard; cDNA; 293 BP.
DE   Human immunoglobulin encoding cDNA SEQ ID No 112.
PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             7.1%;  Score 73;  DB 4;  Length 293;
  Best Local Similarity   62.9%;  Pred. No. 9.4e-12;
RESULT 751
ID   ABA06681 standard; cDNA; 293 BP.
DE   Human cDNA SEQ ID NO: 347.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             7.1%;  Score 73;  DB 4;  Length 293;
  Best Local Similarity   62.9%;  Pred. No. 9.4e-12;
RESULT 752
ID   ABV84018 standard; cDNA; 293 BP.
DE   Human polynucleotide SEQ ID NO 347.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
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PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match             7.1%;  Score 73;  DB 6;  Length 293;
  Best Local Similarity   62.9%;  Pred. No. 9.4e-12;
RESULT 753
ID   ADB31591 standard; cDNA; 293 BP.
DE   Human cDNA encoding a novel protein SEQ ID NO 112.
PN   US2003077606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             7.1%;  Score 73;  DB 10;  Length 293;
  Best Local Similarity   62.9%;  Pred. No. 9.4e-12;
RESULT 754
ID   ADG63286 standard; DNA; 480 BP.
DE   Human OBCAM gene exon 5.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             6.9%;  Score 71.4;  DB 10;  Length 480;
  Best Local Similarity   74.4%;  Pred. No. 3.9e-11;
RESULT 755
ID   AAT42092 standard; cDNA to mRNA; 198 BP.
DE   Human LAMP residues 232-297 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             6.2%;  Score 64.6;  DB 2;  Length 198;
  Best Local Similarity   61.3%;  Pred. No. 3e-09;
RESULT 756
ID   AAT42093 standard; cDNA to mRNA; 198 BP.
DE   Rat LAMP residues 232-297 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
  Query Match             6.1%;  Score 63.4;  DB 2;  Length 198;
  Best Local Similarity   60.7%;  Pred. No. 7.1e-09;
RESULT 757
ID   ADG63282 standard; DNA; 270 BP.
DE   Human OBCAM gene exon 1.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             6.0%;  Score 61.6;  DB 10;  Length 270;
  Best Local Similarity   88.6%;  Pred. No. 3.1e-08;
RESULT 758
ID   ADA71938 standard; DNA; 2000 BP.
DE   Rice gene, SEQ ID 5263.
PN   WO2003000898-A1.
PD   03-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
  Query Match             5.7%;  Score 58.6;  DB 8;  Length 2000;
  Best Local Similarity   9.5%;  Pred. No. 7.9e-07;
RESULT 759
ID   ADG63284 standard; DNA; 420 BP.
DE   Human OBCAM gene exon 3.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
  Query Match             5.6%;  Score 57.6;  DB 10;  Length 420;
  Best Local Similarity   65.6%;  Pred. No. 6.8e-07;
RESULT 760
ID   ACH15235 standard; cDNA; 514 BP.
DE   Human adult brain cDNA #2447.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             5.3%;  Score 54.4;  DB 9;  Length 514;
  Best Local Similarity   62.3%;  Pred. No. 7.5e-06;
RESULT 761
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ID   ABL11515 standard; cDNA; 2010 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 29027.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              5.0%;  Score 52.2;  DB 4;  Length 2010;
  Best Local Similarity   45.6%;  Pred. No. 7.6e-05;
RESULT 762
ID   ABX56303 standard; DNA; 8243 BP.
DE   Human NOV25b CG93858-02 DNA SEQ ID 85.
PN   WO200281625-A2.
PD   17-OCT-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match              4.8%;  Score 50;  DB 8;  Length 8243;
  Best Local Similarity   49.7%;  Pred. No. 0.0008;
RESULT 763
ID   ADA71938 standard; DNA; 2000 BP.
DE   Rice gene, SEQ ID 5263.
PN   WO2003000898-A1.
PD   03-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
  Query Match              4.8%;  Score 49.8;  DB 8;  Length 2000;
  Best Local Similarity    7.7%;  Pred. No. 0.00042;
RESULT 764
ID   ADH72103 standard; DNA; 2136 BP.
DE   Human gene of the invention NOV43b SEQ ID NO:999.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match              4.7%;  Score 48.4;  DB 12;  Length 2136;
  Best Local Similarity   49.4%;  Pred. No. 0.0012;
RESULT 765
ID   ACA10119 standard; cDNA; 2153 BP.
DE   Human NOVX polynucleotide #9.
PN   WO200290504-A2.
PD   14-NOV-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match              4.7%;  Score 48.4;  DB 8;  Length 2153;
  Best Local Similarity   49.4%;  Pred. No. 0.0012;
RESULT 766
ID   ADH72101 standard; DNA; 2153 BP.
DE   Human gene of the invention NOV43a SEQ ID NO:997.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match              4.7%;  Score 48.4;  DB 12;  Length 2153;
  Best Local Similarity   49.4%;  Pred. No. 0.0012;
RESULT 767
ID   ADO08270 standard; cDNA; 2153 BP.
DE   Human NOVX polynucleotide #9.
PN   US2004018594-A1.
PD   29-JAN-2004.
PA   (ALSO/) ALSOBROOK J P.
PA   (ANDE/) ANDERSON D W.
PA   (BOLD/) BOLDOG F L.
PA   (BURG/) BURGESS C E.
PA   (CASM/) CASMAN S J.
PA   (CHAP/) CHAPOVAL A.
PA   (EDIN/) EDINGER S R.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (GUNT/) GUNTHER E.
PA   (GUOX/) GUO X S.
PA   (KEKU/) KEKUDA R.
PA   (LEPL/) LEPLEY D M.
PA   (LILL/) LI L.
PA   (LIUX/) LIU X.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLER C E.
PA   (MILL/) MILLET I.
PA   (PADI/) PADIGARU M.
PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
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PA   (RIEG/) RIEGER D K.
PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (SPYT/) SPYTEK K A.
PA   (TAUP/) TAUPIER R J.
PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
PA   (ZERH/) ZERHUSEN B D.
  Query Match              4.7%;  Score 48.4;  DB 12;  Length 2153;
  Best Local Similarity   49.4%;  Pred. No. 0.0012;
RESULT 768
ID   AAS68120 standard; cDNA; 3910 BP.
DE   DNA encoding novel human diagnostic protein #3924.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              4.7%;  Score 48.4;  DB 5;  Length 3910;
  Best Local Similarity   49.4%;  Pred. No. 0.0017;
RESULT 769
ID   AAI72024 standard; cDNA; 4073 BP.
DE   Human thrombospondin protein, BTL.012, coding sequence.
PN   WO200174852-A2.
PD   11-OCT-2001.
PA   (FARB ) BAYER CORP.
  Query Match              4.7%;  Score 48.4;  DB 6;  Length 4073;
  Best Local Similarity   49.4%;  Pred. No. 0.0017;
RESULT 770
ID   ADL93996 standard; cDNA; 5877 BP.
DE   Human G-coupled protein receptor-related gene #44.
PN   US2004006205-A1.
PD   08-JAN-2004.
PA   (LILL/) LI L.
PA   (GERL/) GERLACH V.
PA   (LIUX/) LIU X.
PA   (MILL/) MILLER C E.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PENA/) PENA C E A.
PA   (SHEN/) SHENOY S G.
PA   (ZHON/) ZHONG H.
PA   (SMIT/) SMITHSON G.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (VOSS/) VOSS E Z.
PA   (VERN/) VERNET C A.
PA   (MACD/) MACDOUGALL J R.
PA   (RAST/) RASTELLI L.
PA   (ANDE/) ANDERSON D W.
PA   (ZHON/) ZHONG M.
PA   (MEZE/) MEZES P S.
PA   (FURT/) FURTAK K.
PA   (PATT/) PATTURAJAN M.
PA   (BURG/) BURGESS C E.
PA   (MALY/) MALYANKAR U M.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (EDIN/) EDINGER S.
PA   (MAZU/) MAZUR A.
  Query Match              4.7%;  Score 48.4;  DB 12;  Length 5877;
  Best Local Similarity   49.4%;  Pred. No. 0.0021;
RESULT 771
ID   ADE16057 standard; DNA; 5935 BP.
DE   G-coupled protein receptor related polypeptide DNA, SEQ ID No 87.
PN   WO200283841-A2.
PD   24-OCT-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match              4.7%;  Score 48.4;  DB 10;  Length 5935;
  Best Local Similarity   49.4%;  Pred. No. 0.0021;
RESULT 772
ID   ABX56304 standard; DNA; 6343 BP.
DE   Human NOV25c CG56914-03 DNA SEQ ID 87.
PN   WO200281625-A2.
PD   17-OCT-2002.
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PA   (CURA-) CURAGEN CORP.
  Query Match             4.7%;  Score 48.4;  DB 8;  Length 6343;
  Best Local Similarity   49.4%;  Pred. No. 0.0022;
RESULT 773
ID   ADH72107 standard; DNA; 6343 BP.
DE   Human gene of the invention NOV43d SEQ ID NO:1003.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             4.7%;  Score 48.4;  DB 12;  Length 6343;
  Best Local Similarity   49.4%;  Pred. No. 0.0022;
RESULT 774
ID   ADK60477 standard; DNA; 8546 BP.
DE   Angiogenesis differentially expressed gene GS-N52.
PN   FR2836687-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
  Query Match             4.7%;  Score 48.4;  DB 12;  Length 8546;
  Best Local Similarity   49.4%;  Pred. No. 0.0026;
RESULT 775
ID   ADK60778 standard; DNA; 8546 BP.
DE   Angiogenesis differentially expressed gene GS-N52.
PN   FR2836686-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
  Query Match             4.7%;  Score 48.4;  DB 12;  Length 8546;
  Best Local Similarity   49.4%;  Pred. No. 0.0026;
RESULT 776
ID   ADP73100 standard; DNA; 8546 BP.
DE   Angiogenesis inhibitor human DNA sequence, GS-N52.
PN   FR2843753-A1.
PD   27-FEB-2004.
PA   (GENE/) GENE S.
PA   (ALMS/) AL M S.
  Query Match             4.7%;  Score 48.4;  DB 12;  Length 8546;
  Best Local Similarity   49.4%;  Pred. No. 0.0026;
RESULT 777
ID   ADS09799 standard; DNA; 8546 BP.
DE   Human therapeutic DNA - SEQ ID 36.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
  Query Match             4.7%;  Score 48.4;  DB 13;  Length 8546;
  Best Local Similarity   49.4%;  Pred. No. 0.0026;
RESULT 778
ID   ADO08272 standard; cDNA; 15659 BP.
DE   Human NOVX polynucleotide #10.
PN   US2004018594-A1.
PD   29-JAN-2004.
PA   (ALSO/) ALSOBROOK J P.
PA   (ANDE/) ANDERSON D W.
PA   (BOLD/) BOLDOG F L.
PA   (BURG/) BURGESS C E.
PA   (CASM/) CASMAN S J.
PA   (CHAP/) CHAPOVAL A.
PA   (EDIN/) EDINGER S R.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (GUNT/) GUNTHER E.
PA   (GUOX/) GUO X S.
PA   (KEKU/) KEKUDA R.
PA   (LEPL/) LEPLEY D M.
PA   (LILL/) LI L.
PA   (LIUX/) LIU X.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLER C E.
PA   (MILL/) MILLET I.
PA   (PADI/) PADIGARU M.
PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
PA   (RIEG/) RIEGER D K.
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PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (SPYT/) SPYTEK K A.
PA   (TAUP/) TAUPIER R J.
PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
PA   (ZERH/) ZERHUSEN B D.
  Query Match             4.7%;  Score 48.4;  DB 12;  Length 15659;
  Best Local Similarity   49.4%;  Pred. No. 0.0036;
RESULT 779
ID   ACA10120 standard; cDNA; 15660 BP.
DE   Human NOVX polynucleotide #10.
PN   WO200290504-A2.
PD   14-NOV-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             4.7%;  Score 48.4;  DB 8;  Length 15660;
  Best Local Similarity   49.4%;  Pred. No. 0.0036;
RESULT 780
ID   ADH72105 standard; DNA; 15660 BP.
DE   Human gene of the invention NOV43c SEQ ID NO:1001.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
  Query Match             4.7%;  Score 48.4;  DB 12;  Length 15660;
  Best Local Similarity   49.4%;  Pred. No. 0.0036;
RESULT 781
ID   ABQ86156 standard; DNA; 16908 BP.
DE   Novel human gene. SEQ ID 27.
PN   WO200250105-A1.
PD   27-JUN-2002.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
  Query Match             4.7%;  Score 48.4;  DB 6;  Length 16908;
  Best Local Similarity   49.4%;  Pred. No. 0.0037;
RESULT 782
ID   ADK60455 standard; DNA; 18207 BP.
DE   Angiogenesis differentially expressed gene GS-N29.
PN   FR2836687-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
  Query Match             4.7%;  Score 48.4;  DB 12;  Length 18207;
  Best Local Similarity   49.4%;  Pred. No. 0.0039;
RESULT 783
ID   ADK60756 standard; DNA; 18207 BP.
DE   Angiogenesis differentially expressed gene GS-N29.
PN   FR2836686-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
  Query Match             4.7%;  Score 48.4;  DB 12;  Length 18207;
  Best Local Similarity   49.4%;  Pred. No. 0.0039;
RESULT 784
ID   ADP73078 standard; DNA; 18207 BP.
DE   Angiogenesis inhibitor human DNA sequence, GS-N29.
PN   FR2843753-A1.
PD   27-FEB-2004.
PA   (GENE/) GENE S.
PA   (ALMS/) AL M S.
  Query Match             4.7%;  Score 48.4;  DB 12;  Length 18207;
  Best Local Similarity   49.4%;  Pred. No. 0.0039;
RESULT 785
ID   ADQ22570 standard; DNA; 18248 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5390.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             4.7%;  Score 48.4;  DB 12;  Length 18248;
  Best Local Similarity   49.4%;  Pred. No. 0.0039;
RESULT 786
ID   ACH14951 standard; cDNA; 467 BP.
DE   Human adult brain cDNA #2163.
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PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             4.1%;  Score 42.8;  DB 9;  Length 467;
  Best Local Similarity   50.5%;  Pred. No. 0.028;
RESULT 787
ID   ABD33040 standard; cDNA; 3588 BP.
DE   Human cancer-associated cDNA HR22-025.1.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
  Query Match             4.1%;  Score 42.4;  DB 13;  Length 3588;
  Best Local Similarity   47.4%;  Pred. No. 0.11;
RESULT 788
ID   AAI64283 standard; DNA; 4548 BP.
DE   Human transient axonal glycoprotein (tag-1) DNA.
PN   WO200188546-A2.
PD   22-NOV-2001.
PA   (UNMI ) UNIV MICHIGAN.
  Query Match             4.1%;  Score 42.4;  DB 6;  Length 4548;
  Best Local Similarity   47.4%;  Pred. No. 0.13;
RESULT 789
ID   ABD33041 standard; cDNA; 6137 BP.
DE   Human cancer-associated cDNA HR22-025.2.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
  Query Match             4.1%;  Score 42.4;  DB 13;  Length 6137;
  Best Local Similarity   47.4%;  Pred. No. 0.15;
RESULT 790
ID   ADQ23368 standard; DNA; 7625 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 6188.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             4.1%;  Score 42.4;  DB 12;  Length 7625;
  Best Local Similarity   47.4%;  Pred. No. 0.17;
RESULT 791
ID   ADQ24513 standard; DNA; 7625 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             4.1%;  Score 42.4;  DB 12;  Length 7625;
  Best Local Similarity   47.4%;  Pred. No. 0.17;
RESULT 792
ID   ADO28580 standard; cDNA; 7650 BP.
DE   Human axonin-1 precursor (AXO1) encoding cDNA SEQ ID NO:9.
PN   WO2004044178-A2.
PD   27-MAY-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             4.1%;  Score 42.4;  DB 12;  Length 7650;
  Best Local Similarity   47.4%;  Pred. No. 0.17;
RESULT 793
ID   AAV31988 standard; cDNA; 6413 BP.
DE   Human Down syndrome-cell adhesion molecule DS-CAM2 cDNA.
PN   WO9817795-A1.
PD   30-APR-1998.
PA   (CEDA-) CEDARS SINAI MEDICAL CENT.
  Query Match             4.0%;  Score 41.6;  DB 2;  Length 6413;
  Best Local Similarity   45.8%;  Pred. No. 0.28;
RESULT 794
ID   AAV31981 standard; cDNA; 6604 BP.
DE   Human Down syndrome-cell adhesion molecule DS-CAM1 cDNA.
PN   WO9817795-A1.
PD   30-APR-1998.
PA   (CEDA-) CEDARS SINAI MEDICAL CENT.
  Query Match             4.0%;  Score 41.6;  DB 2;  Length 6604;
  Best Local Similarity   45.8%;  Pred. No. 0.28;
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RESULT 795
ID   ADK71086 standard; DNA; 6649 BP.
DE   Human MP21 polypeptide encoding DNA.
PN   WO2004015073-A2.
PD   19-FEB-2004.
PA   (EXEL-) EXELIXIS INC.
  Query Match             4.0%;  Score 41.6;  DB 12;  Length 6649;
  Best Local Similarity   45.8%;  Pred. No. 0.29;
RESULT 796
ID   AAL57278 standard; DNA; 1267 BP.
DE   DKFZp761A179 'human modifier of p53 pathway' DNA.
PN   WO2003035833-A2.
PD   01-MAY-2003.
PA   (EXEL-) EXELIXIS INC.
  Query Match             4.0%;  Score 41.2;  DB 8;  Length 1267;
  Best Local Similarity   54.7%;  Pred. No. 0.15;
RESULT 797
ID   ABK34766 standard; cDNA; 1869 BP.
DE   Human cDNA for novel secreted protein, SEQ ID 535.
PN   WO200177290-A2.
PD   18-OCT-2001.
PA   (GEMY ) GENETICS INST INC.
  Query Match             4.0%;  Score 41.2;  DB 6;  Length 1869;
  Best Local Similarity   54.7%;  Pred. No. 0.19;
RESULT 798
ID   ABX03572 standard; DNA; 2083 BP.
DE   Human nervous system leucine rich repeat protein (HLRRNS1) EST.
PN   WO200274959-A2.
PD   26-SEP-2002.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
  Query Match             4.0%;  Score 41.2;  DB 6;  Length 2083;
  Best Local Similarity   54.7%;  Pred. No. 0.2;
RESULT 799
ID   AAS62318 standard; cDNA; 2090 BP.
DE   cDNA sequence #105 encoding novel human secreted protein.
PN   WO200177291-A2.
PD   18-OCT-2001.
PA   (GEMY ) GENETICS INST INC.
  Query Match             4.0%;  Score 41.2;  DB 6;  Length 2090;
  Best Local Similarity   54.7%;  Pred. No. 0.2;
RESULT 800
ID   ABX70472 standard; DNA; 2316 BP.
DE   DNA encoding human GPCR related protein NOV31a.
PN   WO200279398-A2.
PD   10-OCT-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             4.0%;  Score 41.2;  DB 8;  Length 2316;
  Best Local Similarity   54.7%;  Pred. No. 0.21;
RESULT 801
ID   ADL24096 standard; cDNA; 2316 BP.
DE   Human NOVX cDNA #71.
PN   US2004002120-A1.
PD   01-JAN-2004.
PA   (KEKU/) KEKUDA R.
PA   (TCHE/) TCHERNEV V T.
PA   (LIUX/) LIU X.
PA   (SPYT/) SPYTEK K A.
PA   (PATT/) PATTURAJAN M.
PA   (BURG/) BURGESS C E.
PA   (VERN/) VERNET C A M.
PA   (LILL/) LI L.
PA   (GORM/) GORMAN L.
PA   (MALY/) MALYANKAR U M.
PA   (BOLD/) BOLDOG F L.
PA   (GUOX/) GUO X.
PA   (SHEN/) SHENOY S G.
PA   (PADI/) PADIGARU M.
PA   (TAUP/) TAUPIER R J.
PA   (MILL/) MILLER C E.
PA   (CASM/) CASMAN S J.
PA   (PENA/) PENA C E A.
PA   (GANG/) GANGOLLI E A.
PA   (GUSE/) GUSEV V Y.
PA   (SMIT/) SMITHSON G.
PA   (ZERH/) ZERHUSEN B D.
PA   (GERL/) GERLACH V.
PA   (POCH/) POCHART P F.
PA   (FERN/) FERNANDES E R.
PA   (SHIM/) SHIMKETS R A.
PA   (RAST/) RASTELLI L.
PA   (SPAD/) SPADERNA S K.
PA   (LARO/) LAROCHELLE W J.
PA   (ZHON/) ZHONG M.
PA   (KHRA/) KHRAMTSOV N V.
PA   (VOSS/) VOSS E Z.
PA   (HERR/) HERRMANN J L.
  Query Match             4.0%;  Score 41.2;  DB 12;  Length 2316;
  Best Local Similarity   54.7%;  Pred. No. 0.21;
RESULT 802
ID   ABK62093 standard; cDNA; 2397 BP.
DE   Human cDNA encoding novel secreted protein LP223(b).
PN   WO200214358-A2.
PD   21-FEB-2002.
PA   (ELIL ) LILLY & CO ELI.
  Query Match             4.0%;  Score 41.2;  DB 6;  Length 2397;
  Best Local Similarity   54.7%;  Pred. No. 0.22;
RESULT 803
ID   ABX03571 standard; DNA; 2450 BP.
DE   DNA encoding human nervous system leucine rich repeat protein #1.
PN   WO200274959-A2.
PD   26-SEP-2002.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
  Query Match             4.0%;  Score 41.2;  DB 6;  Length 2450;
  Best Local Similarity   54.7%;  Pred. No. 0.22;
RESULT 804
ID   AAD21287 standard; cDNA; 2493 BP.
DE   Human leucine-rich repeat (LRR) family member cDNA.
PN   WO200175105-A2.
PD   11-OCT-2001.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match             4.0%;  Score 41.2;  DB 5;  Length 2493;
  Best Local Similarity   54.7%;  Pred. No. 0.22;
RESULT 805
ID   AAD54734 standard; cDNA; 2522 BP.
DE   Human CGDD-1 cDNA.
PN   WO2002102310-A2.
PD   27-DEC-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             4.0%;  Score 41.2;  DB 10;  Length 2522;
  Best Local Similarity   54.7%;  Pred. No. 0.22;
RESULT 806
ID   ADD25618 standard; DNA; 2633 BP.
DE   Binding domain-immunoglobulin fusion protein-associated DNA #93.
PN   US2003118592-A1.
PD   26-JUN-2003.
PA   (GENE-) GENECRAFT INC.
  Query Match             4.0%;  Score 41.2;  DB 10;  Length 2633;
  Best Local Similarity   50.0%;  Pred. No. 0.23;
RESULT 807
ID   ADI31624 standard; cDNA; 2633 BP.
DE   Human cDNA #950.
PN   US6607879-B1.
PD   19-AUG-2003.
PA   (INCY-) INCYTE CORP.
  Query Match             4.0%;  Score 41.2;  DB 11;  Length 2633;
  Best Local Similarity   50.0%;  Pred. No. 0.23;
RESULT 808
ID   ABX03577 standard; DNA; 2756 BP.
DE   DNA encoding human nervous system leucine rich repeat protein #2.
PN   WO200274959-A2.
PD   26-SEP-2002.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
  Query Match             4.0%;  Score 41.2;  DB 6;  Length 2756;
  Best Local Similarity   54.7%;  Pred. No. 0.23;
RESULT 809
ID   ADI24496 standard; cDNA; 2960 BP.
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DE   Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:46.
PN   WO2004004785-A1.
PD   15-JAN-2004.
PA   (EXEL-) EXELIXIS INC.
  Query Match             4.0%;  Score 41.2;  DB 12;  Length 2960;
  Best Local Similarity   50.0%;  Pred. No. 0.24;
RESULT 810
ID   ABK62087 standard; cDNA; 3027 BP.
DE   Human cDNA encoding novel secreted protein LP223(a).
PN   WO200214358-A2.
PD   21-FEB-2002.
PA   (ELIL ) LILLY & CO ELI.
  Query Match             4.0%;  Score 41.2;  DB 6;  Length 3027;
  Best Local Similarity   54.7%;  Pred. No. 0.25;
RESULT 811
ID   ADQ24300 standard; DNA; 3110 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7120.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             4.0%;  Score 41.2;  DB 12;  Length 3110;
  Best Local Similarity   54.7%;  Pred. No. 0.25;
RESULT 812
ID   ADA53985 standard; cDNA; 3309 BP.
DE   Human coding sequence, SEQ ID 1553.
PN   EP1293569-A2.
PD   19-MAR-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match             4.0%;  Score 41.2;  DB 10;  Length 3309;
  Best Local Similarity   50.0%;  Pred. No. 0.26;
RESULT 813
ID   AAL62047 standard; cDNA; 3360 BP.
DE   Human cell adhesion and extracellular matrix protein (CADECM)-35 cDNA.
PN   WO2003047526-A2.
PD   12-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             4.0%;  Score 41.2;  DB 9;  Length 3360;
  Best Local Similarity   50.0%;  Pred. No. 0.26;
RESULT 814
ID   AAH98595 standard; cDNA; 4710 BP.
DE   Human EST-derived coding sequence SEQ ID NO: 452.
PN   WO200154477-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             4.0%;  Score 41.2;  DB 4;  Length 4710;
  Best Local Similarity   50.0%;  Pred. No. 0.31;
RESULT 815
ID   AAH98610 standard; cDNA; 4710 BP.
DE   Human EST-derived coding sequence SEQ ID NO: 467.
PN   WO200154477-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             4.0%;  Score 41.2;  DB 4;  Length 4710;
  Best Local Similarity   50.0%;  Pred. No. 0.31;
RESULT 816
ID   ABX63089 standard; cDNA; 4978 BP.
DE   Human cDNA #89 differentially expressed in activated vascular tissue.
PN   US2002137081-A1.
PD   26-SEP-2002.
PA   (BAND/) BANDMAN O.
  Query Match             4.0%;  Score 41.2;  DB 8;  Length 4978;
  Best Local Similarity   50.0%;  Pred. No. 0.32;
RESULT 817
ID   ADL12516 standard; cDNA; 5807 BP.
DE   Human steroid-induced C3A liver cell cDNA #245.
PN   US6673549-B1.
PD   06-JAN-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             4.0%;  Score 41.2;  DB 12;  Length 5807;
  Best Local Similarity   50.0%;  Pred. No. 0.35;
RESULT 818
ID   AAD14203 standard; DNA; 8513 BP.
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DE   MESVR/EGFP/IRESNCAMPro(ori) vector.
PN   WO200155371-A1.
PD   02-AUG-2001.
PA   (SCRI ) SCRIPPS RES INST.
  Query Match              4.0%;  Score 41.2;  DB 4;  Length 8513;
  Best Local Similarity   50.0%;  Pred. No. 0.44;
RESULT 819
ID   ABT17038 standard; DNA; 4620 BP.
DE   Human MP21 gene neogenin SEQ ID No 12.
PN   WO2003006990-A1.
PD   23-JAN-2003.
PA   (EXEL-) EXELIXIS INC.
  Query Match              3.9%;  Score 40.2;  DB 10;  Length 4620;
  Best Local Similarity   49.3%;  Pred. No. 0.63;
RESULT 820
ID   AAS70835 standard; cDNA; 4650 BP.
DE   DNA encoding novel human diagnostic protein #6639.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              3.9%;  Score 40.2;  DB 5;  Length 4650;
  Best Local Similarity   49.3%;  Pred. No. 0.64;
RESULT 821
ID   ADE09880 standard; DNA; 4650 BP.
DE   Novel DNA-related contig nucleotide sequence #602.
PN   WO2003054152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match              3.9%;  Score 40.2;  DB 10;  Length 4650;
  Best Local Similarity   49.3%;  Pred. No. 0.64;
RESULT 822
ID   ABV94279 standard; cDNA; 5297 BP.
DE   Breast carcinoma related nucleotide sequence SEQ ID NO:270.
PN   WO200246467-A2.
PD   13-JUN-2002.
PA   (IPSO-) IPSOGEN.
  Query Match              3.9%;  Score 40.2;  DB 6;  Length 5297;
  Best Local Similarity   49.3%;  Pred. No. 0.68;
RESULT 823
ID   ADS99922 standard; cDNA; 5297 BP.
DE   Human neogenin homologue 1 (NEO1), cDNA.
PN   US2003148327-A1.
PD   07-AUG-2003.
PA   (OLEK/) OLEK A.
PA   (PIEP/) PIEPENBROCK C.
PA   (BERL/) BERLIN K.
  Query Match              3.9%;  Score 40.2;  DB 7;  Length 5297;
  Best Local Similarity   49.3%;  Pred. No. 0.68;
RESULT 824
ID   ABX10384 standard; DNA; 5297 BP.
DE   DNA encoding protein differentially regulated in prostate cancer #53.
PN   WO200281638-A2.
PD   17-OCT-2002.
PA   (ORIG-) ORIGENE TECHNOLOGIES INC.
  Query Match              3.9%;  Score 40.2;  DB 8;  Length 5297;
  Best Local Similarity   49.3%;  Pred. No. 0.68;
RESULT 825
ID   ADQ18519 standard; DNA; 5297 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 1338.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              3.9%;  Score 40.2;  DB 12;  Length 5297;
  Best Local Similarity   49.3%;  Pred. No. 0.68;
RESULT 826
ID   ADL12801 standard; cDNA; 5506 BP.
DE   Human steroid-induced C3A liver cell cDNA #530.
PN   US6673549-B1.
PD   06-JAN-2004.
PA   (INCY-) INCYTE CORP.
  Query Match              3.9%;  Score 40.2;  DB 12;  Length 5506;
  Best Local Similarity   49.3%;  Pred. No. 0.7;
RESULT 827
ID   AAL62014 standard; cDNA; 5543 BP.
DE   Human cell adhesion and extracellular matrix protein (CADECM)-2 cDNA.
PN   WO2003047526-A2.
PD   12-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match              3.9%;  Score 40.2;  DB 9;  Length 5543;
  Best Local Similarity   49.3%;  Pred. No. 0.7;
RESULT 828
ID   ADQ23000 standard; DNA; 5544 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5820.
PN · WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              3.9%;  Score 40.2;  DB 12;  Length 5544;
  Best Local Similarity   49.3%;  Pred. No. 0.7;
RESULT 829
ID   ABS76362 standard; DNA; 5553 BP.
DE   DNA encoding human immunoglobulin superfamily protein IGSFP-7.
PN   WO200272794-A2.
PD   19-SEP-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match              3.9%;  Score 40.2;  DB 6;  Length 5553;
  Best Local Similarity   49.3%;  Pred. No. 0.7;
RESULT 830
ID   ADF83428 standard; DNA; 1623 BP.
DE   Bread wheat phytase enzyme coding sequence #1.
PN   WO200183763-A2.
PD   08-NOV-2001.
PA   (RISO-) RISOE FORSKNINGSCENTER.
  Query Match              3.8%;  Score 39.8;  DB 6;  Length 1623;
  Best Local Similarity   49.8%;  Pred. No. 0.47;
RESULT 831
ID   ABV75372 standard; DNA; 31024 BP.
DE   Human IGFBP-2 gene sequence.
PN   WO200290580-A1.
PD   14-NOV-2002.
PA   (NACA-) NAT CANCER CENT SINGAPORE PTE LTD.
PA   (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
PA   (ARGA/) ARGAET V P.
  Query Match              3.8%;  Score 39.8;  DB 10;  Length 31024;
  Best Local Similarity   47.1%;  Pred. No. 2.4;
RESULT 832
ID   ADC08783 standard; DNA; 741 BP.
DE   Wheat DNA sequence Seq ID1088 related to grain filling.
PN   WO2003000905-A2.
PD   03-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
  Query Match              3.8%;  Score 39.4;  DB 10;  Length 741;
  Best Local Similarity   46.8%;  Pred. No. 0.41;
RESULT 833
ID   ADQ18218 standard; DNA; 2650 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 1035.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              3.8%;  Score 39.4;  DB 12;  Length 2650;
  Best Local Similarity   46.0%;  Pred. No. 0.83;
RESULT 834
ID   ADP25365 standard; cDNA; 2650 BP.
DE   PRO polypeptide encoding cDNA SEQ ID NO:479.
PN   WO2004041170-A2.
PD   21-MAY-2004.
PA   (GETH ) GENENTECH INC.
  Query Match              3.8%;  Score 39.4;  DB 13;  Length 2650;
  Best Local Similarity   46.0%;  Pred. No. 0.83;
RESULT 835
ID   ADS19466 standard; DNA; 2650 BP.
DE   Glucose-6-phosphate dehydrogenase DNA, a therapeutic gene.
PN   WO2004083404-A2.
PD   30-SEP-2004.
PA   (ISOG-) ISOGENIS INC.
  Query Match              3.8%;  Score 39.4;  DB 13;  Length 2650;
  Best Local Similarity   46.0%;  Pred. No. 0.83;
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RESULT 836
ID   AAK92784 standard; cDNA; 518 BP.
DE   Human cDNA 3'-end sequence, SEQ ID NO: 1244.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
  Query Match              3.8%;  Score 39;  DB 4;  Length 518;
  Best Local Similarity   53.6%;  Pred. No. 0.45;
RESULT 837
ID   AAK94072 standard; cDNA; 518 BP.
DE   Human cDNA clone representative sequence, SEQ ID NO: 2532.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
  Query Match              3.8%;  Score 39;  DB 4;  Length 518;
  Best Local Similarity   53.6%;  Pred. No. 0.45;
RESULT 838
ID   ADL29211 standard; cDNA; 518 BP.
DE   3' end of a human cDNA molecule SeqID 1244.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match              3.8%;  Score 39;  DB 12;  Length 518;
  Best Local Similarity   53.6%;  Pred. No. 0.45;
RESULT 839
ID   ADL30499 standard; cDNA; 518 BP.
DE   3' end of a representative human cDNA cluster SeqID 2532.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match              3.8%;  Score 39;  DB 12;  Length 518;
  Best Local Similarity   53.6%;  Pred. No. 0.45;
RESULT 840
ID   ABL19627 standard; DNA; 1883 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 10354.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.8%;  Score 39;  DB 4;  Length 1883;
  Best Local Similarity   49.7%;  Pred. No. 0.91;
RESULT 841
ID   AAK94366 standard; cDNA; 2742 BP.
DE   Human full-length cDNA, SEQ ID NO: 3089.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
  Query Match              3.8%;  Score 39;  DB 4;  Length 2742;
  Best Local Similarity   53.6%;  Pred. No. 1.1;
RESULT 842
ID   ADL31056 standard; cDNA; 2742 BP.
DE   Full length human cDNA clone SeqID 3089.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match              3.8%;  Score 39;  DB 12;  Length 2742;
  Best Local Similarity   53.6%;  Pred. No. 1.1;
RESULT 843
ID   ADT44512 standard; cDNA; 3390 BP.
DE   Bacterial polynucleotide #19263.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match              3.8%;  Score 39;  DB 13;  Length 3390;
  Best Local Similarity   48.1%;  Pred. No. 1.3;
RESULT 844
ID   ABL19626 standard; DNA; 4012 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 10351.
PN   WO200171042-A2.
PD   27-SEP-2001.
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PA   (PEKE ) PE CORP NY.
  Query Match              3.8%;  Score 39;  DB 4;  Length 4012;
  Best Local Similarity   49.7%;  Pred. No. 1.4;
RESULT 845
ID   ABL19624 standard; DNA; 4057 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 10345.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.8%;  Score 39;  DB 4;  Length 4057;
  Best Local Similarity   49.7%;  Pred. No. 1.4;
RESULT 846
ID   ADT42073 standard; cDNA; 2952 BP.
DE   Bacterial polynucleotide #16824.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match              3.7%;  Score 38.8;  DB 13;  Length 2952;
  Best Local Similarity   53.2%;  Pred. No. 1.3;
RESULT 847
ID   ABL25336 standard; DNA; 4285 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 27481.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.7%;  Score 38.8;  DB 4;  Length 4285;
  Best Local Similarity   57.4%;  Pred. No. 1.7;
RESULT 848
ID   ABD32648 standard; cDNA; 5913 BP.
DE   Mouse cancer-associated cDNA MR13-036.1.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
  Query Match              3.7%;  Score 38.8;  DB 13;  Length 5913;
  Best Local Similarity   49.0%;  Pred. No. 2;
RESULT 849
ID   ADB61924 standard; cDNA; 2462 BP.
DE   Human cDNA encoding clone BNGH42007798.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match              3.7%;  Score 38.6;  DB 10;  Length 2462;
  Best Local Similarity   65.9%;  Pred. No. 1.4;
RESULT 850
ID   ADH18905 standard; cDNA; 4000 BP.
DE   Human cell adhesion and extracellular matrix CADECM-1 cDNA - SEQ 32.
PN   WO2003094843-A2.
PD   20-NOV-2003.
PA   (INCY-) INCYTE CORP.
  Query Match              3.7%;  Score 38.6;  DB 12;  Length 4000;
  Best Local Similarity   65.9%;  Pred. No. 1.8;
RESULT 851
ID   ACN42224 standard; cDNA; 4045 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:1099.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match              3.7%;  Score 38.6;  DB 13;  Length 4045;
  Best Local Similarity   65.9%;  Pred. No. 1.8;
RESULT 852
ID   ACN42225 standard; cDNA; 4053 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:1100.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match              3.7%;  Score 38.6;  DB 13;  Length 4053;
  Best Local Similarity   65.9%;  Pred. No. 1.8;
RESULT 853
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ID   AAD49595 standard; cDNA; 4080 BP.
DE   Human cytoskeleton-associated protein, CSAP-6 cDNA.
PN   WO200279404-A2.
PD   10-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             3.7%;  Score 38.6;  DB 8;  Length 4080;
  Best Local Similarity   65.9%;  Pred. No. 1.9;
RESULT 854
ID   ABT16046 standard; DNA; 4131 BP.
DE   NOVX related polynucleotide SEQ ID No 59.
PN   WO200299062-A2.
PD   12-DEC-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             3.7%;  Score 38.6;  DB 8;  Length 4131;
  Best Local Similarity   65.9%;  Pred. No. 1.9;
RESULT 855
ID   ADO41693 standard; cDNA; 4131 BP.
DE   Novel human polypeptide NOV22a cDNA.
PN   US2004018555-A1.
PD   29-JAN-2004.
PA   (ANDE/) ANDERSON D W.
PA   (ZERH/) ZERHUSEN B D.
PA   (LILL/) LI L.
PA   (ZHON/) ZHONG M.
PA   (CASM/) CASMAN S J.
PA   (GERL/) GERLACH V.
PA   (SHIM/) SHIMKETS R A.
PA   (GORM/) GORMAN L.
PA   (PENA/) PENA C E A.
PA   (KEKU/) KEKUDA R.
PA   (PATT/) PATTURAJAN M.
PA   (SPYT/) SPYTEK K A.
PA   (LEIT/) LEITE M W.
PA   (RAST/) RASTELLI L.
PA   (MACD/) MACDOUGALL J R.
PA   (TAUP/) TAUPIER R J.
PA   (GUOX/) GUO X S.
PA   (MILL/) MILLER C E.
PA   (SHEN/) SHENOY S G.
PA   (HJAL/) HJALT T.
PA   (VOSS/) VOSS E Z.
PA   (BOLD/) BOLDOG F L.
PA   (MALY/) MALYANKAR U M.
PA   (PADI/) PADIGARU M.
PA   (JIWW/) JI W.
PA   (SMIT/) SMITHSON G.
PA   (EDIN/) EDINGER S R.
PA   (MILL/) MILLET I.
PA   (ELLE/) ELLERMAN K.
  Query Match             3.7%;  Score 38.6;  DB 12;  Length 4131;
  Best Local Similarity   65.9%;  Pred. No. 1.9;
RESULT 856
ID   AAD49596 standard; cDNA; 4360 BP.
DE   Human cytoskeleton-associated protein, CSAP-7 cDNA.
PN   WO200279404-A2.
PD   10-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             3.7%;  Score 38.6;  DB 8;  Length 4360;
  Best Local Similarity   65.9%;  Pred. No. 1.9;
RESULT 857
ID   ACN42223 standard; cDNA; 4633 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:1098.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.7%;  Score 38.6;  DB 13;  Length 4633;
  Best Local Similarity   65.9%;  Pred. No. 2;
RESULT 858
ID   AAK51847 standard; cDNA; 4694 BP.
DE   Human polynucleotide SEQ ID NO 392.
PN   WO200157190-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             3.7%;  Score 38.6;  DB 4;  Length 4694;
  Best Local Similarity   65.9%;  Pred. No. 2;
RESULT 859
ID   AAK51848 standard; cDNA; 4739 BP.
DE   Human polynucleotide SEQ ID NO 393.
PN   WO200157190-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             3.7%;  Score 38.6;  DB 4;  Length 4739;
  Best Local Similarity   65.9%;  Pred. No. 2;
RESULT 860
ID   ACN42222 standard; cDNA; 4834 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:1097.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.7%;  Score 38.6;  DB 13;  Length 4834;
  Best Local Similarity   65.9%;  Pred. No. 2;
RESULT 861
ID   ADQ18863 standard; DNA; 4955 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 1682.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             3.7%;  Score 38.6;  DB 12;  Length 4955;
  Best Local Similarity   65.9%;  Pred. No. 2.1;
RESULT 862
ID   ADR14752 standard; DNA; 5244 BP.
DE   Nucleotide sequence of human MAPCAX orthologue #10.
PN   WO2004066948-A2.
PD   12-AUG-2004.
PA   (EXEL-) EXELIXIS INC.
  Query Match             3.7%;  Score 38.6;  DB 13;  Length 5244;
  Best Local Similarity   65.9%;  Pred. No. 2.1;
RESULT 863
ID   ADH82128 standard; DNA; 366 BP.
DE   Enterococcus faecalis polynucleotide #13.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
  Query Match             3.7%;  Score 38.4;  DB 10;  Length 366;
  Best Local Similarity   51.1%;  Pred. No. 0.56;
RESULT 864
ID   ABD02016 standard; DNA; 366 BP.
DE   Pseudomonas aeruginosa polynucleotide #620.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.7%;  Score 38.4;  DB 11;  Length 366;
  Best Local Similarity   51.1%;  Pred. No. 0.56;
RESULT 865
ID   ADH82126 standard; DNA; 591 BP.
DE   Enterococcus faecalis polynucleotide #11.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
  Query Match             3.7%;  Score 38.4;  DB 10;  Length 591;
  Best Local Similarity   51.1%;  Pred. No. 0.74;
RESULT 866
ID   ABD02170 standard; DNA; 912 BP.
DE   Pseudomonas aeruginosa polynucleotide #774.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.7%;  Score 38.4;  DB 11;  Length 912;
  Best Local Similarity   51.1%;  Pred. No. 0.93;
RESULT 867
ID   ABD02039 standard; DNA; 948 BP.
DE   Pseudomonas aeruginosa polynucleotide #643.
PN   US6551795-B1.
PD   22-APR-2003.
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PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match              3.7%;  Score 38.4;  DB 11;  Length 948;
  Best Local Similarity   51.1%;  Pred. No. 0.96;
RESULT 868
ID   AAL49438 standard; DNA; 984 BP.
DE   Cell adhesion molecule coding sequence SEQ ID NO: 1.
PN   WO200264771-A1.
PD   22-AUG-2002.
PA   (MOCH ) MOCHIDA PHARM CO LTD.
  Query Match              3.7%;  Score 38.4;  DB 6;  Length 984;
  Best Local Similarity   53.3%;  Pred. No. 0.97;
RESULT 869
ID   ADT43022 standard; cDNA; 1281 BP.
DE   Bacterial polynucleotide #17773.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match              3.7%;  Score 38.4;  DB 13;  Length 1281;
  Best Local Similarity   47.5%;  Pred. No. 1.1;
RESULT 870
ID   AAL39652 standard; DNA; 1500 BP.
DE   Human secreted protein DNA SEQ ID No 96.
PN   WO200238602-A2.
PD   16-MAY-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match              3.7%;  Score 38.4;  DB 6;  Length 1500;
  Best Local Similarity   53.3%;  Pred. No. 1.2;
RESULT 871
ID   ADD69626 standard; cDNA; 1513 BP.
DE   Human REMAP cDNA - SEQ ID 55.
PN   WO2003048305-A2.
PD   12-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match              3.7%;  Score 38.4;  DB 10;  Length 1513;
  Best Local Similarity   53.3%;  Pred. No. 1.2;
RESULT 872
ID   AAL49439 standard; DNA; 1523 BP.
DE   Cell adhesion molecule related DNA #14.
PN   WO200264771-A1.
PD   22-AUG-2002.
PA   (MOCH ) MOCHIDA PHARM CO LTD.
  Query Match              3.7%;  Score 38.4;  DB 6;  Length 1523;
  Best Local Similarity   53.3%;  Pred. No. 1.2;
RESULT 873
ID   ADB63075 standard; cDNA; 2375 BP.
DE   Human cDNA encoding clone SMINT20017310.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match              3.7%;  Score 38.4;  DB 10;  Length 2375;
  Best Local Similarity   53.3%;  Pred. No. 1.6;
RESULT 874
ID   ADM02018 standard; cDNA; 2735 BP.
DE   Human cDNA of the invention SEQ ID NO:703.
PN   EP1347046-A1.
PD   24-SEP-2003.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match              3.7%;  Score 38.4;  DB 11;  Length 2735;
  Best Local Similarity   53.3%;  Pred. No. 1.7;
RESULT 875
ID   ABL13797 standard; cDNA; 4808 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 35873.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.7%;  Score 38.4;  DB 4;  Length 4808;
  Best Local Similarity   58.9%;  Pred. No. 2.3;
RESULT 876
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ID   AAD60168 standard; cDNA; 4890 BP.
DE   Drosophila melanogaster VEGFR cDNA #2.
PN   US6599717-B1.
PD   29-JUL-2003.
PA   (EXEL-) EXELIXIS INC.
  Query Match              3.7%;  Score 38.4;  DB 10;  Length 4890;
  Best Local Similarity   58.9%;  Pred. No. 2.4;
RESULT 877
ID   AAD60170 standard; cDNA; 4943 BP.
DE   Drosophila melanogaster VEGFR isolated mutant cDNA.
PN   US6599717-B1.
PD   29-JUL-2003.
PA   (EXEL-) EXELIXIS INC.
  Query Match              3.7%;  Score 38.4;  DB 10;  Length 4943;
  Best Local Similarity   58.9%;  Pred. No. 2.4;
RESULT 878
ID   AAD60169 standard; cDNA; 5170 BP.
DE   Drosophila melanogaster VEGFR cDNA #3.
PN   US6599717-B1.
PD   29-JUL-2003.
PA   (EXEL-) EXELIXIS INC.
  Query Match              3.7%;  Score 38.4;  DB 10;  Length 5170;
  Best Local Similarity   58.9%;  Pred. No. 2.4;
RESULT 879
ID   ABL13796 standard; cDNA; 20311 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 35870.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.7%;  Score 38.4;  DB 4;  Length 20311;
  Best Local Similarity   58.9%;  Pred. No. 5.2;
RESULT 880
ID   ABL25337 standard; DNA; 1242 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 27484.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.7%;  Score 38;  DB 4;  Length 1242;
  Best Local Similarity   60.8%;  Pred. No. 1.5;
RESULT 881
ID   AAA52631 standard; DNA; 885 BP.
DE   Eosinophil activating peptide gene 24.
PN   WO200032630-A2.
PD   08-JUN-2000.
PA   (SEAR ) SEARLE & CO G D.
  Query Match              3.7%;  Score 37.8;  DB 3;  Length 885;
  Best Local Similarity   45.7%;  Pred. No. 1.4;
RESULT 882
ID   ABZ83196 standard; cDNA; 1024 BP.
DE   Toxicologically relevant human nucleotide sequence #355.
PN   WO2003016500-A2.
PD   27-FEB-2003.
PA   (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
  Query Match              3.7%;  Score 37.8;  DB 10;  Length 1024;
  Best Local Similarity   45.7%;  Pred. No. 1.5;
RESULT 883
ID   ABL20249 standard; DNA; 1605 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 12220.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.7%;  Score 37.8;  DB 4;  Length 1605;
  Best Local Similarity   48.4%;  Pred. No. 2;
RESULT 884
ID   ADF61833 standard; DNA; 2631 BP.
DE   Human glucose-6-phosphate dehydrogenase DNA.
PN   WO2003088910-A2.
PD   30-OCT-2003.
PA   (RIGE-) RIGEL PHARM INC.
  Query Match              3.7%;  Score 37.8;  DB 10;  Length 2631;
  Best Local Similarity   45.7%;  Pred. No. 2.6;
RESULT 885
ID   ADQ86257 standard; cDNA; 2631 BP.
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DE   Human tumour-associated antigenic target (TAT) cDNA sequence #3129.
PN   WO2004060270-A2.
PD   22-JUL-2004.
PA   (GETH ) GENENTECH INC.
PA   (WUTD/) WU T D.
PA   (ZHOU/) ZHOU Y.
  Query Match             3.7%;  Score 37.8;  DB 12;  Length 2631;
  Best Local Similarity   45.7%;  Pred. No. 2.6;
RESULT 886
ID   ADQ87416 standard; cDNA; 2631 BP.
DE   Human tumour-associated antigenic target (TAT) cDNA sequence #4293.
PN   WO2004060270-A2.
PD   22-JUL-2004.
PA   (GETH ) GENENTECH INC.
PA   (WUTD/) WU T D.
PA   (ZHOU/) ZHOU Y.
  Query Match             3.7%;  Score 37.8;  DB 12;  Length 2631;
  Best Local Similarity   45.7%;  Pred. No. 2.6;
RESULT 887
ID   ACN41102 standard; cDNA; 2631 BP.
DE   Tumour-associated antigenic target (TAT) cDNA DNA327111, SEQ ID NO:6320.
PN   WO2004030615-A2.
PD   15-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.7%;  Score 37.8;  DB 13;  Length 2631;
  Best Local Similarity   45.7%;  Pred. No. 2.6;
RESULT 888
ID   ADQ22767 standard; DNA; 2680 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5587.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             3.7%;  Score 37.8;  DB 12;  Length 2680;
  Best Local Similarity   45.7%;  Pred. No. 2.6;
RESULT 889
ID   AAF21697 standard; DNA; 2803 BP.
DE   Human breast and ovarian cancer associated antigen gene SEQ ID 84.
PN   WO200055173-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.7%;  Score 37.8;  DB 3;  Length 2803;
  Best Local Similarity   45.7%;  Pred. No. 2.7;
RESULT 890
ID   ABL20248 standard; DNA; 9680 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 12217.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match             3.7%;  Score 37.8;  DB 4;  Length 9680;
  Best Local Similarity   48.4%;  Pred. No. 5.3;
RESULT 891
ID   AAX35377 standard; DNA; 384 BP.
DE   SEQ ID 52 of WO9916889.
PN   WO9916889-A1.
PD   08-APR-1999.
PA   (SEAR ) SEARLE & CO G D.
  Query Match             3.6%;  Score 37.6;  DB 2;  Length 384;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 892
ID   ADG48023 standard; DNA; 387 BP.
DE   Human variant TTR (C10A/G83C) DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 893
ID   ADG48019 standard; DNA; 387 BP.
DE   Human variant TTR (C10A) DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
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PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 894
ID   ADG48020 standard; DNA; 387 BP.
DE   Human variant TTR (C10A/A37C) DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 895
ID   ADG48024 standard; DNA; 387 BP.
DE   Human variant TTR (C10A/K15A/G83C) DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 896
ID   ADG48021 standard; DNA; 387 BP.
DE   Human variant TTR (C10A/D38C) DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 897
ID   ADG48018 standard; DNA; 387 BP.
DE   Human transthyretin (TTR) DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 898
ID   ADG68775 standard; cDNA; 387 BP.
DE   Human mutant transthyretin (TTR)  cDNA #1.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 899
ID   ADG68779 standard; cDNA; 387 BP.
DE   Human mutant transthyretin (TTR)  cDNA #5.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 900
ID   ADG68774 standard; cDNA; 387 BP.
DE   Human transthyretin (TTR)  cDNA.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 901
ID   ADG68777 standard; cDNA; 387 BP.
DE   Human mutant transthyretin (TTR)  cDNA #3.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
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  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 902
ID   ADG68776 standard; cDNA; 387 BP.
DE   Human mutant transthyretin (TTR)  cDNA #2.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 903
ID   ADG68780 standard; cDNA; 387 BP.
DE   Human mutant transthyretin (TTR)  cDNA #6.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 387;
  Best Local Similarity   50.6%;  Pred. No. 1;
RESULT 904
ID   ADG48033 standard; DNA; 439 BP.
DE   Human TTR (C10A/G83C)-bradykinin variant fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 439;
  Best Local Similarity   50.6%;  Pred. No. 1.1;
RESULT 905
ID   ADG68789 standard; cDNA; 439 BP.
DE   Human mutant transthyretin (TTR)  cDNA #15.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 439;
  Best Local Similarity   50.6%;  Pred. No. 1.1;
RESULT 906
ID   ABZ83385 standard; cDNA; 483 BP.
DE   Toxicologically relevant human nucleotide sequence #544.
PN   WO2003016500-A2.
PD   27-FEB-2003.
PA   (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
  Query Match             3.6%;  Score 37.6;  DB 10;  Length 483;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 907
ID   ADG48089 standard; DNA; 495 BP.
DE   Human TMP-TTR (C10A/K15A/G83C) fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 495;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 908
ID   ADG48027 standard; DNA; 495 BP.
DE   Human TMP-TTR (C10A/D38C) variant fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 495;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 909
ID   ADG48029 standard; DNA; 495 BP.
DE   Human TMP-TTR (C10A/G83C) variant fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 495;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
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RESULT 910
ID   ADG48091 standard; DNA; 495 BP.
DE   Human TMP-TTR (C10A/K15A/A37C) fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 495;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 911
ID   ADG48025 standard; DNA; 495 BP.
DE   Human TMP-TTR fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 495;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 912
ID   ADG48026 standard; DNA; 495 BP.
DE   Human TMP-TTR (C10A/A37C) variant fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 495;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 913
ID   ADG68785 standard; cDNA; 495 BP.
DE   Human mutant transthyretin (TTR)  cDNA #11.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 495;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 914
ID   ADG68782 standard; cDNA; 495 BP.
DE   Human mutant transthyretin (TTR)  cDNA #8.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 495;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 915
ID   ADG68781 standard; cDNA; 495 BP.
DE   Human mutant transthyretin (TTR)  cDNA #7.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 495;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 916
ID   ADG68783 standard; cDNA; 495 BP.
DE   Human mutant transthyretin (TTR)  cDNA #9.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 495;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 917
ID   ADG48084 standard; DNA; 510 BP.
DE   Human TTR-TMP fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 510;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 918
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ID   ADG48088 standard; DNA; 510 BP.
DE   Human TTR (C10A/K15A/G83C)-TMP fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 510;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 919
ID   ADG48086 standard; DNA; 510 BP.
DE   Human TTR (C10A/K15A/A37C)-TMP fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 510;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 920
ID   ADG48085 standard; DNA; 510 BP.
DE   Human TTR (C10A/K15A)-TMP fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 510;
  Best Local Similarity   50.6%;  Pred. No. 1.2;
RESULT 921
ID   ADE76836 standard; cDNA; 572 BP.
DE   Human cDNA differentially expressed in a liver disorder #1.
PN   US2003108871-A1.
PD   12-JUN-2003.
PA   (KASE/) KASER M R.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 572;
  Best Local Similarity   50.6%;  Pred. No. 1.3;
RESULT 922
ID   ADG48065 standard; DNA; 591 BP.
DE   Human GLP-1-TTR (C10A/K15A/G83C) variant fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 591;
  Best Local Similarity   50.6%;  Pred. No. 1.3;
RESULT 923
ID   ADG48064 standard; DNA; 594 BP.
DE   Human GLP-1-TTR (C10A/G83C) variant fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 594;
  Best Local Similarity   50.6%;  Pred. No. 1.3;
RESULT 924
ID   ABQ78304 standard; DNA; 615 BP.
DE   Nucleotide sequence of transthyretin polypeptide.
PN   WO200259621-A2.
PD   01-AUG-2002.
PA   (FARB ) BAYER CORP.
  Query Match             3.6%;  Score 37.6;  DB 6;  Length 615;
  Best Local Similarity   50.6%;  Pred. No. 1.3;
RESULT 925
ID   ABQ78305 standard; DNA; 615 BP.
DE   Nucleotide sequence of transthyretin polypeptide.
PN   WO200259621-A2.
PD   01-AUG-2002.
PA   (FARB ) BAYER CORP.
  Query Match             3.6%;  Score 37.6;  DB 6;  Length 615;
  Best Local Similarity   50.6%;  Pred. No. 1.3;
RESULT 926
ID   AAN60839 standard; cDNA; 631 BP.
DE   Cloned pre-albumin DNA.
PN   JP61052292-A.
PD   14-MAR-1986.
PA   (MITH ) MITSUI PHARM INC.
  Query Match             3.6%;  Score 37.6;  DB 1;  Length 631;
  Best Local Similarity   50.6%;  Pred. No. 1.3;
RESULT 927
ID   AAN90103 standard; cDNA; 669 BP.
DE   Human prealbumin cDNA.
PN   JP01117790-A.
PD   10-MAY-1989.
PA   (KAGA ) KAGAKU OYOBI KESSEI RYOHO.
  Query Match             3.6%;  Score 37.6;  DB 1;  Length 669;
  Best Local Similarity   50.6%;  Pred. No. 1.4;
RESULT 928
ID   ADG48078 standard; DNA; 723 BP.
DE   Human immunoglobulin CH2 domain-TTR (C10A) fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 723;
  Best Local Similarity   50.6%;  Pred. No. 1.5;
RESULT 929
ID   ADG48072 standard; DNA; 735 BP.
DE   Human TTR (C10A)-immunoglobulin CH2 domain fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 735;
  Best Local Similarity   50.6%;  Pred. No. 1.5;
RESULT 930
ID   ADG48081 standard; DNA; 831 BP.
DE   Human TMP-immunoglobulin CH2 domain-TTR (C10A) fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 831;
  Best Local Similarity   50.6%;  Pred. No. 1.6;
RESULT 931
ID   ADG48031 standard; DNA; 843 BP.
DE   Human IL-1ra-TTR (C10A) variant fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 843;
  Best Local Similarity   50.6%;  Pred. No. 1.6;
RESULT 932
ID   ADG48075 standard; DNA; 843 BP.
DE   Human TTR (C10A)-CH2-TMP fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 843;
  Best Local Similarity   50.6%;  Pred. No. 1.6;
RESULT 933
ID   ADG48073 standard; DNA; 843 BP.
DE   Human TMP-TTR (C10A)-immunoglobulin CH2 domain fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 843;
  Best Local Similarity   50.6%;  Pred. No. 1.6;
RESULT 934
ID   ADG68787 standard; cDNA; 843 BP.
DE   Human mutant transthyretin (TTR)  cDNA #13.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 843;
  Best Local Similarity   50.6%;  Pred. No. 1.6;
RESULT 935
ID   ADG48032 standard; DNA; 855 BP.
DE   Human TTR (C10A)-IL-1ra variant fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 855;
  Best Local Similarity   50.6%;  Pred. No. 1.6;
RESULT 936
ID   ADG68788 standard; cDNA; 855 BP.
DE   Human mutant transthyretin (TTR)  cDNA #14.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 855;
  Best Local Similarity   50.6%;  Pred. No. 1.6;
RESULT 937
ID   ADS45904 standard; cDNA; 1017 BP.
DE   Bacterial polynucleotide #647.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match             3.6%;  Score 37.6;  DB 13;  Length 1017;
  Best Local Similarity   47.5%;  Pred. No. 1.8;
RESULT 938
ID   ADF83430 standard; DNA; 1370 BP.
DE   Bread wheat phytase enzyme coding sequence #2.
PN   WO200183763-A2.
PD   08-NOV-2001.
PA   (RISO-) RISOE FORSKNINGSCENTER.
  Query Match             3.6%;  Score 37.6;  DB 6;  Length 1370;
  Best Local Similarity   49.0%;  Pred. No. 2.1;
RESULT 939
ID   ADI14335 standard; DNA; 5198 BP.
DE   Human Neogenin nucleic acid.
PN   WO2004003150-A2.
PD   08-JAN-2004.
PA   (UYYA ) UNIV YALE.
  Query Match             3.6%;  Score 37.6;  DB 12;  Length 5198;
  Best Local Similarity   48.6%;  Pred. No. 4.3;
RESULT 940
ID   ADQ62949 standard; cDNA; 1829 BP.
DE   Novel human cDNA sequence #110.
PN   EP1440981-A2.
PD   28-JUL-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match             3.6%;  Score 37.4;  DB 12;  Length 1829;
  Best Local Similarity   53.0%;  Pred. No. 2.8;
RESULT 941
ID   AAI61348 standard; cDNA; 2265 BP.
DE   Human polynucleotide SEQ ID NO 5337.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             3.6%;  Score 37.4;  DB 4;  Length 2265;
  Best Local Similarity   53.0%;  Pred. No. 3.2;
RESULT 942
ID   ABL15323 standard; cDNA; 2472 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 40451.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match             3.6%;  Score 37.4;  DB 4;  Length 2472;
  Best Local Similarity   57.1%;  Pred. No. 3.3;
RESULT 943
ID   ADM93822 standard; DNA; 2916 BP.
DE   DNA encoding human NOV protein #21.
PN   US2004009480-A1.
PD   15-JAN-2004.
PA   (ANDE/) ANDERSON D W.
PA   (BAUM/) BAUMGARTNER J C.
PA   (BOLD/) BOLDOG F L.
PA   (CASM/) CASMAN S J.
PA   (EDIN/) EDINGER S R.
PA   (GANG/) GANGOLLI E A.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (GUOX/) GUO X S.
PA   (HJAL/) HJALT T.
PA   (KEKU/) KEKUDA R.
PA   (LILL/) LI L.
PA   (MACD/) MACDOUGALL J R.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLET I.
PA   (PADI/) PADIGARU M.
PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
PA   (RAST/) RASTELLI L.
PA   (SHIM/) SHIMKETS R A.
PA   (STON/) STONE D J.
PA   (SPYT/) SPYTEK K A.
PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
PA   (ZERH/) ZERHUSEN B D.
  Query Match             3.6%;  Score 37.4;  DB 12;  Length 2916;
  Best Local Similarity   47.6%;  Pred. No. 3.6;
RESULT 944
ID   AAC84449 standard; cDNA; 3705 BP.
DE   Nucleotide sequence of mddt cDNA clone ID No: 243096.6.
PN   WO200075298-A2.
PD   14-DEC-2000.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             3.6%;  Score 37.4;  DB 4;  Length 3705;
  Best Local Similarity   53.0%;  Pred. No. 4.1;
RESULT 945
ID   AAA30430 standard; DNA; 925 BP.
DE   Human RaceACAM DNA sequence.
PN   WO200032633-A1.
PD   08-JUN-2000.
PA   (ICOS-) ICOS CORP.
  Query Match             3.6%;  Score 37;  DB 3;  Length 925;
  Best Local Similarity   49.5%;  Pred. No. 2.6;
RESULT 946
ID   ADT44452 standard; cDNA; 1857 BP.
DE   Bacterial polynucleotide #19203.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match             3.6%;  Score 37;  DB 13;  Length 1857;
  Best Local Similarity   49.2%;  Pred. No. 3.8;
RESULT 947
ID   ADL13892 standard; DNA; 2832 BP.
DE   Osteoarthritis-associated polymorphic nucleotide #424.
PN   WO2003054166-A2.
PD   03-JUL-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             3.6%;  Score 37;  DB 10;  Length 2832;
  Best Local Similarity   47.6%;  Pred. No. 4.8;
RESULT 948
ID   ADP74597 standard; DNA; 4091 BP.
DE   Nucleotide sequence of tyrosine kinase-like orphan receptor 2.
PN   WO2004048540-A2.
PD   10-JUN-2004.
PA   (EXEL-) EXELIXIS INC.
  Query Match             3.6%;  Score 37;  DB 12;  Length 4091;
  Best Local Similarity   47.6%;  Pred. No. 5.8;
RESULT 949
ID   AAV70230 standard; DNA; 4092 BP.
DE   Human receptor tyrosine kinase ROR-2 encoding DNA.
PN   US5843749-A.
PD   01-DEC-1998.
PA   (REGE-) REGENERON PHARM INC.
  Query Match             3.6%;  Score 37;  DB 2;  Length 4092;
  Best Local Similarity   47.6%;  Pred. No. 5.8;
RESULT 950
ID   ADL13891 standard; DNA; 4092 BP.
DE   Osteoarthritis-associated polymorphic nucleotide #423.
PN   WO2003054166-A2.
PD   03-JUL-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             3.6%;  Score 37;  DB 10;  Length 4092;
  Best Local Similarity   47.6%;  Pred. No. 5.8;
RESULT 951
ID   ADQ19268 standard; DNA; 4092 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 2087.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             3.6%;  Score 37;  DB 12;  Length 4092;
  Best Local Similarity   47.6%;  Pred. No. 5.8;
RESULT 952
ID   ADQ89065 standard; cDNA; 4092 BP.
DE   Human urological disorder related protein 5410 encoding cDNA SEQ:17.
PN   WO2004065576-A2.
PD   05-AUG-2004.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match             3.6%;  Score 37;  DB 13;  Length 4092;
  Best Local Similarity   47.6%;  Pred. No. 5.8;
RESULT 953
ID   ADQ23542 standard; DNA; 4132 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 6362.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             3.6%;  Score 37;  DB 12;  Length 4132;
  Best Local Similarity   47.6%;  Pred. No. 5.9;
RESULT 954
ID   ABK84529 standard; cDNA; 7195 BP.
DE   Human cDNA differentially expressed in granulocytic cells #1100.
PN   WO200228999-A2.
PD   11-APR-2002.
PA   (GENE-) GENE LOGIC INC.
  Query Match             3.6%;  Score 37;  DB 6;  Length 7195;
  Best Local Similarity   53.0%;  Pred. No. 8;
RESULT 955
ID   AAH48024 standard; DNA; 14041 BP.
DE   Internal control B19c #1.
PN   WO200146463-A2.
PD   28-JUN-2001.
PA   (BAXT ) BAXTER AG.
  Query Match             3.6%;  Score 37;  DB 4;  Length 14041;
  Best Local Similarity   17.4%;  Pred. No. 12;
RESULT 956
ID   ABD11363 standard; DNA; 546 BP.
DE   Pseudomonas aeruginosa polynucleotide #9967.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.6%;  Score 36.8;  DB 11;  Length 546;
  Best Local Similarity   50.0%;  Pred. No. 2.2;
RESULT 957
ID   ABD11580 standard; DNA; 1350 BP.
DE   Pseudomonas aeruginosa polynucleotide #10184.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.6%;  Score 36.8;  DB 11;  Length 1350;
  Best Local Similarity   50.0%;  Pred. No. 3.6;
RESULT 958
ID   ABD11441 standard; DNA; 3639 BP.
DE   Pseudomonas aeruginosa polynucleotide #10045.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.6%;  Score 36.8;  DB 11;  Length 3639;
  Best Local Similarity   50.0%;  Pred. No. 6.3;
RESULT 959
ID   ABD11188 standard; DNA; 3717 BP.
DE   Pseudomonas aeruginosa polynucleotide #9792.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.6%;  Score 36.8;  DB 11;  Length 3717;
  Best Local Similarity   50.0%;  Pred. No. 6.4;
RESULT 960
ID   AAD60167 standard; cDNA; 5220 BP.
DE   Drosophila melanogaster VEGFR cDNA #1.
PN   US6599717-B1.
PD   29-JUL-2003.
PA   (EXEL-) EXELIXIS INC.
  Query Match             3.6%;  Score 36.8;  DB 10;  Length 5220;
  Best Local Similarity   58.0%;  Pred. No. 7.7;
RESULT 961
ID   AAV89551 standard; cDNA; 397 BP.
DE   EST clone CR1162.
PN   WO9845436-A2.
PD   15-OCT-1998.
PA   (GEMY ) GENETICS INST INC.
  Query Match             3.5%;  Score 36.4;  DB 2;  Length 397;
  Best Local Similarity   49.5%;  Pred. No. 2.5;
RESULT 962
ID   AAH06394 standard; cDNA; 820 BP.
DE   Human cDNA clone (5'-primer) SEQ ID NO:3229.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
  Query Match             3.5%;  Score 36.4;  DB 4;  Length 820;
  Best Local Similarity   49.5%;  Pred. No. 3.7;
RESULT 963
ID   AAD04299 standard; cDNA; 1242 BP.
DE   Human brain immunoglobulin superfamily receptor (BIgR) cDNA.
PN   WO200129083-A1.
PD   26-APR-2001.
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
  Query Match             3.5%;  Score 36.4;  DB 5;  Length 1242;
  Best Local Similarity   49.5%;  Pred. No. 4.6;
RESULT 964
ID   AAD04351 standard; cDNA; 1242 BP.
DE   Alternative version of human BIgR cDNA.
PN   WO200129083-A1.
PD   26-APR-2001.
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
  Query Match             3.5%;  Score 36.4;  DB 5;  Length 1242;
  Best Local Similarity   49.5%;  Pred. No. 4.6;
RESULT 965
ID   ABT17389 standard; DNA; 1242 BP.
DE   Human IG gene related nucleic acid SEQ ID No 15.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1242;
  Best Local Similarity   49.5%;  Pred. No. 4.6;
RESULT 966
ID   ABT17386 standard; DNA; 1274 BP.
DE   Human IG gene related nucleic acid SEQ ID No 12.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1274;
  Best Local Similarity   49.5%;  Pred. No. 4.7;
RESULT 967
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ID   ABT17388 standard; DNA; 1299 BP.
DE   Human IG gene related nucleic acid SEQ ID No 14.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match              3.5%;  Score 36.4;  DB 8;  Length 1299;
  Best Local Similarity   49.5%;  Pred. No. 4.7;
RESULT 968
ID   AAA13653 standard; cDNA; 1302 BP.
DE   Human Beat-like 1 (BL1) cDNA coding sequence.
PN   CN1242376-A.
PD   26-JAN-2000.
PA   (BASI-) BASIC MEDICAL SCI RES INST CHINESE ACAD.
  Query Match              3.5%;  Score 36.4;  DB 3;  Length 1302;
  Best Local Similarity   49.5%;  Pred. No. 4.7;
RESULT 969
ID   ABT17387 standard; DNA; 1376 BP.
DE   Human IG gene related nucleic acid SEQ ID No 13.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
  Query Match              3.5%;  Score 36.4;  DB 8;  Length 1376;
  Best Local Similarity   49.5%;  Pred. No. 4.9;
RESULT 970
ID   ACA38048 standard; DNA; 1515 BP.
DE   Prokaryotic essential gene #19705.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
  Query Match              3.5%;  Score 36.4;  DB 8;  Length 1515;
  Best Local Similarity   49.0%;  Pred. No. 5.2;
RESULT 971
ID   AAV84523 standard; DNA; 1542 BP.
DE   Human secreted protein gene 113 clone HCE3Q10.
PN   WO9854963-A2.
PD   10-DEC-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.5%;  Score 36.4;  DB 2;  Length 1542;
  Best Local Similarity   49.5%;  Pred. No. 5.2;
RESULT 972
ID   ABA83441 standard; cDNA; 1542 BP.
DE   Human secreted protein related cDNA SEQ ID NO:1244.
PN   WO200162891-A2.
PD   30-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.5%;  Score 36.4;  DB 4;  Length 1542;
  Best Local Similarity   49.5%;  Pred. No. 5.2;
RESULT 973
ID   ACH04807 standard; cDNA; 1542 BP.
DE   Novel human secreted protein #113 cDNA.
PN   US2003065160-A1.
PD   03-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1542;
  Best Local Similarity   49.5%;  Pred. No. 5.2;
RESULT 974
ID   ACD44617 standard; cDNA; 1542 BP.
DE   Human cDNA from novel secreted protein gene 113.
PN   US6525174-B1.
PD   25-FEB-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1542;
  Best Local Similarity   49.5%;  Pred. No. 5.2;
RESULT 975
ID   AAZ08540 standard; cDNA; 1614 BP.
DE   Human MBGP1 encoding cDNA.
PN   EP939124-A2.
PD   01-SEP-1999.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
  Query Match              3.5%;  Score 36.4;  DB 2;  Length 1614;
  Best Local Similarity   49.5%;  Pred. No. 5.3;
RESULT 976
ID   AAX52229 standard; DNA; 1685 BP.
DE   Protein PRO258 cDNA clone DNA35918-1174.
PN   WO9914328-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 2;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 977
ID   ADC78403 standard; cDNA; 1685 BP.
DE   Human PRO258 cDNA.
PN   WO200015796-A2.
PD   23-MAR-2000.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 3;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 978
ID   AAF72387 standard; cDNA; 1685 BP.
DE   Human PRO258 cDNA.
PN   WO200104311-A1.
PD   18-JAN-2001.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 4;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 979
ID   AAS21417 standard; cDNA; 1685 BP.
DE   Human cDNA sequence encoding for PRO258 polypeptide.
PN   WO200140466-A2.
PD   07-JUN-2001.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 4;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 980
ID   AAC97445 standard; cDNA; 1685 BP.
DE   Human angiogenesis-associated protein PRO258 cDNA, SEQ ID NO:100.
PN   WO200053753-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 4;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 981
ID   ABL88093 standard; cDNA; 1685 BP.
DE   Human PRO258 cDNA sequence SEQ ID NO:43.
PN   WO200200690-A2.
PD   03-JAN-2002.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 6;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 982
ID   ABL95582 standard; cDNA; 1685 BP.
DE   Human angiogenesis related cDNA PRO258 SEQ ID NO: 43.
PN   WO200208284-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match              3.5%;  Score 36.4;  DB 6;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 983
ID   ACA60068 standard; cDNA; 1685 BP.
DE   Human cDNA for secreted/transmembrane protein PRO258.
PN   US2003003530-A1.
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PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 984
ID   ACD07468 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2002197671-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 985
ID   ACA03776 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003036180-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 986
ID   ABX71516 standard; cDNA; 1685 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO258.
PN   US2002132240-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 987
ID   ACH06848 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane polypeptide PRO258 cDNA.
PN   US2003044839-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 988
ID   ABX89314 standard; cDNA; 1685 BP.
DE   DNA encoding novel secreted and transmembrane protein PRO258.
PN   US2003017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 989
ID   ACD41968 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #174.
PN   US2003036179-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 990
ID   ABX96085 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2002160374-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 991
ID   ACA05406 standard; cDNA; 1685 BP.
DE   cDNA encoding human secreted protein PRO258.
PN   US2003023054-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 992
ID   ACD20073 standard; cDNA; 1685 BP.
DE   Human secreted / transmembrane polypeptide PRO258 cDNA.
PN   US2003036060-A1.
PD   20-FEB-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 993
ID   ACA04197 standard; cDNA; 1685 BP.
DE   Human cDNA encoding a secreted/transmembrane protein, SEQ ID 347.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 994
ID   ACA54876 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003017463-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 8;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 995
ID   ACD19711 standard; cDNA; 1685 BP.
DE   Human secreted / transmembrane polypeptide PRO258 cDNA.
PN   US2003027143-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 996
ID   ADA45866 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 997
ID   ADA76297 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 998
ID   ADB29288 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003092002-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 999
ID   ADA18947 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003054517-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1000
ID   ADA61570 standard; cDNA; 1685 BP.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1001
ID   ADB19355 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1002
ID   ADB27896 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1003
ID   ADA86375 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1004
ID   ADB15939 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1005
ID   ADA47725 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1006
ID   ADA18144 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003039971-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1007
ID   ACD66858 standard; cDNA; 1685 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO258.
PN   US2003045693-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1008
ID   ADA67520 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1009
ID   ADB30527 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003068794-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1010
ID   ADA85823 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082693-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1011
ID   ADA97035 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082705-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1012
ID   ADA79339 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082763-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1013
ID   ADA87478 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087345-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1014
ID   ADB16680 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003087349-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1015
ID   ACD83019 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #15.
PN   US2003044793-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1016
ID   ADA16119 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003049621-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1017
ID   ADA91772 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082694-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1018
ID   ADB14835 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003087351-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1019
ID   ADB18796 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003073211-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
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RESULT 1020
ID   ADA94011 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003077722-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1021
ID   ADB19907 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082691-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1022
ID   ADB13219 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082710-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1023
ID   ACD98597 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003044945-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1024
ID   ADA74473 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003068798-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1025
ID   ADA42264 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003054401-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1026
ID   ADB24706 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide SEQ ID NO 347.
PN   US2003077713-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1027
ID   ADA82230 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082701-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1028
ID   ADA75193 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003073216-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1029
ID   ADA85271 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082695-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1030
ID   ADA84719 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1031
ID   ACD23197 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #15.
PN   US2003064367-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1032
ID   ADB29975 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1033
ID   ADA80503 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1034
ID   ADA75745 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082703-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1035
ID   ADA46970 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003073210-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1036
ID   ADB25266 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide SEQ ID NO 347.
PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1037
ID   ADA93442 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003077721-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1038
ID   ADB26792 standard; cDNA; 1685 BP.
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DE   cDNA encoding human PRO polypeptide #174.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1039
ID   ADB31079 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1040
ID   ADA61007 standard; cDNA; 1685 BP.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1041
ID   ADB24154 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide SEQ ID NO 347.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1042
ID   ADA96483 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082690-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1043
ID   ADA81055 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082702-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1044
ID   ADA95931 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1045
ID   ADB26240 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1046
ID   ADB21725 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1047
ID   ADA77504 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
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PN   US2003068797-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1048
ID   ADB18244 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003077710-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1049
ID   ADA86927 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082709-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1050
ID   ADA16543 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003039969-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1051
ID   ADA12972 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003049622-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1052
ID   ADA41840 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003082540-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1053
ID   ADA88030 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082700-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1054
ID   ADA46418 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003054516-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1055
ID   ADA17187 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003017498-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1056
ID   ADA42690 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003054351-A1.
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PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1057
ID   ADB28448 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003082699-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1058
ID   ADB29000 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003082706-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1059
ID   ADA76952 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003059909-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1060
ID   ADA88582 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003073213-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1061
ID   ADA97587 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082686-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1062
ID   ADB27344 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003022239-A1.
PD   30-JAN-2003.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1063
ID   ADB22277 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087344-A1.
PD   08-MAY-2003.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1064
ID   ACD23559 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #15.
PN   US2003064923-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1065
ID   ADA66968 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003068793-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1066
ID   ADB22829 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003077711-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1067
ID   ADB23602 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide SEQ ID NO 347.
PN   US2003077712-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1068
ID   ADA92324 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082712-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1069
ID   ADB15387 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003087352-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1070
ID   ADB38639 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082766-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1071
ID   ADB38087 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087347-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1072
ID   ADB66559 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082689-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1073
ID   ADB89639 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082698-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1074
ID   ADB90371 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082762-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
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RESULT 1075
ID   ADB77609 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003077654-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1076
ID   ADB39472 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082764-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1077
ID   ADB74745 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003082542-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1078
ID   ADB47095 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082687-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1079
ID   ADB86702 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003082697-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1080
ID   ADB77307 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082696-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1081
ID   ADB34464 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide SEQ ID NO 347.
PN   US2003077717-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1082
ID   ADB35568 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide SEQ ID NO 347.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1083
ID   ADB33912 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide SEQ ID NO 347.
PN   US2003077716-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1084
ID   ADB35016 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide SEQ ID NO 347.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1085
ID   ADB36120 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide SEQ ID NO 347.
PN   US2003077720-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1086
ID   ADB46515 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003082692-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1087
ID   ADC28391 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003059772-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1088
ID   ADC39591 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003059828-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1089
ID   ADC40105 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003059829-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1090
ID   ADC18933 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003036061-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1091
ID   ADC34229 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003036094-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1092
ID   ADC29284 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003049676-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1093
ID   ADC28815 standard; cDNA; 1685 BP.
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DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003049677-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1094
ID   ADC40700 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003054400-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1095
ID   ADC19357 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003054441-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1096
ID   ADC33805 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003073077-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1097
ID   ADC12875 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003073079-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1098
ID   ADC50388 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003092106-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1099
ID   ADC71935 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1100
ID   ADC59914 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1101
ID   ADC52921 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID347.
PN   US2003087365-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1102
ID   ADC57275 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID347.
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PN   US2003087366-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1103
ID   ADC60466 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1104
ID   ADC50941 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1105
ID   ADC65468 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1106
ID   ADC54566 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID347.
PN   US2003087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1107
ID   ADC53527 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID347.
PN   US2003087364-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1108
ID   ADC59050 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID347.
PN   US2003087359-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1109
ID   ADC55928 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID347.
PN   US2003087360-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1110
ID   ADC58498 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID347.
PN   US2003087346-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1111
ID   ADC12327 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003082541-A1.
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PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1112
ID   ADD03172 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003092104-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1113
ID   ADC90164 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087348-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1114
ID   ADC69583 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003194770-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1115
ID   ADC48472 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003194773-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1116
ID   ADD10001 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1117
ID   ADD04576 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1118
ID   ADC80532 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1119
ID   ADD11039 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1120
ID   ADD10332 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #22.
PN   US2003105011-A1.
PD   05-JUN-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1121
ID   ADC47920 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1122
ID   ADD04882 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003104469-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1123
ID   ADC79980 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1124
ID   ADD11292 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #22.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1125
ID   ADD09449 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1126
ID   ADD03888 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003104381-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1127
ID   ADD03464 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003108983-A1.
PD   12-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1128
ID   ADD41162 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1129
ID   ADD52301 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1130
ID   ADD53041 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1131
ID   ADD53593 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003203437-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1132
ID   ADD37085 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #22.
PN   US2003105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1133
ID   ADD51749 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1134
ID   ADD02548 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003203431-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1135
ID   ADD01982 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003203430-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1136
ID   ADD54164 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003203432-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1137
ID   ADD92481 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199030-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1138
ID   ADD91377 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199055-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1139
ID   ADE03991 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199057-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1140
ID   ADE32288 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003194765-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1141
ID   ADE22220 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003199056-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1142
ID   ADD79444 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003203428-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1143
ID   ADE41980 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003194772-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1144
ID   ADE17797 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199023-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1145
ID   ADD91929 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199053-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1146
ID   ADE33392 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003194767-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1147
ID   ADE33944 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003194791-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
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RESULT 1148
ID   ADD79996 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003207417-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1149
ID   ADD93033 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003194768-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1150
ID   ADE19453 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199025-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1151
ID   ADE34716 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003077583-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1152
ID   ADE18901 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199026-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1153
ID   ADE43097 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1154
ID   ADD95886 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199059-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1155
ID   ADE22772 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1156
ID   ADD78890 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1157
ID   ADE32840 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1158
ID   ADE42532 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1159
ID   ADD80548 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1160
ID   ADD89576 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1161
ID   ADE40860 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1162
ID   ADE04659 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1163
ID   ADE92788 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003194777-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1164
ID   ADG21497 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1165
ID   ADG23138 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1166
ID   ADF97473 standard; cDNA; 1685 BP.
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DE   Human PRO polynucleotide #174.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1167
ID   ADG80537 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1168
ID   ADG79985 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1169
ID   ADH59199 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003039972-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1170
ID   ADH55277 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207381-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1171
ID   ADH55829 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207379-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1172
ID   ADI37978 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003054352-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1173
ID   ADI64048 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207385-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1174
ID   ADI64997 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207386-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1175
ID   ADI63496 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207387-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1176
ID   ADH81910 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207388-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1177
ID   ADH81358 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207377-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1178
ID   ACA58964 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #15.
PN   US2002146709-A1.
PD   10-OCT-2002.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1179
ID   ACD24026 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003032156-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1180
ID   ACA58361 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #15.
PN   US2002192659-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1181
ID   ACA67167 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003004311-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1182
ID   ADJ26246 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003054349-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 10;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1183
ID   ADM82527 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087355-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 11;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1184
ID   ADN15926 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087353-A1.
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PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 11;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1185
ID   ADN16555 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087385-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 11;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1186
ID   ADN15374 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087356-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 11;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1187
ID   ADN14822 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003087357-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 11;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1188
ID   ADC81084 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003092115-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1189
ID   ADE79161 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003135025-A1.
PD   17-JUL-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1190
ID   ADD76532 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003100087-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1191
ID   ADD87896 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003092113-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1192
ID   ADD86300 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003203440-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1193
ID   ADE79585 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003130489-A1.
PD   10-JUL-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1194
ID   ADE75748 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003211571-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1195
ID   ADE73261 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003129592-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1196
ID   ADE41293 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #22.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1197
ID   ADE23324 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003092108-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1198
ID   ADE23876 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003092110-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1199
ID   ADE24519 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003092111-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1200
ID   ADD87344 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1201
ID   ADE89210 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1202
ID   ADE73796 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003148370-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1203
ID   ADE18349 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003194794-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1204
ID   ADE88658 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1205
ID   ADE99350 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003211576-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1206
ID   ADE94678 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003199027-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1207
ID   ADE91089 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1208
ID   ADE95230 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1209
ID   ADE93340 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1210
ID   ADF34921 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003199029-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1211
ID   ADE98469 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003211569-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
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  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1212
ID   ADE92236 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1213
ID   ADE90537 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1214
ID   ADE91684 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1215
ID   ADE98896 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003211568-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity . 49.5%;  Pred. No. 5.5;
RESULT 1216
ID   ADG40366 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003225253-A1.
PD   04-DEC-2003.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1217
ID   ADF73760 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003180312-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1218
ID   ADG02263 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1219
ID   ADG22049 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1220
ID   ADG20119 standard; cDNA; 1685 BP.
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DE   cDNA encoding human PRO polypeptide #174.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1221
ID   ADF98025 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1222
ID   ADG24242 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207426-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1223
ID   ADF98596 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1224
ID   ADG03427 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1225
ID   ADF99148 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1226
ID   ADG16733 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1227
ID   ADG05192 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1228
ID   ADG19459 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1229
ID   ADF73336 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
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PN   US2003166051-A1.
PD   04-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1230
ID   ADG13296 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1231
ID   ADG08353 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1232
ID   ADG15523 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1233
ID   ADF96921 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1234
ID   ADG06106 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1235
ID   ADG23690 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1236
ID   ADG03979 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1237
ID   ADG24880 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1238
ID   ADG07177 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207350-A1.
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PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1239
ID   ADG07729 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207356-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1240
ID   ADG55224 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1241
ID   ADG60888 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1242
ID   ADG61992 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1243
ID   ADG92179 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003027145-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1244
ID   ADG82193 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1245
ID   ADG57432 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1246
ID   ADG56880 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1247
ID   ADG55776 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207365-A1.
PD   06-NOV-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1248
ID   ADG58536 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1249
ID   ADG70902 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1250
ID   ADG92606 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003027146-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1251
ID   ADG57984 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1252
ID   ADG53568 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1253
ID   ADG71454 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1254
ID   ADG81641 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003207805-A1.
PD   06-NOV-2003.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1255
ID   ADH30603 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1256
ID   ADH11970 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1257
ID   ADG52392 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1258
ID   ADG54120 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1259
ID   ADG81089 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1260
ID   ADG56328 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1261
ID   ADH12594 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1262
ID   ADG61440 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1263
ID   ADH28527 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1264
ID   ADG54672 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1265
ID   ADG59712 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
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RESULT 1266
ID   ADH20395 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2004005553-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1267
ID   ADH43476 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #22.
PN   US2003224984-A1.
PD   04-DEC-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1268
ID   ADH07250 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2004006211-A1.
PD   08-JAN-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1269
ID   ADH59795 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003215904-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1270
ID   ADH06823 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2004005665-A1.
PD   08-JAN-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1271
ID   ADI81136 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2003207361-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1272
ID   ADI18565 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003152999-A1.
PD   14-AUG-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1273
ID   ADI65285 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003148419-A1.
PD   07-AUG-2003.
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PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1274
ID   ADI37548 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003096340-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1275
ID   ADG09879 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2004009548-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1276
ID   ADH97352 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003190610-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1277
ID   ADI15350 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207382-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1278
ID   ADG09227 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2004009547-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1279
ID   ADI65712 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003148371-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1280
ID   ADI14682 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207383-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1281
ID   ADH60455 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2004023331-A1.
PD   05-FEB-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
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RESULT 1282
ID   ADI18277 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207349-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1283
ID   ADJ99512 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003187238-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1284
ID   ADL08705 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003186358-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1285
ID   ADM25050 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003096233-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1286
ID   ADJ63558 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1287
ID   ADM29796 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003190611-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1288
ID   ADJ77453 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #174.
PN   US2004038336-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1289
ID   ADK82821 standard; cDNA; 1685 BP.
DE   Human PRO polynucleotide #22.
PN   US2004043927-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1290
ID   ADJ65575 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2004038335-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1291
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ID   ADM27711 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2004048333-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1292
ID   ADM42435 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2004058424-A1.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1293
ID   ADO06118 standard; cDNA; 1685 BP.
DE   Human.PRO polynucleotide #17.
PN   US6686451-B1.
PD   03-FEB-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1294
ID   ADM28297 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
PN   US2004077064-A1.
PD   22-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1295
ID   ADR10970 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2004137561-A1.
PD   15-JUL-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 12;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1296
ID   ADR17879 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2004147017-A1.
PD   29-JUL-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI C J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (MATH/) MATHER J P.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             3.5%;  Score 36.4;  DB 13;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1297
ID   ADI95779 standard; cDNA; 1685 BP.
DE   cDNA encoding human PRO polypeptide #174.
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PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 13;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1298
ID   ADI96331 standard; cDNA; 1685 BP.
DE   Novel human secreted and transmembrane protein PRO258 cDNA.
PN   US2003207354-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 13;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1299
ID   ADT03555 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane protein cDNA, #17.
PN   US2003152922-A1.
PD   14-AUG-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 36.4;  DB 13;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1300
ID   ADS74518 standard; cDNA; 1685 BP.
DE   Human secreted/transmembrane cDNA #17.
PN   US2004185531-A1.
PD   23-SEP-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI C J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (MATH/) MATHER J P.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             3.5%;  Score 36.4;  DB 13;  Length 1685;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1301
ID   AAZ61418 standard; DNA; 1718 BP.
DE   DNA encoding the short extracellular form of human B7-1 (CD80).
PN   WO200008057-A2.
PD   17-FEB-2000.
PA   (IMMV ) IMMUNEX CORP.
  Query Match             3.5%;  Score 36.4;  DB 3;  Length 1718;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1302
ID   AAZ50887 standard; DNA; 1718 BP.
DE   Human LDCAM binding protein, B7L-1 short form encoding DNA.
PN   WO200008158-A2.
PD   17-FEB-2000.
PA   (IMMV ) IMMUNEX CORP.
  Query Match             3.5%;  Score 36.4;  DB 3;  Length 1718;
  Best Local Similarity   49.5%;  Pred. No. 5.5;
RESULT 1303
ID   ACH87501 standard; DNA; 1739 BP.
DE   Human genome derived single exon probe #20696.
PN   US2003194704-A1.
PD   16-OCT-2003.
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PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 1739;
  Best Local Similarity   47.1%;  Pred. No. 5.6;
RESULT 1304
ID   AAZ61416 standard; DNA; 1820 BP.
DE   DNA encoding the long extracellular form of human B7-1 (CD80).
PN   WO200008057-A2.
PD   17-FEB-2000.
PA   (IMMV ) IMMUNEX CORP.
  Query Match              3.5%;  Score 36.4;  DB 3;  Length 1820;
  Best Local Similarity   49.5%;  Pred. No. 5.7;
RESULT 1305
ID   AAZ50886 standard; DNA; 1820 BP.
DE   Human LDCAM binding protein, B7L-1 long form encoding DNA.
PN   WO200008158-A2.
PD   17-FEB-2000.
PA   (IMMV ) IMMUNEX CORP.
  Query Match              3.5%;  Score 36.4;  DB 3;  Length 1820;
  Best Local Similarity   49.5%;  Pred. No. 5.7;
RESULT 1306
ID   AAA30423 standard; cDNA; 2224 BP.
DE   Human cDNA clone ACAM#6 nucleotide sequence.
PN   WO200032633-A1.
PD   08-JUN-2000.
PA   (ICOS-) ICOS CORP.
  Query Match              3.5%;  Score 36.4;  DB 3;  Length 2224;
  Best Local Similarity   49.5%;  Pred. No. 6.4;
RESULT 1307
ID   AAH14434 standard; cDNA; 2463 BP.
DE   Human cDNA sequence SEQ ID NO:11895.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
  Query Match              3.5%;  Score 36.4;  DB 4;  Length 2463;
  Best Local Similarity   49.5%;  Pred. No. 6.8;
RESULT 1308
ID   AAV63189 standard; cDNA; 2496 BP.
DE   cDNA from clone cr1162_25 which encodes a secreted protein.
PN   WO9844113-A1.
PD   08-OCT-1998.
PA   (GEMY ) GENETICS INST INC.
  Query Match              3.5%;  Score 36.4;  DB 2;  Length 2496;
  Best Local Similarity   49.5%;  Pred. No. 6.8;
RESULT 1309
ID   ABQ92039 standard; cDNA; 2496 BP.
DE   Human polynucleotide SEQ ID NO 36.
PN   US2002065394-A1.
PD   30-MAY-2002.
PA   (JACO/) JACOBS K.
PA   (MCCO/) MCCOY J M.
PA   (LAVA/) LAVALLIE E R.
PA   (COLL/) COLLINS-RACIE L A.
PA   (EVAN/) EVANS C.
PA   (MERB/) MERBERG D.
PA   (TREA/) TREACY M.
PA   (SPAU/) SPAULDING V.
  Query Match              3.5%;  Score 36.4;  DB 6;  Length 2496;
  Best Local Similarity   49.5%;  Pred. No. 6.8;
RESULT 1310
ID   ADI03925 standard; DNA; 2496 BP.
DE   Human B7-L1 polypeptide encoding DNA.
PN   WO2003105887-A1.
PD   24-DEC-2003.
PA   (AMHP ) WYETH.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 2496;
  Best Local Similarity   49.5%;  Pred. No. 6.8;
RESULT 1311
ID   ABA83306 standard; cDNA; 2537 BP.
DE   Human secreted protein gene 113 SEQ ID NO:123.
PN   WO200162891-A2.
PD   30-AUG-2001.
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PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.5%;  Score 36.4;  DB 4;  Length 2537;
  Best Local Similarity   49.5%;  Pred. No. 6.9;
RESULT 1312
ID   AAA13652 standard; cDNA; 2543 BP.
DE   Human Beat-like 1 (BL1) cDNA sequence.
PN   CN1242376-A.
PD   26-JAN-2000.
PA   (BASI-) BASIC MEDICAL SCI RES INST CHINESE ACAD.
  Query Match              3.5%;  Score 36.4;  DB 3;  Length 2543;
  Best Local Similarity   49.5%;  Pred. No. 6.9;
RESULT 1313
ID   ACN43565 standard; cDNA; 2642 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:2440.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match              3.5%;  Score 36.4;  DB 13;  Length 2642;
  Best Local Similarity   49.5%;  Pred. No. 7;
RESULT 1314
ID   AAA30424 standard; cDNA; 2837 BP.
DE   Human cDNA clone ACAM#4 nucleotide sequence.
PN   WO200032633-A1.
PD   08-JUN-2000.
PA   (ICOS-) ICOS CORP.
  Query Match              3.5%;  Score 36.4;  DB 3;  Length 2837;
  Best Local Similarity   49.5%;  Pred. No. 7.3;
RESULT 1315
ID   ADA24421 standard; DNA; 3557 BP.
DE   Human tumour suppressor gene, TSLL1.
PN   US2003109016-A1.
PD   12-JUN-2003.
PA   (PRES-) PRESIDENT NAT CANCER CENT.
PA   (BMLB-) BML INC.
  Query Match              3.5%;  Score 36.4;  DB 9;  Length 3557;
  Best Local Similarity   49.5%;  Pred. No. 8.3;
RESULT 1316
ID   AAS81244 standard; cDNA; 14934 BP.
DE   DNA encoding novel human diagnostic protein #17048.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              3.5%;  Score 36.4;  DB 5;  Length 14934;
  Best Local Similarity   47.1%;  Pred. No. 18;
RESULT 1317
ID   AAS88024 standard; cDNA; 14934 BP.
DE   DNA encoding novel human diagnostic protein #23828.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              3.5%;  Score 36.4;  DB 5;  Length 14934;
  Best Local Similarity   47.1%;  Pred. No. 18;
RESULT 1318
ID   AAS87217 standard; cDNA; 14948 BP.
DE   DNA encoding novel human diagnostic protein #23021.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match              3.5%;  Score 36.4;  DB 5;  Length 14948;
  Best Local Similarity   47.1%;  Pred. No. 18;
RESULT 1319
ID   AAK83212 standard; DNA; 68356 BP.
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38024.
PN   WO200157182-A2.
PD   09-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.5%;  Score 36.4;  DB 4;  Length 68356;
  Best Local Similarity   47.1%;  Pred. No. 42;
RESULT 1320
ID   AAK67283 standard; DNA; 68356 BP.
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22095.
PN   WO200157182-A2.
PD   09-AUG-2001.
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PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.5%;  Score 36.4;  DB 4;  Length 68356;
  Best Local Similarity   47.1%;  Pred. No. 42;
RESULT 1321
ID   ADQ59443 standard; DNA; 352938 BP.
DE   Human cancer-associated (CA) gene sequence SEQ ID NO:79.
PN   WO2004058288-A1.
PD   15-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 110000;
  Best Local Similarity   50.6%;  Pred. No. 55;
RESULT 1322
  Query Match              3.5%;  Score 36.4;  DB 12;  Length 110000;
  Best Local Similarity   50.6%;  Pred. No. 55;
RESULT 1323
ID   ADJ83882 standard; DNA; 321 BP.
DE   HERV-K HML-2 subgroup cORF (Rec) optimised DNA.
PN   WO2003106634-A2.
PD   24-DEC-2003.
PA   (CHIR ) CHIRON CORP.
  Query Match              3.5%;  Score 36.2;  DB 12;  Length 321;
  Best Local Similarity   50.3%;  Pred. No. 2.5;
RESULT 1324
ID   ADJ83884 standard; DNA; 438 BP.
DE   HERV-K HML-2 subgroup PCAP5 optimised DNA.
PN   WO2003106634-A2.
PD   24-DEC-2003.
PA   (CHIR ) CHIRON CORP.
  Query Match              3.5%;  Score 36.2;  DB 12;  Length 438;
  Best Local Similarity   50.3%;  Pred. No. 3;
RESULT 1325
ID   ADJ83906 standard; DNA; 2103 BP.
DE   HERV-K HML-2 subgroup env (envelope) optimised DNA.
PN   WO2003106634-A2.
PD   24-DEC-2003.
PA   (CHIR ) CHIRON CORP.
  Query Match              3.5%;  Score 36.2;  DB 12;  Length 2103;
  Best Local Similarity   50.3%;  Pred. No. 7.1;
RESULT 1326
ID   ADJ83875 standard; DNA; 4657 BP.
DE   HERV-K HML-2 subgroup-related vector pCMVKm2-cORFopt HML-2 DNA.
PN   WO2003106634-A2.
PD   24-DEC-2003.
PA   (CHIR ) CHIRON CORP.
  Query Match              3.5%;  Score 36.2;  DB 12;  Length 4657;
  Best Local Similarity   50.3%;  Pred. No. 11;
RESULT 1327
ID   ADJ83876 standard; DNA; 4773 BP.
DE   HERV-K HML-2 subgroup-related vector pCMVKm2-pCAP5opt HML-2 DNA.
PN   WO2003106634-A2.
PD   24-DEC-2003.
PA   (CHIR ) CHIRON CORP.
  Query Match              3.5%;  Score 36.2;  DB 12;  Length 4773;
  Best Local Similarity   50.3%;  Pred. No. 11;
RESULT 1328
ID   ABD33039 standard; DNA; 33294 BP.
DE   Human cancer-associated genomic DNA HD22-025.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
  Query Match              3.5%;  Score 36.2;  DB 13;  Length 33294;
  Best Local Similarity   51.6%;  Pred. No. 33;
RESULT 1329
ID   ADG48022 standard; DNA; 387 BP.
DE   Human variant TTR (C10A/A81C) DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match              3.5%;  Score 36;  DB 12;  Length 387;
  Best Local Similarity   50.0%;  Pred. No. 3.2;
RESULT 1330
ID   ADG68778 standard; cDNA; 387 BP.
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DE   Human mutant transthyretin (TTR)  cDNA #4.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match              3.5%;  Score 36;  DB 12;  Length 387;
  Best Local Similarity   50.0%;  Pred. No. 3.2;
RESULT 1331
ID   ADG48030 standard; DNA; 489 BP.
DE   Human PTH-TTR (C10A/K15A/G83C) variant fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match              3.5%;  Score 36;  DB 12;  Length 489;
  Best Local Similarity   50.0%;  Pred. No. 3.7;
RESULT 1332
ID   ADG48059 standard; DNA; 489 BP.
DE   Human PTH-TTR (C10A/K15A/A81C) variant fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match              3.5%;  Score 36;  DB 12;  Length 489;
  Best Local Similarity   50.0%;  Pred. No. 3.7;
RESULT 1333
ID   ADG68786 standard; cDNA; 489 BP.
DE   Human mutant transthyretin (TTR)  cDNA #12.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match              3.5%;  Score 36;  DB 12;  Length 489;
  Best Local Similarity   50.0%;  Pred. No. 3.7;
RESULT 1334
ID   ADG48028 standard; DNA; 495 BP.
DE   Human  TMP-TTR (C10A/A81C) variant fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match              3.5%;  Score 36;  DB 12;  Length 495;
  Best Local Similarity   50.0%;  Pred. No. 3.7;
RESULT 1335
ID   ADG48090 standard; DNA; 495 BP.
DE   Human TMP-TTR (C10A/K15A/A81C) fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match              3.5%;  Score 36;  DB 12;  Length 495;
  Best Local Similarity   50.0%;  Pred. No. 3.7;
RESULT 1336
ID   ADG68784 standard; cDNA; 495 BP.
DE   Human mutant transthyretin (TTR)  cDNA #10.
PN   US2003191056-A1.
PD   09-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match              3.5%;  Score 36;  DB 12;  Length 495;
  Best Local Similarity   50.0%;  Pred. No. 3.7;
RESULT 1337
ID   ADG48087 standard; DNA; 510 BP.
DE   Human TTR (C10A/K15A/A81C)-TMP fusion DNA.
PN   US2003195154-A1.
PD   16-OCT-2003.
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
  Query Match              3.5%;  Score 36;  DB 12;  Length 510;
  Best Local Similarity   50.0%;  Pred. No. 3.8;
RESULT 1338
ID   AAL03221 standard; DNA; 1348 BP.
DE   Human reproductive system related antigen DNA SEQ ID NO: 5909.
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PN   WO200155320-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.5%;  Score 35.8;  DB 4;  Length 1348;
  Best Local Similarity   59.2%;  Pred. No. 7.4;
RESULT 1339
ID   ABK74382 standard; DNA; 1731 BP.
DE   Bacillus licheniformis genomic sequence tag (GST) #1673.
PN   WO200229113-A2.
PD   11-APR-2002.
PA   (NOVO ) NOVOZYMES BIOTECH INC.
PA   (NOVO ) NOVOZYMES AS.
  Query Match             3.5%;  Score 35.8;  DB 6;  Length 1731;
  Best Local Similarity   48.3%;  Pred. No. 8.5;
RESULT 1340
ID   ADG32035 standard; DNA; 2734 BP.
DE   DNA encoding a mutant B_licheniformis secreted polypeptide SeqID 5.
PN   WO2003093453-A2.
PD   13-NOV-2003.
PA   (NOVO ) NOVOZYMES AS.
  Query Match             3.5%;  Score 35.8;  DB 12;  Length 2734;
  Best Local Similarity   48.3%;  Pred. No. 11;
RESULT 1341
ID   ACD03633 standard; cDNA; 2916 BP.
DE   Novel human GPCR related protein NOV9b cDNA.
PN   WO200299116-A2.
PD   12-DEC-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             3.5%;  Score 35.8;  DB 8;  Length 2916;
  Best Local Similarity   47.2%;  Pred. No. 11;
RESULT 1342
ID   ADB53259 standard; DNA; 3170 BP.
DE   Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3801.
PN   WO2003065993-A2.
PD   14-AUG-2003.
PA   (GENE-) GENE LOGIC INC.
  Query Match             3.5%;  Score 35.8;  DB 10;  Length 3170;
  Best Local Similarity   48.3%;  Pred. No. 12;
RESULT 1343
ID   AAV62739 standard; cDNA; 3997 BP.
DE   Human neural cell adhesion molecule NrCAMvar cDNA.
PN   WO9836062-A1.
PD   20-AUG-1998.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
  Query Match             3.5%;  Score 35.8;  DB 2;  Length 3997;
  Best Local Similarity   65.8%;  Pred. No. 14;
RESULT 1344
ID   AAZ38152 standard; DNA; 4134 BP.
DE   Human Nr-CAM gene sequence.
PN   WO9955380-A1.
PD   04-NOV-1999.
PA   (PACI-) PACIFIC NORTHWEST CANCER FOUND.
  Query Match             3.5%;  Score 35.8;  DB 3;  Length 4134;
  Best Local Similarity   65.8%;  Pred. No. 14;
RESULT 1345
ID   ACN43499 standard; cDNA; 5084 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:2374.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.5%;  Score 35.8;  DB 13;  Length 5084;
  Best Local Similarity   65.8%;  Pred. No. 15;
RESULT 1346
ID   ACN41814 standard; cDNA; 5126 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:689.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.5%;  Score 35.8;  DB 13;  Length 5126;
  Best Local Similarity   65.8%;  Pred. No. 16;
RESULT 1347
ID   ACN41813 standard; cDNA; 5232 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:688.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.5%;  Score 35.8;  DB 13;  Length 5232;
  Best Local Similarity   65.8%;  Pred. No. 16;
RESULT 1348
ID   ACN43498 standard; cDNA; 5366 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:2373.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.5%;  Score 35.8;  DB 13;  Length 5366;
  Best Local Similarity   65.8%;  Pred. No. 16;
RESULT 1349
ID   ACN41812 standard; cDNA; 5371 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:687.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.5%;  Score 35.8;  DB 13;  Length 5371;
  Best Local Similarity   65.8%;  Pred. No. 16;
RESULT 1350
ID   ACN41811 standard; cDNA; 5387 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:686.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.5%;  Score 35.8;  DB 13;  Length 5387;
  Best Local Similarity   65.8%;  Pred. No. 16;
RESULT 1351
ID   ACN43497 standard; cDNA; 5393 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:2372.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.5%;  Score 35.8;  DB 13;  Length 5393;
  Best Local Similarity   65.8%;  Pred. No. 16;
RESULT 1352
ID   ACN43496 standard; cDNA; 5396 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:2371.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.5%;  Score 35.8;  DB 13;  Length 5396;
  Best Local Similarity   65.8%;  Pred. No. 16;
RESULT 1353
ID   ACN43495 standard; cDNA; 5398 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:2370.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.5%;  Score 35.8;  DB 13;  Length 5398;
  Best Local Similarity   65.8%;  Pred. No. 16;
RESULT 1354
ID   ADN95537 standard; DNA; 6218 BP.
DE   Human BEC/LEC-related gene sequence SeqID460.
PN   WO2003080640-A1.
PD   02-OCT-2003.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (LICN ) LICENTIA LTD.
  Query Match             3.5%;  Score 35.8;  DB 11;  Length 6218;
  Best Local Similarity   65.8%;  Pred. No. 17;
RESULT 1355
ID   ADQ20706 standard; DNA; 6218 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 3526.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             3.5%;  Score 35.8;  DB 12;  Length 6218;
  Best Local Similarity   65.8%;  Pred. No. 17;
RESULT 1356
ID   ADR14186 standard; DNA; 6218 BP.
DE   Human NF-kappaB pathway-associated gene SeqID187.
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PN   WO2004065577-A2.
PD   05-AUG-2004.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
  Query Match             3.5%;  Score 35.8;  DB 13;  Length 6218;
  Best Local Similarity   65.8%;  Pred. No. 17;
RESULT 1357
ID   ADR14795 standard; DNA; 6218 BP.
DE   Nucleotide sequence of human MAPCAX orthologue #27.
PN   WO2004066948-A2.
PD   12-AUG-2004.
PA   (EXEL-) EXELIXIS INC.
  Query Match             3.5%;  Score 35.8;  DB 13;  Length 6218;
  Best Local Similarity   65.8%;  Pred. No. 17;
RESULT 1358
ID   ADQ24679 standard; DNA; 6234 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7499.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             3.5%;  Score 35.8;  DB 12;  Length 6234;
  Best Local Similarity   65.8%;  Pred. No. 17;
RESULT 1359
ID   AAA64155 standard; cDNA; 6253 BP.
DE   Nucleotide sequence of secreted protein clone CO722_1.
PN   WO200050592-A1.
PD   31-AUG-2000.
PA   (GEMY ) GENETICS INST INC.
  Query Match             3.5%;  Score 35.8;  DB 3;  Length 6253;
  Best Local Similarity   65.8%;  Pred. No. 17;
RESULT 1360
ID   AAV40887 standard; cDNA; 6254 BP.
DE   Coding sequence of clone CO722_1.
PN   WO9824905-A2.
PD   11-JUN-1998.
PA   (GEMY ) GENETICS INST INC.
  Query Match             3.5%;  Score 35.8;  DB 2;  Length 6254;
  Best Local Similarity   65.8%;  Pred. No. 17;
RESULT 1361
ID   AAF98452 standard; cDNA; 6254 BP.
DE   Human cDNA clone CO722_1 sequence SEQ ID 129.
PN   WO200119988-A1.
PD   22-MAR-2001.
PA   (GEMY ) GENETICS INST INC.
  Query Match             3.5%;  Score 35.8;  DB 5;  Length 6254;
  Best Local Similarity   65.8%;  Pred. No. 17;
RESULT 1362
ID   ADE77114 standard; cDNA; 6384 BP.
DE   Human cDNA differentially expressed in a liver disorder #206.
PN   US2003108871-A1.
PD   12-JUN-2003.
PA   (KASE/) KASER M R.
  Query Match             3.5%;  Score 35.8;  DB 12;  Length 6384;
  Best Local Similarity   65.8%;  Pred. No. 18;
RESULT 1363
ID   ADL12995 standard; cDNA; 6384 BP.
DE   Human steroid-induced C3A liver cell cDNA #724.
PN   US6673549-B1.
PD   06-JAN-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.5%;  Score 35.8;  DB 12;  Length 6384;
  Best Local Similarity   65.8%;  Pred. No. 18;
RESULT 1364
ID   ADJ87608 standard; DNA; 6385 BP.
DE   Nervous system disease differentially expressed gene #10.
PN   WO2003103474-A2.
PD   18-DEC-2003.
PA   (INCY-) INCYTE CORP.
  Query Match             3.5%;  Score 35.8;  DB 12;  Length 6385;
  Best Local Similarity   65.8%;  Pred. No. 18;
RESULT 1365
ID   AAA01952 standard; cDNA; 718 BP.
DE   Human colon cancer cell line polynucleotide sequence SEQ ID NO:1943.
PN   WO9958675-A2.
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PD   18-NOV-1999.
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
  Query Match             3.4%;  Score 35.6;  DB 3;  Length 718;
  Best Local Similarity   48.6%;  Pred. No. 6;
RESULT 1366
ID   ACA44307 standard; DNA; 1199 BP.
DE   Prokaryotic essential gene #25964.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
  Query Match             3.4%;  Score 35.6;  DB 8;  Length 1199;
  Best Local Similarity   53.6%;  Pred. No. 8;
RESULT 1367
ID   AAF61080 standard; DNA; 1932 BP.
DE   P. putida KT2440-associated DNA ORF09354.
PN   DE19935088-A1.
PD   01-FEB-2001.
PA   (TIGR-) TIGR INST GENOMIC RES.
PA   (QUIA-) QUIAGEN GMBH.
PA   (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
PA   (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
PA   (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
  Query Match             3.4%;  Score 35.6;  DB 4;  Length 1932;
  Best Local Similarity   53.6%;  Pred. No. 10;
RESULT 1368
ID   ADB08265 standard; DNA; 2298 BP.
DE   Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:2205.
PN   WO2003048304-A2.
PD   12-JUN-2003.
PA   (AMHP ) WYETH HOLDINGS CORP.
  Query Match             3.4%;  Score 35.6;  DB 9;  Length 2298;
  Best Local Similarity   60.2%;  Pred. No. 12;
RESULT 1369
ID   ADB08267 standard; DNA; 2298 BP.
DE   Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:2207.
PN   WO2003048304-A2.
PD   12-JUN-2003.
PA   (AMHP ) WYETH HOLDINGS CORP.
  Query Match             3.4%;  Score 35.6;  DB 9;  Length 2298;
  Best Local Similarity   60.2%;  Pred. No. 12;
RESULT 1370
ID   ABL15322 standard; cDNA; 4734 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 40448.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match             3.4%;  Score 35.6;  DB 4;  Length 4734;
  Best Local Similarity   57.0%;  Pred. No. 17;
RESULT 1371
  Query Match             3.4%;  Score 35.6;  DB 9;  Length 110000;
  Best Local Similarity   60.2%;  Pred. No. 98;
RESULT 1372
ID   ABD09108 standard; DNA; 840 BP.
DE   Pseudomonas aeruginosa polynucleotide #7712.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.4%;  Score 35.4;  DB 11;  Length 840;
  Best Local Similarity   44.7%;  Pred. No. 7.6;
RESULT 1373
ID   ABL24133 standard; DNA; 843 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 23872.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match             3.4%;  Score 35.4;  DB 4;  Length 843;
  Best Local Similarity   50.3%;  Pred. No. 7.6;
RESULT 1374
ID   ABD09246 standard; DNA; 1221 BP.
DE   Pseudomonas aeruginosa polynucleotide #7850.
PN   US6551795-B1.
PD   22-APR-2003.
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PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match              3.4%;  Score 35.4;  DB 11;  Length 1221;
  Best Local Similarity   44.7%;  Pred. No. 9.4;
RESULT 1375
ID   ACH95924 standard; DNA; 3324 BP.
DE   Klebsiella pneumoniae polynucleotide seqid 1719.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match              3.4%;  Score 35.4;  DB 11;  Length 3324;
  Best Local Similarity   45.5%;  Pred. No. 16;
RESULT 1376
ID   AAA10595 standard; DNA; 6741 BP.
DE   Gene encoding a subunit of cellulose synthase.
PN   JP2000060568-A.
PD   29-FEB-2000.
PA   (MIZU/) MIZUNO K.
PA   (OJIP ) OJI PAPER CO.
  Query Match              3.4%;  Score 35.4;  DB 3;  Length 6741;
  Best Local Similarity   19.0%;  Pred. No. 24;
RESULT 1377
ID   ABL20787 standard; DNA; 10242 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 13834.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.4%;  Score 35.2;  DB 4;  Length 10242;
  Best Local Similarity   49.0%;  Pred. No. 35;
RESULT 1378
ID   ABL20786 standard; DNA; 20978 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 13831.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.4%;  Score 35.2;  DB 4;  Length 20978;
  Best Local Similarity   49.0%;  Pred. No. 52;
RESULT 1379
ID   AAQ94572 standard; DNA; 879 BP.
DE   Pseudomonas mendocina SD702 lipase gene.
PN   WO9514783-A1.
PD   01-JUN-1995.
PA   (SHOW ) SHOWA DENKO KK.
  Query Match              3.4%;  Score 35;  DB 2;  Length 879;
  Best Local Similarity   49.2%;  Pred. No. 10;
RESULT 1380
ID   ABD10093 standard; DNA; 1005 BP.
DE   Pseudomonas aeruginosa polynucleotide #8697.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match              3.4%;  Score 35;  DB 11;  Length 1005;
  Best Local Similarity   47.9%;  Pred. No. 11;
RESULT 1381
ID   ACA36139 standard; DNA; 1731 BP.
DE   Prokaryotic essential gene #17796.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
  Query Match              3.4%;  Score 35;  DB 8;  Length 1731;
  Best Local Similarity   56.5%;  Pred. No. 15;
RESULT 1382
ID   ACH99754 standard; DNA; 1749 BP.
DE   Klebsiella pneumoniae polynucleotide seqid 5549.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match              3.4%;  Score 35;  DB 11;  Length 1749;
  Best Local Similarity   56.5%;  Pred. No. 15;
RESULT 1383
ID   ABD10478 standard; DNA; 2706 BP.
DE   Pseudomonas aeruginosa polynucleotide #9082.
PN   US6551795-B1.
PD   22-APR-2003.
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PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match              3.4%;  Score 35;  DB 11;  Length 2706;
  Best Local Similarity   47.9%;  Pred. No. 19;
RESULT 1384
ID   ABT16074 standard; DNA; 3693 BP.
DE   NOVX related polynucleotide SEQ ID No 115.
PN   WO200299062-A2.
PD   12-DEC-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match              3.4%;  Score 35;  DB 8;  Length 3693;
  Best Local Similarity   49.8%;  Pred. No. 23;
RESULT 1385
ID   ADO41749 standard; cDNA; 3693 BP.
DE   Novel human polypeptide NOV37b cDNA.
PN   US2004018555-A1.
PD   29-JAN-2004.
PA   (ANDE/) ANDERSON D W.
PA   (ZERH/) ZERHUSEN B D.
PA   (LILL/) LI L.
PA   (ZHON/) ZHONG M.
PA   (CASM/) CASMAN S J.
PA   (GERL/) GERLACH V.
PA   (SHIM/) SHIMKETS R A.
PA   (GORM/) GORMAN L.
PA   (PENA/) PENA C E A.
PA   (KEKU/) KEKUDA R.
PA   (PATT/) PATTURAJAN M.
PA   (SPYT/) SPYTEK K A.
PA   (LEIT/) LEITE M W.
PA   (RAST/) RASTELLI L.
PA   (MACD/) MACDOUGALL J R.
PA   (TAUP/) TAUPIER R J.
PA   (GUOX/) GUO X S.
PA   (MILL/) MILLER C E.
PA   (SHEN/) SHENOY S G.
PA   (HJAL/) HJALT T.
PA   (VOSS/) VOSS E Z.
PA   (BOLD/) BOLDOG F L.
PA   (MALY/) MALYANKAR U M.
PA   (PADI/) PADIGARU M.
PA   (JIWW/) JI W.
PA   (SMIT/) SMITHSON G.
PA   (EDIN/) EDINGER S R.
PA   (MILL/) MILLET I.
PA   (ELLE/) ELLERMAN K.
  Query Match              3.4%;  Score 35;  DB 12;  Length 3693;
  Best Local Similarity   49.8%;  Pred. No. 23;
RESULT 1386
ID   ADQ23001 standard; DNA; 4053 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5821.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              3.4%;  Score 35;  DB 12;  Length 4053;
  Best Local Similarity   49.8%;  Pred. No. 24;
RESULT 1387
ID   ABD08885 standard; DNA; 1077 BP.
DE   Pseudomonas aeruginosa polynucleotide #7489.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match              3.4%;  Score 34.8;  DB 11;  Length 1077;
  Best Local Similarity   50.0%;  Pred. No. 13;
RESULT 1388
ID   ABL04261 standard; cDNA; 1110 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 7265.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.4%;  Score 34.8;  DB 4;  Length 1110;
  Best Local Similarity   58.8%;  Pred. No. 14;
RESULT 1389
ID   ADT45810 standard; cDNA; 1242 BP.
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DE   Bacterial polynucleotide #20561.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match              3.4%;  Score 34.8;  DB 13;  Length 1242;
  Best Local Similarity   46.3%;  Pred. No. 14;
RESULT 1390
ID   ABD08604 standard; DNA; 2748 BP.
DE   Pseudomonas aeruginosa polynucleotide #7208.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match              3.4%;  Score 34.8;  DB 11;  Length 2748;
  Best Local Similarity   50.0%;  Pred. No. 22;
RESULT 1391
ID   AAI71055 standard; cDNA; 3357 BP.
DE   Benign prostatic hyperplasia associated cDNA clone JT156897.
PN   WO200198456-A2.
PD   27-DEC-2001.
PA   (GENE-) GENE LOGIC INC.
PA   (NISB ) JAPAN TOBACCO INC.
  Query Match              3.4%;  Score 34.8;  DB 6;  Length 3357;
  Best Local Similarity   50.9%;  Pred. No. 25;
RESULT 1392
ID   ABL04260 standard; cDNA; 3426 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 7262.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.4%;  Score 34.8;  DB 4;  Length 3426;
  Best Local Similarity   58.8%;  Pred. No. 25;
RESULT 1393
ID   ABL14607 standard; cDNA; 4645 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 38303.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match              3.4%;  Score 34.8;  DB 4;  Length 4645;
  Best Local Similarity   62.8%;  Pred. No. 30;
RESULT 1394
ID   ADQ89651 standard; DNA; 4645 BP.
DE   Antagonist of cell cycle progression nucleotide sequence #41.
PN   WO2004063362-A2.
PD   29-JUL-2004.
PA   (CYCL-) CYCLACEL LTD.
  Query Match              3.4%;  Score 34.8;  DB 13;  Length 4645;
  Best Local Similarity   62.8%;  Pred. No. 30;
RESULT 1395
ID   ABV99327 standard; DNA; 8554 BP.
DE   Human NOV1a coding sequence.
PN   WO200272771-A2.
PD   19-SEP-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match              3.4%;  Score 34.8;  DB 6;  Length 8554;
  Best Local Similarity   50.9%;  Pred. No. 42;
RESULT 1396
ID   AAS28894 standard; DNA; 8895 BP.
DE   Human immunoglobulin encoding genomic DNA SEQ ID No 256.
PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.4%;  Score 34.8;  DB 4;  Length 8895;
  Best Local Similarity   50.9%;  Pred. No. 43;
RESULT 1397
ID   AAS28888 standard; DNA; 8895 BP.
DE   Human immunoglobulin encoding genomic DNA SEQ ID No 250.
PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.4%;  Score 34.8;  DB 4;  Length 8895;
  Best Local Similarity   50.9%;  Pred. No. 43;
RESULT 1398
ID   ABA06851 standard; DNA; 8895 BP.
DE   Human genomic DNA SEQ ID NO: 937.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.4%;  Score 34.8;  DB 4;  Length 8895;
  Best Local Similarity   50.9%;  Pred. No. 43;
RESULT 1399
ID   ABA06801 standard; DNA; 8895 BP.
DE   Human genomic DNA SEQ ID NO: 887.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.4%;  Score 34.8;  DB 4;  Length 8895;
  Best Local Similarity   50.9%;  Pred. No. 43;
RESULT 1400
ID   ABV84188 standard; DNA; 8895 BP.
DE   Human polynucleotide SEQ ID NO 937.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match              3.4%;  Score 34.8;  DB 6;  Length 8895;
  Best Local Similarity   50.9%;  Pred. No. 43;
RESULT 1401
ID   ABV84138 standard; DNA; 8895 BP.
DE   Human polynucleotide SEQ ID NO 887.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match              3.4%;  Score 34.8;  DB 6;  Length 8895;
  Best Local Similarity   50.9%;  Pred. No. 43;
RESULT 1402
ID   ADB31735 standard; DNA; 8895 BP.
DE   Human novel protein DNA SEQ ID NO 256.
PN   US2003077606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.4%;  Score 34.8;  DB 10;  Length 8895;
  Best Local Similarity   50.9%;  Pred. No. 43;
RESULT 1403
ID   ADB31729 standard; DNA; 8895 BP.
DE   Human novel protein DNA SEQ ID NO 250.
PN   US2003077606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.4%;  Score 34.8;  DB 10;  Length 8895;
  Best Local Similarity   50.9%;  Pred. No. 43;
RESULT 1404
ID   ABK90048 standard; DNA; 9109 BP.
DE   DNA encoding predicted human adlican-2 protein.
PN   WO200246364-A2.
PD   13-JUN-2002.
PA   (QUAR-) QUARK BIOTECH INC.
  Query Match              3.4%;  Score 34.8;  DB 6;  Length 9109;
  Best Local Similarity   50.9%;  Pred. No. 44;
RESULT 1405
ID   ADL02249 standard; cDNA; 9109 BP.
DE   Human OCP cDNA #9.
PN   US2004053301-A1.
PD   18-MAR-2004.
PA   (QUAR-) QUARK BIOTECH INC.
  Query Match              3.4%;  Score 34.8;  DB 12;  Length 9109;
  Best Local Similarity   50.9%;  Pred. No. 44;
RESULT 1406
ID   AAS28884 standard; DNA; 9656 BP.
DE   Human immunoglobulin encoding genomic DNA SEQ ID No 246.
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PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.4%;  Score 34.8;  DB 4;  Length 9656;
  Best Local Similarity   50.9%;  Pred. No. 45;
RESULT 1407
ID   AAS28893 standard; DNA; 9656 BP.
DE   Human immunoglobulin encoding genomic DNA SEQ ID No 255.
PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.4%;  Score 34.8;  DB 4;  Length 9656;
  Best Local Similarity   50.9%;  Pred. No. 45;
RESULT 1408
ID   ABA06800 standard; DNA; 9656 BP.
DE   Human genomic DNA SEQ ID NO: 886.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.4%;  Score 34.8;  DB 4;  Length 9656;
  Best Local Similarity   50.9%;  Pred. No. 45;
RESULT 1409
ID   ABA06847 standard; DNA; 9656 BP.
DE   Human genomic DNA SEQ ID NO: 933.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.4%;  Score 34.8;  DB 4;  Length 9656;
  Best Local Similarity   50.9%;  Pred. No. 45;
RESULT 1410
ID   ABV84137 standard; DNA; 9656 BP.
DE   Human polynucleotide SEQ ID NO 886.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match             3.4%;  Score 34.8;  DB 6;  Length 9656;
  Best Local Similarity   50.9%;  Pred. No. 45;
RESULT 1411
ID   ABV84184 standard; DNA; 9656 BP.
DE   Human polynucleotide SEQ ID NO 933.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match             3.4%;  Score 34.8;  DB 6;  Length 9656;
  Best Local Similarity   50.9%;  Pred. No. 45;
RESULT 1412
ID   ADB31734 standard; DNA; 9656 BP.
DE   Human novel protein DNA SEQ ID NO 255.
PN   US2003077606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.4%;  Score 34.8;  DB 10;  Length 9656;
  Best Local Similarity   50.9%;  Pred. No. 45;
RESULT 1413
ID   ADB31725 standard; DNA; 9656 BP.
DE   Human novel protein DNA SEQ ID NO 246.
PN   US2003077606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.4%;  Score 34.8;  DB 10;  Length 9656;
  Best Local Similarity   50.9%;  Pred. No. 45;
RESULT 1414
ID   ACC00398 standard; cDNA; 10569 BP.
DE   Human cell adhesion and extracellular matrix protein, CADECM-7, DNA.
PN   WO2003027230-A2.
PD   03-APR-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             3.4%;  Score 34.8;  DB 8;  Length 10569;
  Best Local Similarity   50.9%;  Pred. No. 47;
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RESULT 1415
ID   ABL14606 standard; cDNA; 20348 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 38300.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match             3.4%;  Score 34.8;  DB 4;  Length 20348;
  Best Local Similarity   62.8%;  Pred. No. 68;
RESULT 1416
ID   ACN45090 standard; DNA; 350764 BP.
DE   Human genomic sequence hCG22125.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
  Query Match             3.4%;  Score 34.8;  DB 11;  Length 110000;
  Best Local Similarity   57.3%;  Pred. No. 1.7e+02;
RESULT 1417
ID   AAC70680 standard; DNA; 440 BP.
DE   Single nucleotide polymorphism containing sequence #170.
PN   WO200058519-A2.
PD   05-OCT-2000.
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
  Query Match             3.3%;  Score 34.6;  DB 3;  Length 440;
  Best Local Similarity   47.8%;  Pred. No. 9.4;
RESULT 1418
ID   ADK68389 standard; cDNA; 668 BP.
DE   Amorphophallus konjac a-Lectin-encoding cDNA.
PN   CN1384196-A.
PD   11-DEC-2002.
PA   (FUDA-) FUDANDIEN BIOTECHNOLOGY CO LTD SHANGHAI.
  Query Match             3.3%;  Score 34.6;  DB 10;  Length 668;
  Best Local Similarity   50.9%;  Pred. No. 12;
RESULT 1419
ID   ABA06474 standard; cDNA; 942 BP.
DE   Human cDNA SEQ ID NO: 140.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.3%;  Score 34.6;  DB 4;  Length 942;
  Best Local Similarity   48.6%;  Pred. No. 14;
RESULT 1420
ID   ABV83811 standard; cDNA; 942 BP.
DE   Human polynucleotide SEQ ID NO 140.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match             3.3%;  Score 34.6;  DB 6;  Length 942;
  Best Local Similarity   48.6%;  Pred. No. 14;
RESULT 1421
ID   AAS28819 standard; cDNA; 1020 BP.
DE   Human immunoglobulin encoding cDNA SEQ ID No 65.
PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.3%;  Score 34.6;  DB 4;  Length 1020;
  Best Local Similarity   48.6%;  Pred. No. 15;
RESULT 1422
ID   ADB31544 standard; cDNA; 1020 BP.
DE   Human cDNA encoding a novel protein SEQ ID NO 65.
PN   US2003077606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.3%;  Score 34.6;  DB 10;  Length 1020;
  Best Local Similarity   48.6%;  Pred. No. 15;
RESULT 1423
ID   ACC59920 standard; cDNA; 1539 BP.
DE   Human REMAP-33 encoding cDNA SEQ ID NO:69.
PN   WO2003025130-A2.
PD   27-MAR-2003.
PA   (INCY-) INCYTE GENOMICS INC.
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  Query Match             3.3%;  Score 34.6;  DB 9;  Length 1539;
  Best Local Similarity   51.6%;  Pred. No. 19;
RESULT 1424
ID   ADQ21633 standard; DNA; 3613 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 4453.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             3.3%;  Score 34.6;  DB 12;  Length 3613;
  Best Local Similarity   48.6%;  Pred. No. 30;
RESULT 1425
ID   AAC42222 standard; DNA; 3695 BP.
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 34740.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match             3.3%;  Score 34.6;  DB 3;  Length 3695;
  Best Local Similarity   58.1%;  Pred. No. 31;
RESULT 1426
ID   ADQ25448 standard; DNA; 4176 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 8268.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match             3.3%;  Score 34.6;  DB 12;  Length 4176;
  Best Local Similarity   48.6%;  Pred. No. 33;
RESULT 1427
ID   AAS28869 standard; cDNA; 573 BP.
DE   Human immunoglobulin encoding cDNA SEQ ID No 115.
PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.3%;  Score 34.4;  DB 4;  Length 573;
  Best Local Similarity   48.0%;  Pred. No. 13;
RESULT 1428
ID   ABA06680 standard; cDNA; 573 BP.
DE   Human cDNA SEQ ID NO: 346.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.3%;  Score 34.4;  DB 4;  Length 573;
  Best Local Similarity   48.0%;  Pred. No. 13;
RESULT 1429
ID   ABV84017 standard; cDNA; 573 BP.
DE   Human polynucleotide SEQ ID NO 346.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match             3.3%;  Score 34.4;  DB 6;  Length 573;
  Best Local Similarity   48.0%;  Pred. No. 13;
RESULT 1430
ID   ADB31594 standard; cDNA; 573 BP.
DE   Human cDNA encoding a novel protein SEQ ID NO 115.
PN   US2003077606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.3%;  Score 34.4;  DB 10;  Length 573;
  Best Local Similarity   48.0%;  Pred. No. 13;
RESULT 1431
ID   AAF75378 standard; DNA; 1179 BP.
DE   Ralstonia eutropha nucleotide sequence #1.
PN   WO200111014-A1.
PD   15-FEB-2001.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA   (RIKE ) RIKEN KK.
  Query Match             3.3%;  Score 34.4;  DB 5;  Length 1179;
  Best Local Similarity   52.0%;  Pred. No. 19;
RESULT 1432
ID   ABX17282 standard; DNA; 1179 BP.
DE   DNA encoding Poly3-hydroxybutanoate synthase associated protein #5.
PN   JP2002199890-A.
PD   16-JUL-2002.
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PA   (RIKA ) RIKAGAKU KENKYUSHO.
  Query Match             3.3%;  Score 34.4;  DB 6;  Length 1179;
  Best Local Similarity   52.0%;  Pred. No. 19;
RESULT 1433
ID   AAF84263 standard; DNA; 1181 BP.
DE   Beta-ketothiolase gene, phbA.
PN   EP1076095-A1.
PD   14-FEB-2001.
PA   (RIKE ) RIKEN KK.
  Query Match             3.3%;  Score 34.4;  DB 4;  Length 1181;
  Best Local Similarity   52.0%;  Pred. No. 19;
RESULT 1434
ID   AAQ67910 standard; DNA; 1182 BP.
DE   Alcaligenes eutrophus ketothiolase gene.
PN   WO9412014-A1.
PD   09-JUN-1994.
PA   (CETU ) AGRACETUS INC.
  Query Match             3.3%;  Score 34.4;  DB 2;  Length 1182;
  Best Local Similarity   52.0%;  Pred. No. 19;
RESULT 1435
ID   ADP83239 standard; DNA; 1182 BP.
DE   PhaA without signal sequence DNA.
PN   WO2004006657-A1.
PD   22-JAN-2004.
PA   (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.
PA   (UYQU ) UNIV QUEENSLAND.
  Query Match             3.3%;  Score 34.4;  DB 12;  Length 1182;
  Best Local Similarity   52.0%;  Pred. No. 19;
RESULT 1436
ID   ADP83241 standard; DNA; 1280 BP.
DE   Modified PhaA without signal sequence DNA.
PN   WO2004006657-A1.
PD   22-JAN-2004.
PA   (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.
PA   (UYQU ) UNIV QUEENSLAND.
  Query Match             3.3%;  Score 34.4;  DB 12;  Length 1280;
  Best Local Similarity   52.0%;  Pred. No. 20;
RESULT 1437
ID   ADF14870 standard; cDNA; 1360 BP.
DE   Sunflower resistance gene analogue RS7-4 cDNA #2.
PN   US6608240-B1.
PD   19-AUG-2003.
PA   (PION-) PIONEER HI-BRED INT INC.
  Query Match             3.3%;  Score 34.4;  DB 10;  Length 1360;
  Best Local Similarity   53.8%;  Pred. No. 20;
RESULT 1438
ID   ADP83248 standard; DNA; 1428 BP.
DE   Full length PhaA DNA.
PN   WO2004006657-A1.
PD   22-JAN-2004.
PA   (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.
PA   (UYQU ) UNIV QUEENSLAND.
  Query Match             3.3%;  Score 34.4;  DB 12;  Length 1428;
  Best Local Similarity   52.0%;  Pred. No. 21;
RESULT 1439
ID   AAQ85641 standard; DNA; 1431 BP.
DE   Acetyl-CoA-acyltransferase (3-ketothiolase) DNA.
PN   WO9505472-A2.
PD   23-FEB-1995.
PA   (UNMS ) UNIV MICHIGAN STATE.
  Query Match             3.3%;  Score 34.4;  DB 2;  Length 1431;
  Best Local Similarity   52.0%;  Pred. No. 21;
RESULT 1440
ID   ADP83250 standard; DNA; 1529 BP.
DE   Modified full length PhaA DNA.
PN   WO2004006657-A1.
PD   22-JAN-2004.
PA   (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.
PA   (UYQU ) UNIV QUEENSLAND.
  Query Match             3.3%;  Score 34.4;  DB 12;  Length 1529;
  Best Local Similarity   52.0%;  Pred. No. 22;
RESULT 1441
ID   AAN91209 standard; DNA; 2327 BP.
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DE   Beta-ketothiolase and acetyl-CoA reductase genes.
PN   WO8900202-A.
PD   12-JAN-1989.
PA   (MASI ) MASSACHUSETTS INST TECHNOLOGY.
  Query Match              3.3%;  Score 34.4;  DB 1;  Length 2327;
  Best Local Similarity   52.0%;  Pred. No. 27;
RESULT 1442
ID   AAQ10501 standard; DNA; 2328 BP.
DE   Clone pAeT3 contg. thiolase and acetoacetyl CoA reductase genes.
PN   WO9100917-A.
PD   24-JAN-1991.
PA   (MASI ) MASSACHUSETTS INST TECHNOLOGY.
  Query Match              3.3%;  Score 34.4;  DB 2;  Length 2328;
  Best Local Similarity   52.0%;  Pred. No. 27;
RESULT 1443
ID   AAZ31774 standard; DNA; 2328 BP.
DE   Acetoacetyl-CoA reductase, phbB, coding sequence.
PN   JP11276180-A.
PD   12-OCT-1999.
PA   (RIKA ) RIKAGAKU KENKYUSHO.
PA   (NAKA/) NAKASHITA H.
PA   (YOSH/) YOSHIOKA K.
  Query Match              3.3%;  Score 34.4;  DB 2;  Length 2328;
  Best Local Similarity   52.0%;  Pred. No. 27;
RESULT 1444
ID   AAD03827 standard; DNA; 2328 BP.
DE   Ralstonia eutropha 3-ketoacyl-CoA reductase DNA.
PN   WO200123580-A2.
PD   05-APR-2001.
PA   (PION-) PIONEER HI-BRED INT INC.
  Query Match              3.3%;  Score 34.4;  DB 4;  Length 2328;
  Best Local Similarity   52.0%;  Pred. No. 27;
RESULT 1445
ID   AAD07038 standard; DNA; 2328 BP.
DE   Ralstonia eutropha 3-ketoacyl-CoA reductase DNA.
PN   WO200123596-A2.
PD   05-APR-2001.
PA   (PION-) PIONEER HI-BRED INT INC.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
  Query Match              3.3%;  Score 34.4;  DB 4;  Length 2328;
  Best Local Similarity   52.0%;  Pred. No. 27;
RESULT 1446
ID   ADF14868 standard; cDNA; 3456 BP.
DE   Sunflower resistance gene analogue RS6-8 cDNA #2.
PN   US6608240-B1.
PD   19-AUG-2003.
PA   (PION-) PIONEER HI-BRED INT INC.
  Query Match              3.3%;  Score 34.4;  DB 10;  Length 3456;
  Best Local Similarity   53.8%;  Pred. No. 34;
RESULT 1447
ID   ACC84741 standard; DNA; 4193 BP.
DE   R. eutropha PHA biosynthesis-related enzymes (PHAE) gene fragment.
PN   WO2003046159-A1.
PD   05-JUN-2003.
PA   (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
  Query Match              3.3%;  Score 34.4;  DB 9;  Length 4193;
  Best Local Similarity   52.0%;  Pred. No. 38;
RESULT 1448
ID   AAQ36660 standard; DNA; 4980 BP.
DE   A. eutrophus polyhydroxybutyrate (PHB) operon including PHB synthase
DE   gene, the 3-ketothiolase gene and the acetoacetyl-CoA reductase gene.
PN   WO9302187-A1.
PD   04-FEB-1993.
PA   (UNMS ) UNIV MICHIGAN STATE.
  Query Match              3.3%;  Score 34.4;  DB 2;  Length 4980;
  Best Local Similarity   52.0%;  Pred. No. 42;
RESULT 1449
ID   AAV18986 standard; DNA; 4984 BP.
DE   Polyhydroxyalkanoate biosynthetic operon in pUC18.
PN   WO9804713-A1.
PD   05-FEB-1998.
PA   (MASI ) MASSACHUSETTS INST TECHNOLOGY.
  Query Match              3.3%;  Score 34.4;  DB 2;  Length 4984;
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  Best Local Similarity   52.0%;  Pred. No. 42;
RESULT 1450
ID   AAF84261 standard; DNA; 4984 BP.
DE   phb operon.
PN   EP1076095-A1.
PD   14-FEB-2001.
PA   (RIKE ) RIKEN KK.
  Query Match              3.3%;  Score 34.4;  DB 4;  Length 4984;
  Best Local Similarity   52.0%;  Pred. No. 42;
RESULT 1451
ID   AAC62287 standard; cDNA; 7928 BP.
DE   cDNA encoding a splice variant of a signal transduction polypeptide.
PN   WO200063381-A1.
PD   26-OCT-2000.
PA   (SCIO-) SCIOS INC.
  Query Match              3.3%;  Score 34.4;  DB 5;  Length 7928;
  Best Local Similarity   45.5%;  Pred. No. 54;
RESULT 1452
ID   ABX11641 standard; cDNA; 8106 BP.
DE   Human serine/threonine or protein kinase 59079, cDNA.
PN   US2002168742-A1.
PD   14-NOV-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match              3.3%;  Score 34.4;  DB 8;  Length 8106;
  Best Local Similarity   45.5%;  Pred. No. 54;
RESULT 1453
ID   ADQ22881 standard; DNA; 20489 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5701.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
  Query Match              3.3%;  Score 34.4;  DB 12;  Length 20489;
  Best Local Similarity   45.5%;  Pred. No. 91;
RESULT 1454
ID   ABX11642 standard; cDNA; 24120 BP.
DE   Human serine/threonine or protein kinase 12599, cDNA.
PN   US2002168742-A1.
PD   14-NOV-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match              3.3%;  Score 34.4;  DB 8;  Length 24120;
  Best Local Similarity   45.5%;  Pred. No. 99;
RESULT 1455
ID   ACH39035 standard; cDNA; 458 BP.
DE   Human foetal brain cDNA #402.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match              3.3%;  Score 34.2;  DB 9;  Length 458;
  Best Local Similarity   47.0%;  Pred. No. 13;
RESULT 1456
ID   AAT30562 standard; cDNA; 640 BP.
DE   Eukaryotic cell growth inhibiting factor cDNA clone pTB1671.
PN   WO9617933-A2.
PD   13-JUN-1996.
PA   (TAKE ) TAKEDA CHEM IND LTD.
  Query Match              3.3%;  Score 34.2;  DB 2;  Length 640;
  Best Local Similarity   58.3%;  Pred. No. 15;
RESULT 1457
ID   ADA69968 standard; DNA; 1353 BP.
DE   Rice gene, SEQ ID 3291.
PN   WO2003000898-A1.
PD   03-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
  Query Match              3.3%;  Score 34.2;  DB 8;  Length 1353;
  Best Local Similarity   48.6%;  Pred. No. 23;
RESULT 1458
ID   AAA92302 standard; DNA; 31422 BP.
DE   S. avermitilis avermectin aglycon synthase DNA aveAII SEQ ID NO:2.
PN   WO200050605-A1.
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PD   31-AUG-2000.
PA   (KITA ) KITASATO INST.
  Query Match             3.3%;  Score 34.2;  DB 3;  Length 31422;
  Best Local Similarity   54.3%;  Pred. No. 1.3e+02;
RESULT 1459
ID   AAH79278 standard; DNA; 31422 BP.
DE   Streptomyces avermitilis coding sequences SEQ ID NO: 2.
PN   WO200162939-A1.
PD   30-AUG-2001.
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (KITA ) KITASATO INST.
  Query Match             3.3%;  Score 34.2;  DB 4;  Length 31422;
  Best Local Similarity   54.3%;  Pred. No. 1.3e+02;
RESULT 1460
ID   ADL08124 standard; DNA; 176080 BP.
DE   Human gene associated with low HDL-C LRPAP1.
PN   US2004043389-A1.
PD   04-MAR-2004.
PA   (VITI-) VITIVITY INC.
  Query Match             3.3%;  Score 34.2;  DB 12;  Length 176080;
  Best Local Similarity   46.8%;  Pred. No. 3.4e+02;
RESULT 1461
ID   ABL21947 standard; DNA; 648 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 17314.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match             3.3%;  Score 34;  DB 4;  Length 648;
  Best Local Similarity   54.9%;  Pred. No. 18;
RESULT 1462
ID   AAC68637 standard; cDNA; 1746 BP.
DE   Novel human transporter protein cDNA SEQ ID NO: 5.
PN   WO200065055-A2.
PD   02-NOV-2000.
PA   (LEXI-) LEXICON GENETICS INC.
  Query Match             3.3%;  Score 34;  DB 3;  Length 1746;
  Best Local Similarity   45.0%;  Pred. No. 31;
RESULT 1463
ID   AAC68640 standard; cDNA; 1746 BP.
DE   Novel human transporter protein cDNA SEQ ID NO: 11.
PN   WO200065055-A2.
PD   02-NOV-2000.
PA   (LEXI-) LEXICON GENETICS INC.
  Query Match             3.3%;  Score 34;  DB 3;  Length 1746;
  Best Local Similarity   45.0%;  Pred. No. 31;
RESULT 1464
ID   AAC68635 standard; cDNA; 1884 BP.
DE   Novel human transporter protein cDNA SEQ ID NO: 1.
PN   WO200065055-A2.
PD   02-NOV-2000.
PA   (LEXI-) LEXICON GENETICS INC.
  Query Match             3.3%;  Score 34;  DB 3;  Length 1884;
  Best Local Similarity   45.0%;  Pred. No. 32;
RESULT 1465
ID   AAC68639 standard; cDNA; 1884 BP.
DE   Novel human transporter protein cDNA SEQ ID NO: 9.
PN   WO200065055-A2.
PD   02-NOV-2000.
PA   (LEXI-) LEXICON GENETICS INC.
  Query Match             3.3%;  Score 34;  DB 3;  Length 1884;
  Best Local Similarity   45.0%;  Pred. No. 32;
RESULT 1466
ID   AAC68638 standard; cDNA; 1884 BP.
DE   Novel human transporter protein cDNA SEQ ID NO: 7.
PN   WO200065055-A2.
PD   02-NOV-2000.
PA   (LEXI-) LEXICON GENETICS INC.
  Query Match             3.3%;  Score 34;  DB 3;  Length 1884;
  Best Local Similarity   45.0%;  Pred. No. 32;
RESULT 1467
ID   AAC68636 standard; cDNA; 1884 BP.
DE   Novel human transporter protein cDNA SEQ ID NO: 3.
PN   WO200065055-A2.
PD   02-NOV-2000.
PA   (LEXI-) LEXICON GENETICS INC.
  Query Match             3.3%;  Score 34;  DB 3;  Length 1884;
  Best Local Similarity   45.0%;  Pred. No. 32;
RESULT 1468
ID   AAS64404 standard; cDNA; 2631 BP.
DE   DNA encoding novel human diagnostic protein #208.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             3.3%;  Score 34;  DB 5;  Length 2631;
  Best Local Similarity   53.8%;  Pred. No. 39;
RESULT 1469
ID   ABN59863 standard; cDNA; 2878 BP.
DE   Novel human coding sequence SEQ ID NO: 274.
PN   WO200222660-A2.
PD   21-MAR-2002.
PA   (HYSE-) HYSEQ INC.
  Query Match             3.3%;  Score 34;  DB 6;  Length 2878;
  Best Local Similarity   45.0%;  Pred. No. 41;
RESULT 1470
ID   AAC76422 standard; cDNA; 2900 BP.
DE   Human ORFX ORF1977 polynucleotide sequence SEQ ID NO:3953.
PN   WO200058473-A2.
PD   05-OCT-2000.
PA   (CURA-) CURAGEN CORP.
  Query Match             3.3%;  Score 34;  DB 3;  Length 2900;
  Best Local Similarity   45.0%;  Pred. No. 41;
RESULT 1471
ID   AAA93125 standard; cDNA; 2927 BP.
DE   Human secreted protein coding sequence SEQ ID NO: 49.
PN   WO200049134-A1.
PD   24-AUG-2000.
PA   (ALPH-) ALPHAGENE INC.
  Query Match             3.3%;  Score 34;  DB 3;  Length 2927;
  Best Local Similarity   45.0%;  Pred. No. 41;
RESULT 1472
ID   ABL21946 standard; DNA; 3470 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 17311.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match             3.3%;  Score 34;  DB 4;  Length 3470;
  Best Local Similarity   54.9%;  Pred. No. 45;
RESULT 1473
ID   AAI67897 standard; DNA; 4341 BP.
DE   Nucleotide sequence of codon optimised sequence Id No. 3.
PN   EP1156112-A1.
PD   21-NOV-2001.
PA   (GENE-) GENEART GMBH.
  Query Match             3.3%;  Score 34;  DB 6;  Length 4341;
  Best Local Similarity   51.3%;  Pred. No. 51;
RESULT 1474
ID   AAI67896 standard; DNA; 4343 BP.
DE   Nucleotide sequence of optimised GagPol HIV-1IIIB.
PN   EP1156112-A1.
PD   21-NOV-2001.
PA   (GENE-) GENEART GMBH.
  Query Match             3.3%;  Score 34;  DB 6;  Length 4343;
  Best Local Similarity   51.3%;  Pred. No. 51;
RESULT 1475
ID   ABS67999 standard; cDNA; 4376 BP.
DE   DNA encoding LE B-domain-deleted-Factor VIII (FVIII).
PN   WO200264799-A2.
PD   22-AUG-2002.
PA   (TRAN-) TRANSKARYOTIC THERAPIES INC.
  Query Match             3.3%;  Score 34;  DB 6;  Length 4376;
  Best Local Similarity   47.2%;  Pred. No. 51;
RESULT 1476
ID   ABS68000 standard; cDNA; 4384 BP.
DE   DNA encoding 5Arg B-domain-deleted-Factor VIII (FVIII).
PN   WO200264799-A2.
PD   22-AUG-2002.
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PA   (TRAN-) TRANSKARYOTIC THERAPIES INC.
  Query Match              3.3%;  Score 34;  DB 6;  Length 4384;
  Best Local Similarity   47.2%;  Pred. No. 52;
RESULT 1477
ID   ACN44332 standard; DNA; 114633 BP.
DE   Mouse genomic sequence mCG17870.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
  Query Match              3.3%;  Score 34;  DB 11;  Length 114633;
  Best Local Similarity   61.1%;  Pred. No. 3.1e+02;
RESULT 1478
ID   ADP43517 standard; DNA; 347001 BP.
DE   Human MAD1-like 1 DNA #7.
PN   US2004115650-A1.
PD   17-JUN-2004.
PA   (ISIS-) ISIS PHARM INC.
  Query Match              3.3%;  Score 34;  DB 12;  Length 347001;
  Best Local Similarity   49.4%;  Pred. No. 5.7e+02;
RESULT 1479
ID   ACH82331 standard; DNA; 315 BP.
DE   Human genome derived single exon probe #15526.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
  Query Match              3.3%;  Score 33.8;  DB 12;  Length 315;
  Best Local Similarity   56.9%;  Pred. No. 14;
RESULT 1480
ID   ABA54256 standard; DNA; 461 BP.
DE   Human foetal liver single exon nucleic acid probe #2561.
PN   WO200157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
  Query Match              3.3%;  Score 33.8;  DB 4;  Length 461;
  Best Local Similarity   56.9%;  Pred. No. 17;
RESULT 1481
ID   ABA43797 standard; DNA; 461 BP.
DE   Human breast cell single exon nucleic acid probe #2492.
PN   WO200157271-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
  Query Match              3.3%;  Score 33.8;  DB 4;  Length 461;
  Best Local Similarity   56.9%;  Pred. No. 17;
RESULT 1482
ID   ABA24007 standard; DNA; 461 BP.
DE   Probe #2473 for gene expression analysis in human heart cell sample.
PN   WO200157274-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
  Query Match              3.3%;  Score 33.8;  DB 4;  Length 461;
  Best Local Similarity   56.9%;  Pred. No. 17;
RESULT 1483
ID   ABS27557 standard; DNA; 461 BP.
DE   Human liver single exon probe, SEQ ID No 2547.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
  Query Match              3.3%;  Score 33.8;  DB 4;  Length 461;
  Best Local Similarity   56.9%;  Pred. No. 17;
RESULT 1484
ID   AAI02459 standard; DNA; 461 BP.
DE   Probe #2450 used to measure gene expression in human breast sample.
PN   WO200157270-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
  Query Match              3.3%;  Score 33.8;  DB 5;  Length 461;
  Best Local Similarity   56.9%;  Pred. No. 17;
RESULT 1485
ID   ACH68631 standard; DNA; 566 BP.
DE   Human genome derived single exon probe #1826.
PN   US2003194704-A1.
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PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
  Query Match              3.3%;  Score 33.8;  DB 12;  Length 566;
  Best Local Similarity   56.9%;  Pred. No. 19;
RESULT 1486
ID   ADS57570 standard; cDNA; 772 BP.
DE   Bacterial polynucleotide #9557.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match              3.3%;  Score 33.8;  DB 13;  Length 772;
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PN   WO2003100439-A2.
PD   04-DEC-2003.
PA   (UYSH-) UNIV SHEFFIELD.
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RESULT 1488
ID   ADO30229 standard; cDNA; 1032 BP.
DE   Mouse GPCR GPR77 polynucleotide, SEQ ID NO:1332.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
  Query Match              3.3%;  Score 33.8;  DB 12;  Length 1032;
  Best Local Similarity   48.2%;  Pred. No. 27;
RESULT 1489
ID   AAA30433 standard; cDNA; 1122 BP.
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PN   WO200032633-A1.
PD   08-JUN-2000.
PA   (ICOS-) ICOS CORP.
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  Best Local Similarity   54.4%;  Pred. No. 28;
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ID   AAT29035 standard; cDNA; 1321 BP.
DE   Endoglucanase (60 kDa Family 5 cellulase) cDNA sequence.
PN   WO9611262-A1.
PD   18-APR-1996.
PA   (NOVO ) NOVO-NORDISK AS.
  Query Match              3.3%;  Score 33.8;  DB 2;  Length 1321;
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RESULT 1491
ID   ABD12458 standard; DNA; 1416 BP.
DE   Pseudomonas aeruginosa polynucleotide #11062.
PN   US6551795-B1.
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PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match              3.3%;  Score 33.8;  DB 11;  Length 1416;
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ID   AAS26547 standard; cDNA; 1646 BP.
DE   Human cDNA encoding a novel secreted protein, Seq ID 726.
PN   WO200155322-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match              3.3%;  Score 33.8;  DB 4;  Length 1646;
  Best Local Similarity   58.4%;  Pred. No. 35;
RESULT 1493
ID   ABX73888 standard; DNA; 1646 BP.
DE   Human novel polynucleotide #716.
PN   US2002132753-A1.
PD   19-SEP-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
  Query Match              3.3%;  Score 33.8;  DB 8;  Length 1646;
  Best Local Similarity   58.4%;  Pred. No. 35;
RESULT 1494
ID   AAA30440 standard; cDNA; 1694 BP.
DE   Human cDNA sequence encoding ACAM4/IgG4-Fc fusion protein.
PN   WO200032633-A1.
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ID   ABD12590 standard; DNA; 1761 BP.
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ID   ADS56267 standard; cDNA; 1770 BP.
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PD   18-DEC-2003.
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PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match              3.3%;  Score 33.8;  DB 13;  Length 1770;
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ID   AAA30436 standard; cDNA; 1796 BP.
DE   Human cDNA sequence encoding ACAM6/IgG4-Fc fusion protein.
PN   WO200032633-A1.
PD   08-JUN-2000.
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PD   08-JUN-2000.
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PN   WO2003065993-A2.
PD   14-AUG-2003.
PA   (GENE-) GENE LOGIC INC.
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RESULT 1500
ID   AAT86704 standard; DNA; 3147 BP.
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PN   WO9725058-A1.
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PA   (THER-) THERMOGEN INC.
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                     GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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     Pred. No. is the number of results predicted by chance to have a
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 1144   28.6   2.8    906  3  US-09-217-847-24         Sequence 24, Appl
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                                 ALIGNMENTS


RESULT 1
US-09-700-397-2
; Sequence 2, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
;  APPLICANT:  Ono Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION:   No. 6664383el Polypeptides, cDNA encoding the same, and use of
;  FILE REFERENCE:   Q61459
;  CURRENT APPLICATION NUMBER: US/09/700,397
;  CURRENT FILING DATE:  2001-01-05
;  PRIOR APPLICATION NUMBER:   JP 10-131815
;  PRIOR FILING DATE:   1998-05-14
;  PRIOR APPLICATION NUMBER:   PCT/JP99/02485
;  PRIOR FILING DATE:   1999-05-13
;  NUMBER OF SEQ ID NOS:   19
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 1693
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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;   OTHER INFORMATION: Clone OC001 derived from human brain
;   NAME/KEY: CDS
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;   LOCATION: (214)..()
US-09-700-397-2

  Query Match             100.0%;  Score 1035;  DB 4;  Length 1693;
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  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-09-700-397-1
; Sequence 1, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
;  APPLICANT:  Ono Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION:   No. 6664383el Polypeptides, cDNA encoding the same, and use of
;  FILE REFERENCE:    Q61459
;  CURRENT APPLICATION NUMBER: US/09/700,397
;  CURRENT FILING DATE:   2001-01-05
;  PRIOR APPLICATION NUMBER:   JP 10-131815
;  PRIOR FILING DATE:    1998-05-14
;  PRIOR APPLICATION NUMBER:    PCT/JP99/02485
;  PRIOR FILING DATE:    1999-05-13
;  NUMBER OF SEQ ID NOS:   19
;  SOFTWARE:    PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1032
;   TYPE: DNA
;   ORGANISM: Homo sapiens

US-09-700-397-1

  Query Match             99.7%;  Score 1032;  DB 4;  Length 1032;
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Qy        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660
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Db        601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660

Qy        661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720

Qy        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780

Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840

Qy        841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900

Qy        901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960

Qy        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020
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Qy       1021 CTTCTCAAATTT 1032
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Db       1021 CTTCTCAAATTT 1032


RESULT 3
US-09-700-397-5
; Sequence 5, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
;  APPLICANT:  Ono Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION:   No. 6664383el Polypeptides, cDNA encoding the same, and use of
;  FILE REFERENCE:   Q61459
;  CURRENT APPLICATION NUMBER: US/09/700,397
;  CURRENT FILING DATE:  2001-01-05
;  PRIOR APPLICATION NUMBER:   JP 10-131815
;  PRIOR FILING DATE:   1998-05-14
;  PRIOR APPLICATION NUMBER:   PCT/JP99/02485
;  PRIOR FILING DATE:   1999-05-13
;  NUMBER OF SEQ ID NOS:   19
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 939
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-700-397-5

  Query Match             90.7%;  Score 939;  DB 4;  Length 939;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-277;
  Matches  939;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         94 CGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAG 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAG 60

Qy        154 AGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGC 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGC 120

Qy        214 AGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTG 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTG 180

Qy        274 AGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGC 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGC 240

Qy        334 CCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATT 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATT 300

Qy        394 GTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC 360

Qy        454 AATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACAC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACAC 420

Qy        514 ATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATC 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATC 480

Qy        574 ACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTG 633
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTG 540

Qy        634 GTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACA 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACA 600

Qy        694 GGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCA 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCA 660

Qy        754 GAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTG 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTG 720

Qy        814 GAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGG 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGG 780

Qy        874 AACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTT 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTT 840

Qy        934 GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGG 900

Qy        994 CTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 1032
              |||||||||||||||||||||||||||||||||||||||
Db        901 CTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 939


RESULT 4
US-08-414-657D-3
; Sequence 3, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1238 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  56...1069
;      OTHER INFORMATION:
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US-08-414-657D-3

  Query Match             33.0%;  Score 342;  DB 2;  Length 1238;
  Best Local Similarity   61.9%;  Pred. No. 2.6e-94;
  Matches  597;  Conservative    0;  Mismatches  355;  Indels   12;  Gaps    3;

Qy        72 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 131
             |||   |  |||| ||||||| |||||||  |||      ||   |  ||  | ||||||
Db       121 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 174

Qy       132 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 191
             | | || ||  |||||||||| |  |||| |||||||||     | ||  ||  |  | |
Db       175 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 234

Qy       192 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 251
                 ||||||||| | ||||||     |||| |||  |||||  | ||||||||||  ||
Db       235 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 294

Qy       252 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 311
             ||| ||||| || |  ||   ||    |        | | |||||| ||   ||||||||
Db       295 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 354

Qy       312 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 371
              |||||||| ||||| || ||  | ||||| ||||| || |||||| |  |  | || ||
Db       355 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 414

Qy       372 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 431
             |||||||   ||  || | ||||| |||||  |  |||| ||     | || || || ||
Db       415 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 474

Qy       432 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 491
             | || |  | ||||| || | |||| | | |||   |||||| || | |||  | || ||
Db       475 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 534

Qy       492 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 551
              |||    | || ||||||||| |  | ||    |     |  ||||   | ||||| ||
Db       535 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 594

Qy       552 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 611
             |||  |||| || |  ||||||||| |||| ||||||||  | || |||||||  ||  |
Db       595 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 654

Qy       612 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 671
             ||| || ||  || |  | |  ||      ||| |||||||| ||||||||||||||
Db       655 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 714

Qy       672 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 731
             |||  ||||  | ||| | |  |  | | ||   |||| | | |   | ||  | |||||
Db       715 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 774

Qy       732 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 791
             ||||||||| || ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db       775 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 831

Qy       792 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 851
               |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db       832 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 891

Qy       852 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 911
              ||| ||||  |  |||| || ||||| || || |||||  |||||||||| |||  |||
Db       892 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 951

Qy       912 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 971
             |||||||||| |  | || ||  | || ||  | || ||    |  | ||||||  |
Db       952 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAG---AGGAATCAACGGATCCAT 1008

Qy       972 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1031
              ||   ||| |      | ||||||||| |        | ||   ||| ||   |||||
Db      1009 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCCTTCTCAGCAAATG 1068

Qy      1032 TTGA 1035
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Db      1069 TTAA 1072
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RESULT 5
US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1238 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  56...1069
;      OTHER INFORMATION:
US-09-135-080-3

  Query Match             33.0%;  Score 342;  DB 3;  Length 1238;
  Best Local Similarity   61.9%;  Pred. No. 2.6e-94;
  Matches  597;  Conservative    0;  Mismatches  355;  Indels   12;  Gaps    3;

Qy        72 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 131
             |||   |  |||| ||||||| |||||||  |||      ||   |  ||  | ||||||
Db       121 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 174

Qy       132 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 191
             | | || ||  |||||||||| |  |||| |||||||||     | ||  ||  |  | |
Db       175 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 234

Qy       192 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 251
                 ||||||||| | ||||||     |||| |||  |||||  | ||||||||||  ||
Db       235 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 294

Qy       252 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 311
             ||| ||||| || |  ||   ||    |        | | |||||| ||   ||||||||
Db       295 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 354
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Qy        312 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 371
               |||||||| ||||| || ||  | ||||| ||||| || |||||| |  |  | || ||
Db        355 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 414

Qy        372 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 431
              |||||||   ||  || | ||||| |||||  | || || ||     | || || || ||
Db        415 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 474

Qy        432 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 491
              | || |  | ||||| || | |||| | | |||   |||||| || | |||  | || ||
Db        475 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 534

Qy        492 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 551
               |||    | || ||||||||| |  | ||    |     |  ||||   | ||||| ||
Db        535 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 594

Qy        552 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 611
              |||  |||| || |  |||||||| |||| ||||||||  | || |||||||  ||  |
Db        595 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 654

Qy        612 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 671
              ||| || ||  || |  | |  ||      ||| |||||||| |||||||||||||||
Db        655 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 714

Qy        672 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 731
              |||  ||||   | ||| | |  |  | | ||   |||| | | |   | ||  | |||||
Db        715 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 774

Qy        732 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 791
              ||||||||| || ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db        775 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 831

Qy        792 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 851
                |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db        832 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 891

Qy        852 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 911
               ||| ||||  |  |||| || ||||| || || ||||| |||||||||| |||  |||
Db        892 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 951

Qy        912 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 971
              |||||||||| |  | || ||  | || ||  | || ||    |  | ||||||  |
Db        952 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAG---AGGAATCAACGGATCCAT 1008

Qy        972 GAGGAGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1031
               ||   ||| |      | ||||||||| |        | ||   ||| ||   |||||
Db       1009 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCCTTCTCAGCAAATG 1068

Qy       1032 TTGA 1035
              || |
Db       1069 TTAA 1072

RESULT 6
US-08-414-657D-7
; Sequence 7, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  924 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...924
;      OTHER INFORMATION:
US-08-414-657D-7

  Query Match             32.9%;  Score 340.6;  DB 2;  Length 924;
  Best Local Similarity   63.3%;  Pred. No. 5.9e-94;
  Matches  558;  Conservative    0;  Mismatches  314;  Indels    9;  Gaps    2;

Qy         72 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 131
              |||   |  |||| |||| || ||||||||  |||      ||   |  ||  | ||||||
Db         45 TCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 98

Qy        132 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 191
              | | || ||  ||||||||||| |  ||||  ||||||||||  | | ||  ||  |  | |
Db         99 CATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTC 158

Qy        192 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 251
                 |||||||||| | |||||      |||| | | ||||||  ||||||||||||  ||
Db        159 AAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCT 218

Qy        252 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 311
              ||| || || || |  ||    ||    |        | | |||||| ||   ||||||||
Db        219 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAA 278

Qy        312 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 371
               |||||||| ||||| |||||  | ||||| ||||| || |||||| |  |  | || ||
Db        279 GGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAA 338

Qy        372 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 431
              ||||||    ||  || | || || |||||  | || || ||     | || || || ||
Db        339 GACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGA 398

Qy        432 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 491
              | || |  | ||||| || | |||  | |  ||   |||||| || | |||  | || ||
Db        399 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGA 458

Qy        492 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 551
               |||    | || ||||||||| |  | ||  |  |     |  ||||   | ||||| ||
Db        459 ACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 518

Qy        552 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 611
              |||  |||| || |  |||||||| ||||||||||||||  | || |||||||  ||  |
Db        519 ATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGC 578

Qy        612 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 671
              ||| || ||  || || | |  ||      ||| |||||||| ||||||||||| ||
Db        579 CAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCAC 638

Qy        672 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 731
               ||  ||||| ||||| | |  |  | | ||   |||| | | |   ||||  | |||||
Db        639 TATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGA 698

Qy        732 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 791
               ||||| ||||| ||  || | || ||  |||||||||  |||||||||  ||   |||  |
Db        699 GGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 755

Qy        792 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 851
                |    || ||  |  |  |  | | ||        ||  ||    || |   |   |||
Db        756 TAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 815

Qy        852 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 911
               ||| ||||  |  |||| || |||||||| || |||||  |||||||||||||   |||
Db        816 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCAC 875

Qy        912 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 952
              |||||||||| |  | || ||  | || ||   | || || |
Db        876 CAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 916


RESULT 7
US-08-414-657D-1
; Sequence 1, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  2...976
;      OTHER INFORMATION:
US-08-414-657D-1
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  Query Match             32.9%;  Score 340.6;  DB 2;  Length 977;
  Best Local Similarity   63.3%;  Pred. No. 6.1e-94;
  Matches  558;  Conservative    0;  Mismatches  314;  Indels    9;  Gaps    2;

Qy         72 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 131
              |||   |  |||| |||| || ||||||| |||       ||   |  ||  | ||||||
Db         46 TCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 99

Qy        132 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 191
              | | || ||  ||||||||||| |  ||||  ||||||||||  | | ||  ||  |  | |
Db        100 CATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTC 159

Qy        192 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 251
                 ||||||||||| | |||||      |||| | | ||||||  ||||||||||||  ||
Db        160 AAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCT 219

Qy        252 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 311
              ||| || || || |  ||    ||    |        | | |||||| ||   ||||||||
Db        220 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAA 279

Qy        312 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 371
               |||||||| ||||| |||||  | |||||| ||||| || |||||| |  |  | || ||
Db        280 GGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAA 339

Qy        372 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 431
              ||||||    ||  || | || || |||||  | || ||   ||     | || || || ||
Db        340 GACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGA 399

Qy        432 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 491
              | || |  | ||||| || | |||  | | | ||   |||||| || | ||  | || ||
Db        400 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGA 459

Qy        492 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 551
               |||    | || ||||||||| |  | || |  |     |  ||||   | ||||| ||
Db        460 ACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 519

Qy        552 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 611
              |||  |||| || |  ||||||||| ||||||||||||||  | || |||||||  ||  |
Db        520 ATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGC 579

Qy        612 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 671
              ||| || ||  || || | |  ||      ||| |||||||| ||||||||||||| ||
Db        580 CAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCAC 639

Qy        672 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 731
               ||  ||||| ||||| | |  |  | | ||   |||| | | |   ||||  | |||||
Db        640 TATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGA 699

Qy        732 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 791
               ||||| ||||| ||  || | || ||  |||||||||  |||||||||  ||   |||  |
Db        700 GGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 756

Qy        792 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 851
                |    || ||  |  |  |  | | ||        ||  ||    || |   |   |||
Db        757 TAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 816

Qy        852 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 911
               ||| ||||  |  |||| || |||||||| || |||||  |||||||||||||   |||
Db        817 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCAC 876

Qy        912 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 952
              |||||||||| |  | || ||  | || ||   | || || |
Db        877 CAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 917


RESULT 8
US-09-135-080-1
; Sequence 1, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  2...976
;      OTHER INFORMATION:
US-09-135-080-1

  Query Match             32.9%;  Score 340.6;  DB 3;  Length 977;
  Best Local Similarity   63.3%;  Pred. No. 6.1e-94;
  Matches  558;  Conservative    0;  Mismatches  314;  Indels    9;  Gaps    2;

Qy         72 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 131
              |||   |  |||| |||| || |||||||  |||      ||   |  ||  | ||||||
Db         46 TCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 99

Qy        132 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 191
              | | || ||  |||||||||| |  |||| ||||||||||  | | ||  ||  |  | |
Db        100 CATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTC 159

Qy        192 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 251
                 |||||||||| | |||||      |||| | | ||||||  ||||||||||||  ||
Db        160 AAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCT 219

Qy        252 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 311
              ||| || || || |  ||   ||    |        | | |||||| ||   ||||||||
Db        220 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAA 279

Qy        312 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 371
               |||||||| ||||| |||||  | ||||| ||||| || |||||| |  |  | || ||
Db        280 GGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAA 339

Qy        372 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 431
              ||||||    ||  || | || || |||||  | || || ||     | || || || ||
Db        340 GACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGA 399

Qy        432 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 491
              | || |  | ||||| || | |||  | |  ||   |||||| || | |||  | || ||
Db        400 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGA 459

Qy        492 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 551
               |||    | || ||||||||| |  | || |  |     |  ||||   | ||||| ||
Db        460 ACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 519

Qy        552 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 611
              |||  |||| || |  ||||||||| |||||||||||||  | || |||||||  ||  |
Db        520 ATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGC 579

Qy        612 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 671
              ||| || ||  || || | |  ||      ||| |||||||| ||||||||||| ||
Db        580 CAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCAC 639

Qy        672 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 731
               ||  ||||| ||||| | |  |  | | ||   |||| | | |   ||||  | |||||
Db        640 TATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGA 699

Qy        732 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 791
               ||||| ||||| || ||  | || ||  ||||||||  ||||||||  ||   |||  |
Db        700 GGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 756

Qy        792 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 851
                |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db        757 TAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 816

Qy        852 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 911
               ||| ||||  |  |||| || |||||||| ||  ||||  |||||||||||||   |||
Db        817 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCAC 876

Qy        912 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 952
              |||||||||| |  | || ||  | || ||  | || || |
Db        877 CAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 917

RESULT 9
US-08-414-657D-5
; Sequence 5, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1014 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1014
;      OTHER INFORMATION:
US-08-414-657D-5

  Query Match             32.9%;  Score 340.6;  DB 2;  Length 1014;
  Best Local Similarity   61.9%;  Pred. No. 6.2e-94;
  Matches  595;  Conservative    0;  Mismatches  354;  Indels   12;  Gaps    3;

Qy         72 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 131
              |||   |  |||| ||||||| |||||||  |||      ||   |  ||  | ||||||
Db         66 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 119

Qy        132 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 191
              | | || ||  |||||||||| |  |||| |||||||||     | ||  ||  |  | |
Db        120 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 179

Qy        192 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 251
                  ||||||||| | ||||||     |||| |||  |||||  | ||||||||||  ||
Db        180 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 239

Qy        252 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 311
              ||| ||||| || |  ||   ||    |        | | |||||| ||   ||||||||
Db        240 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 299

Qy        312 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 371
               |||||||| ||||| || ||  | ||||| ||||| || |||||| |  |  | || ||
Db        300 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 359

Qy        372 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 431
              |||||||   ||  || | ||||| |||||  | || || ||     | || || || ||
Db        360 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 419

Qy        432 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 491
              | || |  | ||||| || | |||| | | |||   |||||| || | |||  | || ||
Db        420 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 479

Qy        492 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 551
               |||    | || ||||||||| |  | ||    |     |  ||||   | ||||| ||
Db        480 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 539

Qy        552 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 611
              |||  |||| || |  ||||||||| |||| ||||||||  | || |||||||  ||  |
Db        540 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 599

Qy        612 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 671
              ||| || ||  || |  | |  ||      ||| |||||||| ||||||||||||||
Db        600 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659

Qy        672 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 731
              |||  ||||  | ||| | |  |  | | ||   |||| | | |   | ||  | |||||
Db        660 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 719

Qy        732 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 791
              ||||||||| || ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db        720 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 776

Qy        792 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 851
                |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db        777 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 836

Qy        852 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 911
               ||| ||||  |  |||| || ||||| || || |||||  |||||||||| |||  |||
Db        837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 896

Qy        912 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 971
              |||||||||| |  | || ||  | || ||  | || ||    |  | ||||||  |
Db        897 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAG---AGGAATCAACGGATCCAT 953

Qy        972 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1031
               ||   ||| |      | ||||||||| |        | ||   ||| ||   |||||
Db        954 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCCTTCTCAGCAAATG 1013

Qy       1032 T 1032
              |
Db       1014 T 1014

RESULT 10
US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1014 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1014
;      OTHER INFORMATION:
US-09-135-080-7

  Query Match             32.9%;  Score 340.6;  DB 3;  Length 1014;
  Best Local Similarity   61.9%;  Pred. No. 6.2e-94;
  Matches  595;  Conservative    0;  Mismatches  354;  Indels   12;  Gaps    3;

Qy         72 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 131
              |||   |  |||| ||||||| |||||||  |||      ||   |  ||  | ||||||
Db         66 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 119
```

```
Qy         132 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 191
               | | || ||  |||||||||| |  |||| |||||||||     | ||  ||  |  | |
Db         120 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 179

Qy         192 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 251
                   ||||||||| | ||||||     |||| |||  ||||| | ||||||||||  ||
Db         180 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 239

Qy         252 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 311
               ||| ||||| || |  ||   ||  |          | | |||||| ||   ||||||||
Db         240 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 299

Qy         312 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 371
                |||||||| ||||| || ||  | ||||| ||||| || |||||| |  |  | || ||
Db         300 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 359

Qy         372 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 431
               |||||||   ||  || | ||||| |||||  | || || ||     | || || || ||
Db         360 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 419

Qy         432 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 491
               | || |  | ||||| || | |||| | | |||   |||||| || | |||  | || ||
Db         420 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 479

Qy         492 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 551
                |||    | || ||||||||| |  | ||    |     |  ||||   | ||||| ||
Db         480 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 539

Qy         552 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 611
               |||  |||| || |  ||||||||| |||| ||||||||  | || |||||||  ||  |
Db         540 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 599

Qy         612 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 671
               ||| || ||  || |  | |  ||      ||| |||||||| ||||||||||||||
Db         600 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659

Qy         672 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 731
               |||  ||||  | ||| | |  |  | | ||   |||| | | |   | ||  | |||||
Db         660 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 719

Qy         732 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 791
               ||||||||| || ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db         720 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 776

Qy         792 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 851
                 |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db         777 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 836

Qy         852 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 911
                ||| ||||  |  |||| || ||||| || || |||||  |||||||||| |||  |||
Db         837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 896

Qy         912 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTC 971
               |||||||||| |  | || ||  | || ||  | || ||    |  | ||||||  |
Db         897 CAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAG---AGGAATCAACGGATCCAT 953

Qy         972 GAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATT 1031
                ||   ||| |      | ||||||||| |        | ||   ||| ||   |||||
Db         954 CAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTCTGCCTTCTCAGCAAATG 1013

Qy.       1032 T 1032
               |
Db        1014 T 1014

RESULT 11
US-09-976-594-403
; Sequence 403, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 403
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 1640555CB1
US-09-976-594-403

  Query Match             32.9%;  Score 340.6;  DB 4;  Length 1195;
  Best Local Similarity   63.3%;  Pred. No. 6.9e-94;
  Matches  558;  Conservative    0;  Mismatches  314;  Indels    9;  Gaps    2;

Qy          72 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 131
               |||   |  |||| |||| || |||||||  |||      ||   |  ||  | ||||||
Db          66 TCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 119

Qy         132 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 191
               | | || ||  |||||||||| |  |||| ||||||||||  | | ||  ||  |  | |
Db         120 CATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTC 179

Qy         192 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 251
                  |||||||||| | |||||      |||| | | ||||||  ||||||||||||  ||
Db         180 AAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGACAAGTGGTCTCT 239

Qy         252 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 311
               ||| || || || |  ||   ||  |          | | |||||| ||   ||||||||
Db         240 GGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAA 299

Qy         312 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 371
                |||||||| ||||| |||||  | ||||| ||||| || |||||| |  |  | || ||
Db         300 GGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAA 359

Qy         372 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 431
               ||||||    ||  || | || || |||||  | || || ||     | || || || ||
Db         360 GACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGA 419

Qy         432 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 491
               | || |  | ||||| || | |||  | |  ||   |||||| || | |||  | || ||
Db         420 TGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGA 479

Qy         492 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 551
                |||    | || ||||||||| |  | || |  |     |  ||||   | ||||| ||
Db         480 ACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGA 539

Qy         552 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 611
               |||  |||| || |  ||||||||| |||||||||||||  | || |||||||  ||  |
Db         540 ATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGC 599

Qy         612 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 671
               ||| || ||  || || | |  ||      ||| |||||||| ||||||||||| ||
Db         600 CAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCAC 659

Qy         672 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 731
                ||  ||||| ||||| | |  |  | | ||   |||| | | |   ||||  | |||||
Db         660 TATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGA 719

Qy         732 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 791
                ||||| ||||| ||  || | || ||  ||||||||  ||||||||  ||   |||  |
Db         720 GGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACTAG---GATAAA 776

Qy         792 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 851
                 |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db         777 TAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAA 836

Qy         852 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 911
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               ||| ||||  |  |||| || |||||||| || |||||  |||||||||||||   |||
Db        837 CGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGTCAC 896

Qy        912 CAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 952
              |||||||||| |  | || ||  | || ||  | || || |
Db        897 CAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 937

RESULT 12
US-08-414-657D-9
; Sequence 9, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  861 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...861
;      OTHER INFORMATION:
US-08-414-657D-9

  Query Match             32.7%;  Score 338.6;  DB 2;  Length 861;
  Best Local Similarity   63.7%;  Pred. No. 2.3e-93;
  Matches  531;  Conservative    0;  Mismatches  299;  Indels    3;  Gaps    1;

Qy        120 AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGA 179
              ||  | ||||||| | || ||  |||||||||| |  |||| ||||||||||  | | ||
Db         24 AGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGA 83

Qy        180 CAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA 239
                ||  |  | |   |||||||||| | |||||      |||| | | ||||||  ||||
Db         84 AGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGA 143

Qy        240 CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT 299
              ||||||||  ||||| || || || |  ||   ||    |        | | |||||| |
Db        144 CAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCT 203

Qy        300 CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGA 359
              |   |||||||| |||||||| ||||| |||||  | ||||| ||||| || |||||| |
Db        204 CCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACA 263

Qy        360 CAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGA 419
                |  | || ||||||||    ||  || | || || |||||  | || || ||     |
Db        264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAA 323

Qy        420 GATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAAC 479
               || || || ||| || |  | ||||| || | |||  | |  ||   |||||| || |
Db        324 TATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAA 383

Qy        480 TGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT 539
              |||  | || || |||    | || ||||||||| |  | || |  |     |  ||||
Db        384 TGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGA 443

Qy        540 GAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGA 599
                | ||||| |||||  |||| || |  ||||||||| |||||||||||||  | || ||
Db        444 AGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGA 503

Qy        600 GTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAA 659
              |||||  ||  |||| || ||  || || | |  ||      ||| |||||||| |||||
Db        504 GTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAA 563

Qy        660 CTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGAC 719
              |||||| ||    ||  ||||| ||||| | |  |  | | ||   |||| | | |   |
Db        564 CTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTC 623

Qy        720 ACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAA 779
              |||  | ||||| ||||| ||||| ||  || | || ||  ||||||||  ||||||||
Db        624 ACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACAC 683

Qy        780 AAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACT 839
               ||   |||  |  |    || ||  |  |  |  | | ||       ||  ||    ||
Db        684 TAG---GATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCT 740

Qy        840 CATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAA 899
               |   |   ||| ||| ||||  |  |||| || |||||||| || |||||  |||||||
Db        741 GACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAA 800

Qy        900 GCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 952
              ||||||   ||||||||||||| |  | || ||  | || ||  | || || |
Db        801 GCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 853

RESULT 13
US-08-414-657D-6
; Sequence 6, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  912 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...912
;      OTHER INFORMATION:
US-08-414-657D-6

  Query Match             32.7%;  Score 338.6;  DB 2;  Length 912;
  Best Local Similarity   63.7%;  Pred. No. 2.4e-93;
  Matches  531;  Conservative    0;  Mismatches  299;  Indels    3;  Gaps    1;

Qy        120 AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGA 179
              ||  | ||||||| | || ||  |||||||||| |  |||| ||||||||||  | | ||
Db         24 AGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTTCTAGA 83

Qy        180 CAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA 239
                ||  |  | |   |||||||||| | |||||      |||| | | ||||||  ||||
Db         84 AGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGACATGA 143

Qy        240 CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT 299
              ||||||||  ||||| || || || |  ||   ||    |        | | |||||| |
Db        144 CAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATACAGCCT 203

Qy        300 CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGA 359
              |   |||||||| |||||||| ||||| |||||  | ||||| ||||| || |||||| |
Db        204 CCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAGACACA 263

Qy        360 CAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGA 419
                |  | || ||||||||    ||  || | || || |||||  | || || ||     |
Db        264 GCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATCTCCAA 323

Qy        420 GATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAAC 479
               || || || ||| || |  | ||||| || | |||  | |  ||   |||||| || |
Db        324 TATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATGGCCAA 383

Qy        480 TGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT 539
              |||  | || || |||    | || ||||||||| |  | || |  |     |  ||||
Db        384 TGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAATTTGA 443

Qy        540 GAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGA 599
                | ||||| |||||  |||| || |  ||||||||| |||||||||||||  | || ||
Db        444 AGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAATATGA 503

Qy        600 GTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAA 659
              |||||  ||  |||| || ||  || || | |  ||      ||| |||||||| |||||
Db        504 GTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACTGTGAA 563

Qy        660 CTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGAC 719
              |||||| ||    ||  ||||| ||||| | |  |  | | ||   |||| | | |   |
Db        564 CTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAAGCTTC 623

Qy        720 ACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAA 779
              |||  | ||||| ||||| ||||| ||  || | || ||  ||||||||  ||||||||
Db        624 ACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACAC 683
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Qy        780 AAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACT 839
               ||   |||  |  |    || ||  |  |  |  | | ||       ||  ||    ||
Db        684 TAG---GATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCTTCCCT 740

Qy        840 CATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAA 899
               |   |   ||| ||| ||||  |  |||| || |||||||| || |||||  |||||||
Db        741 GACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCCAACAA 800

Qy        900 GCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 952
              ||||||   ||||||||||||| |  | || ||  | || ||  | || || |
Db        801 GCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAG 853

RESULT 14
US-08-414-657D-8
; Sequence 8, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  945 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...945
;      OTHER INFORMATION:
US-08-414-657D-8

  Query Match             32.6%;  Score 337.4;  DB 2;  Length 945;
  Best Local Similarity   63.1%;  Pred. No. 5.8e-93;
  Matches  556;  Conservative    0;  Mismatches  316;  Indels    9;  Gaps    2;

Qy         72 TCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAA 131
              |||   |  |||| ||||||| |||||||  |||      ||   |  ||  | ||||||
Db         66 TCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAA 119

Qy        132 CGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCAC 191
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Db         120 CATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTC 179

Qy         192 CCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCT 251
                   ||||||||| | ||||||     |||| |||  |||||| |  ||||||||||  ||
Db         180 GAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCT 239

Qy         252 GGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAA 311
               ||| ||||| || |  ||   ||    |        | | |||||| ||   ||||||||
Db         240 GGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAA 299

Qy         312 CGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA 371
                |||||||| ||||| || ||  | ||||| ||||| || |||||| |  |  | || ||
Db         300 GGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAA 359

Qy         372 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGA 431
               |||||||   ||  || | ||||| |||||  | || || ||     | || || || ||
Db         360 GACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGA 419

Qy         432 TATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGA 491
               | || |  | ||||| || | |||| | | |||   |||||| || | ||  |  | || ||
Db         420 TGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGA 479

Qy         492 GCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 551
                |||    | || ||||||||| |  | ||    |     |  ||||   | ||||| ||
Db         480 ACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGA 539

Qy         552 ATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC 611
               |||  |||| || |  |||||||| |||| |||||||| | || ||||||||  ||  |
Db         540 ATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGC 599

Qy         612 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATA 671
               ||| || ||  || |  | |  ||      ||| |||||||| ||||||||||||||
Db         600 CAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659

Qy         672 CATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGA 731
               |||  ||||  | ||| | |  |  | | ||   |||| | |   | |  | |||||
Db         660 CATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAAGCTTCCCTCAAATGTGA 719

Qy         732 AGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGA 791
               ||||||||| || ||  |  | || ||  ||||||||  ||||||||  ||   |||  |
Db         720 AGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATAAA 776

Qy         792 AGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAA 851
                 |    || ||  |  |  |  | | ||       ||  ||    || |   |   |||
Db         777 CAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCCTCCCTGACGGTGACCAA 836

Qy         852 TGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACAC 911
                ||| ||||  |  |||| || ||||| ||  || |||||   ||||||||||| |||  |||
Db         837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAAGCTCGGCGTCAC 896

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               |||||||||| |  | || ||  | || ||  | || || |
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RESULT 15
US-08-414-657D-10
; Sequence 10, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  861 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...861
;      OTHER INFORMATION:
US-08-414-657D-10

  Query Match             32.3%;  Score 333.8;  DB 2;  Length 861;
  Best Local Similarity   63.4%;  Pred. No. 6.9e-92;
  Matches  528;  Conservative    0;  Mismatches  302;  Indels    3;  Gaps    1;

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Db          24 AGGCACGGACAACATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTGGTAGA 83

Qy         180 CAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA 239
                 ||  |  | |    |||||||||| | ||||||||     |||| |||  |||||  | ||
Db          84 AGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGA 143

Qy         240 CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT 299
               ||||||||  ||||| ||||| || |  ||   ||    |        | | |||||| |
Db         144 CAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATACAGCCT 203

Qy         300 CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGA 359
               |   |||||||| ||||||||| ||||| || ||  | ||||| ||||| || |||||| |
Db         204 CCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAGACACA 263

Qy         360 CAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGA 419
                 |  | || |||||||||   ||  || | ||||| |||||  | || || ||     |
Db         264 GCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATCTCCAA 323

Qy         420 GATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAAC 479
                || || || ||| || |  | ||||| || | |||| | | |||   |||||| || |
Db         324 CATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATGGCCAA 383

Qy         480 TGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT 539
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Db         384 TGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAATTTGA 443

Qy         540 GAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGA 599
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Db         444 AGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAATATGA 503

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                 ||  | |||||||||||||| || ||  || | || ||  ||||||||  |||||||| 
Db          624 CCTCAAATGTGAAGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACAC 683

Qy          780 AAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACT 839
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Db          741 GACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAA 800

Qy          900 GCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCG 952
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Search completed: June 16, 2005, 10:29:00
Job time : 245.627 secs

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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2005  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:         June 15, 2005, 22:05:42 ; Search time 683.771 Seconds
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Perfect score:  1035
Sequence:       1 atgaaaaccatccagccaaa..........acctgcttctcaaattttga 1035

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6046767 seqs, 3099530249 residues

Total number of hits satisfying chosen parameters:      12093534

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                     SUMMARIES
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Result              Query
  No.    Score  Match Length DB  ID                      Description
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   668  1033.4   99.8   1603  9  US-09-966-545-3          Sequence 3, Appli
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   670  1033.4   99.8   1603  15  US-10-189-940-3          Sequence 3, Appli
   671  1033.4   99.8   2012  9  US-09-966-546-5          Sequence 5, Appli
   672  1033.4   99.8   2012  9  US-09-966-545-5          Sequence 5, Appli
   673  1033.4   99.8   2012  10  US-09-965-212-5          Sequence 5, Appli
   674  1033.4   99.8   2012  15  US-10-189-940-5          Sequence 5, Appli
   675    1032   99.7   1032  18  US-10-657-103-1          Sequence 1, Appli
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   677     955   92.3   1678  13  US-10-098-841-72         Sequence 72, Appl
   678   953.4   92.1   1839  14  US-10-161-572-16         Sequence 16, Appl
   679   953.4   92.1   1839  17  US-10-295-027-455        Sequence 455, App
   680   953.4   92.1   3987  20  US-10-723-860-5804       Sequence 5804, Ap
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   683     912   88.1   1094  14  US-10-161-572-17         Sequence 17, Appl
   684   910.4   88.0   2129  15  US-10-306-133-2          Sequence 2, Appli
   685   872.8   84.3   1130  14  US-10-161-572-18         Sequence 18, Appl
   686   537.2   51.9   1478  14  US-10-161-572-35         Sequence 35, Appl
   687   537.2   51.9   3092  21  US-10-696-639-8          Sequence 8, Appli
   688   537.2   51.9   3110  14  US-10-161-572-32         Sequence 32, Appl
   689   535.6   51.7   1071  14  US-10-161-572-34         Sequence 34, Appl
   690   535.6   51.7   1080  14  US-10-161-572-33         Sequence 33, Appl
   724     492   47.5    503  14  US-10-167-749-524        Sequence 524, App
   760     492   47.5    503  17  US-10-170-481A-524       Sequence 524, App
   762     492   47.5    503  17  US-10-210-028-524        Sequence 524, App
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   779     492   47.5    503  21  US-10-918-851-524        Sequence 524, App
   780     492   47.5    503  21  US-10-805-667-524        Sequence 524, App
   781     492   47.5    503  21  US-10-897-359-524        Sequence 524, App
   782     492   47.5    503  21  US-10-893-802-524        Sequence 524, App
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   794     330   31.9    452  14  US-10-052-283-167        Sequence 167, App
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    77    310    30.0   2798  3  AK028345              AK028345 Mus muscu
    78    306    29.6    780  7  CK313831              CK313831 SB02038B2
c   79  302.2    29.2    759  7  CN094277              CN094277 EC2BBA9CA
    80  301.4    29.1    643  5  BU390882              BU390882 603807132
    81  301.4    29.1    690  7  CN233126              CN233126 WLB057E10
    82  300.4    29.0    513  5  BX279850              BX279850 BX279850
    83  299.2    28.9    704  7  CN228803              CN228803 RJB061B04
    84    295    28.5    764  4  BI752729              BI752729 603028343
    85  292.4    28.3    764  5  BM945665              BM945665 UI-M-EM0-
    86  291.6    28.2    415  7  R18841                R18841 yg22g06.r1
c   87  290.4    28.1    778  7  CN078143              CN078143 EC2BBA14C
    88    290    28.0    290  7  F05894                F05894 HSC0PH101 n
    89  288.8    27.9    567  2  BF078551              BF078551 228917 MA
    90  286.2    27.7    497  2  BB854833              BB854833 BB854833
    91  285.6    27.6    579  2  BB644523              BB644523 BB644523
    92  284.2    27.5    528  2  BB856778              BB856778 BB856778
    93    280    27.1    677  5  BQ444788              BQ444788 UI-M-ER0-
    94  279.8    27.0    677  6  CD217649              CD217649 pgr1n.pk0
    95  275.2    26.6    590  7  CR545391              CR545391 DKFZp459M
c   96  273.8    26.5    394  4  BM684112              BM684112 UI-E-EJ1-
c   97  273.8    26.5    394  4  BM684852              BM684852 UI-E-EJ1-
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c  98    273.8   26.5    394  5  BQ184395                 BQ184395 UI-E-EJ1-
c  99    273.8   26.5    394  5  BQ184512                 BQ184512 UI-E-EJ1-
c 100    273.8   26.5    394  7  CK300895                 CK300895 UI-E-EJ1-
c 101    273.8   26.5    403  4  BM684212                 BM684212 UI-E-EJ1-
  102    273.6   26.4    815  5  BU230452                 BU230452 603320607
  103      272   26.3    390  4  BM719375                 BM719375 UI-E-EJ1-
  104      272   26.3    390  4  BM719757                 BM719757 UI-E-EJ1-
  105      272   26.3    390  5  BM931279                 BM931279 UI-E-EJ1-
  106      272   26.3    608  5  BQ188988                 BQ188988 UI-E-EJ1-
  107      272   26.3    734  5  BQ187606                 BQ187606 UI-E-EJ1-
c 108    271.8   26.3    827  6  CA306798                 CA306798 UI-H-FT1-
  109    271.8   26.3   2096  3  AK035218                 AK035218 Mus muscu
  110      271   26.2    700  5  BQ189788                 BQ189788 UI-E-EJ1-
  111    270.2   26.1   1953  3  AK030503                 AK030503 Mus muscu
c 112    267.6   25.9    858  6  CD325821                 CD325821 AGENCOURT
  113    267.2   25.8    284  7  CR543721                 CR543721 DKFZp459H
  114    264.8   25.6    695  7  CN228731                 CN228731 RJB060E12
c 115      264   25.5    456  1  AI369684                 AI369684 qy71g03.x
  116    263.6   25.5   2534  3  AK039193                 AK039193 Mus muscu
  117      263   25.4   2330  3  BC080168                 BC080168 Xenopus l
c 118    255.8   24.7    754  7  CO043662                 CO043662 UI-M-ER0-
  119    255.2   24.7    587  7  CN088583                 CN088583 EC2BBA30B
  120    252.4   24.4    478  5  BY245406                 BY245406 BY245406
  121      247   23.9    796  7  CO399311                 CO399311 AGENCOURT
  122    246.4   23.8    849  6  CA472810                 CA472810 AGENCOURT
  123    243.8   23.6    652  7  CN078144                 CN078144 EC2BBA14C
  124    240.8   23.3    621  5  BX312928                 BX312928 BX312928
  125    240.6   23.2    496  5  BP201259                 BP201259 BP201259
  126    240.6   23.2    926  6  CD325412                 CD325412 AGENCOURT
  127    240.2   23.2    456  6  CD803885                 CD803885 UI-M-GV0-
  128      239   23.1    511  5  BX493152                 BX493152 DKFZp781G
  129    238.8   23.1    611  7  CN075612                 CN075612 EC2BBA10C
  130      238   23.0    282  7  R75391                   R75391 MDB0556R Mo
  131    235.8   22.8    445  5  BY269882                 BY269882 BY269882
  132    235.6   22.8    788  4  BI767217                 BI767217 603057906
  133    235.4   22.7    492  2  AW967001                 AW967001 EST379075
  134      235   22.7    674  6  CD767791                 CD767791 AGENCOURT
  135      234   22.6    934  7  CN015939                 CN015939 AGENCOURT
  136    233.2   22.5    599  7  CN229507                 CN229507 RJB072D02
  137    231.8   22.4    277  4  BI011319                 BI011319 QV2-EN009
  138    230.8   22.3    481  5  BY256150                 BY256150 BY256150
  139    230.2   22.2    457  5  BY249728                 BY249728 BY249728
c 140    226.4   21.9    772  7  CK776016                 CK776016 967158 MA
c 141    225.8   21.8    564  7  CO602836                 CO602836 DG8-249i1
  142    225.8   21.8    639  7  CV030684                 CV030684 9878 Full
  143      225   21.7    660  7  CR543517                 CR543517 DKFZp459N
  144      225   21.7    795  7  CO395735                 CO395735 AGENCOURT
  145      224   21.6    673  7  CR736885                 CR736885 CR736885
  146      220   21.3    444  1  AA682970                 AA682970 ae89a04.s
c 147    214.6   20.7    697  5  BQ021243                 BQ021243 UI-H-DH1-
  148    213.8   20.7    640  7  CR545244                 CR545244 DKFZp459F
  149      213   20.6    229  1  AA450172                 AA450172 zx42d09.r
  150    212.4   20.5    867  6  CD300857                 CD300857 AGENCOURT
c 151    212.2   20.5    672  6  CA444805                 CA444805 UI-H-DH1-
  152      211   20.4    664  7  CN362538                 CN362538 170006001
  153    210.6   20.3    656  7  CK619540                 CK619540 mk25d06.y
  154      209   20.2    257  2  AW327110                 AW327110 20640 MAR
c 155    208.4   20.1    678  5  BU624639                 BU624639 UI-H-FG1-
  156    208.4   20.1   1148  4  BM466102                 BM466102 AGENCOURT
  157    204.2   19.7    726  5  BX912600                 BX912600 BX912600
  158      204   19.7    357  5  BY303236                 BY303236 BY303236
  159    203.4   19.7    625  2  BB643056                 BB643056 BB643056
  160    203.4   19.7    771  7  CN528825                 CN528825 UI-M-HQ0-
c 161    203.2   19.6    636  7  CK843444                 CK843444 UI-R-BJ2-
c 162    202.8   19.6    656  6  CA307492                 CA307492 UI-H-FT1-
  163    202.6   19.6   1084  6  CD255729                 CD255729 AGENCOURT
c 164    200.2   19.3    719  7  CK465166                 CK465166 936244 MA
  165      200   19.3    786  7  CO811192                 CO811192 AGENCOURT
  166      200   19.3    858  7  CO914076                 CO914076 AGENCOURT
  167    198.6   19.2    663  2  BB633037                 BB633037 BB633037
  168      198   19.1    519  7  CV038761                 CV038761 4136000 B
  169    195.6   18.9    347  7  CN094278                 CN094278 EC2BBA9CA
  170    194.4   18.8    670  7  CN083622                 CN083622 EC2BBA22D
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c 171    194.4   18.8    708  7  CN083621                 CN083621 EC2BBA22D
  172    192.8   18.6    825  5  BP166655                 BP166655 BP166655
c 173    191.4   18.5    294  7  W15256                   W15256 zc16h07.s1
c 174    191.2   18.5    659  2  AW149545                 AW149545 xf39c10.x
  175    189.4   18.3    764  6  CA350929                 CA350929 621861 NC
  176      188   18.2    611  6  CA355517                 CA355517 627428 NC
  177    186.8   18.0    565  2  BE663866                 BE663866 147903 MA
c 178    186.8   18.0    593  7  CK845949                 CK845949 968393 MA
  179    186.8   18.0    880  6  CD303536                 CD303536 AGENCOURT
  180    186.2   18.0    572  6  CB265380                 CB265380 1004285 H
  181      186   18.0    640  7  CO351229                 CO351229 DR_AOV_FL
c 182      186   18.0    753  1  AI589824                 AI589824 tm74g09.x
  183    185.2   17.9    906  5  BU186468                 BU186468 AGENCOURT
  184    184.4   17.8    392  2  BE651010                 BE651010 UI-M-BH3-
  185      183   17.7    410  5  BY276506                 BY276506 BY276506
  186      183   17.7    835  5  BX881962                 BX881962 BX881962
  187      181   17.5    755  5  BX913106                 BX913106 BX913106
  188    180.6   17.4    647  7  CV030870                 CV030870 10123 Ful
  189    179.8   17.4    220  7  H16176                   H16176 ym21g09.r1
c 190    178.2   17.2    578  2  BE121132                 BE121132 UI-R-CA0-
  191      178   17.2    178  6  CB118055                 CB118055 K-EST0164
  192      178   17.2    909  5  BU132565                 BU132565 603120307
  193    175.6   17.0   2296  3  CR592222                 CR592222 full-leng
  194    175.2   16.9    795  1  AU080106                 AU080106 AU080106
  195      175   16.9    666  5  BM951674                 BM951674 UI-M-EG0-
  196    174.6   16.9    867  7  CO543917                 CO543917 LyEST116
c 197    173.4   16.8    572  2  BF407747                 BF407747 UI-R-BJ2-
  198    171.8   16.6    415  5  BY263876                 BY263876 BY263876
  199    171.4   16.6    862  7  CK397022                 CK397022 AGENCOURT
  200    170.6   16.5    768  5  BX868437                 BX868437 BX868437
  201    169.8   16.4    584  5  BP257486                 BP257486 BP257486
c 202    169.6   16.4    637  6  CB528708                 CB528708 UI-H-FT2-
  203      169   16.3    378  2  BF601149                 BF601149 266043 MA
  204      169   16.3    470  5  BX954423                 BX954423 DKFZp781K
  205    167.8   16.2    791  7  CK308721                 CK308721 SB02047A2
  206    167.4   16.2    923  1  AL583491                 AL583491 AL583491
  207      167   16.1    617  6  BY730405                 BY730405 BY730405
c 208    166.6   16.1    458  7  CO667956                 CO667956 DG33-31f8
  209    166.2   16.1    566  7  CF977262                 CF977262 2-84-B04.
c 210    165.8   16.0    541  5  BU735309                 BU735309 UI-E-DW0-
  211    165.6   16.0    535  9  AY409767                 AY409767 Homo sapi
c 212    165.4   16.0    580  7  CN089827                 CN089827 EC2BBA32B
  213      165   15.9    488  5  BX477962                 BX477962 DKFZp686N
c 214    164.6   15.9    544  6  CA439326                 CA439326 UI-H-DT1-
  215    164.4   15.9    651  6  BY726997                 BY726997 BY726997
  216    164.2   15.9    450  5  BY263302                 BY263302 BY263302
  217      164   15.8    773  4  BG208674                 BG208674 RST28306
  218    163.6   15.8    527  5  BY243052                 BY243052 BY243052
  219    163.2   15.8    894  6  CB199088                 CB199088 AGENCOURT
  220    162.4   15.7    535  9  AY409769                 AY409769 Mus muscu
  221    161.8   15.6    936  5  BQ227365                 BQ227365 AGENCOURT
  222    160.8   15.5    892  5  BP462753                 BP462753 BP462753
  223    160.6   15.5    268  1  AA296886                 AA296886 EST112650
  224    158.8   15.3    481  5  BY247646                 BY247646 BY247646
c 225    158.8   15.3    494  1  AA548396                 AA548396 nj14e04.s
  226    157.2   15.2    858  2  BF676478                 BF676478 602086277
  227    156.4   15.1    739  7  CK679857                 CK679857 ZF101-P00
  228    156.4   15.1    884  5  BU323269                 BU323269 603405983
  229    155.8   15.1    815  1  AU079716                 AU079716 AU079716
  230    155.2   15.0    431  5  BY276402                 BY276402 BY276402
c 231    154.6   14.9    733  7  CO619752                 CO619752 DG9-1d13
  232      151   14.6    411  5  BY288341                 BY288341 BY288341
  233    150.2   14.5    456  5  BY249027                 BY249027 BY249027
  234    149.2   14.4    497  7  CV036959                 CV036959 4134532 B
c 235    148.4   14.3    465  1  AI934791                 AI934791 wp89e04.x
  236    147.4   14.2    429  5  BY272572                 BY272572 BY272572
  237    146.4   14.1    600  6  CA526928                 CA526928 8023-83 M
  238    146.2   14.1    862  5  BP462754                 BP462754 BP462754
  239    145.4   14.0    386  6  CB806970                 CB806970 AMGNNUC:N
  240    144.8   14.0    703  7  CF530869                 CF530869 UI-M-GH0-
  241    144.6   14.0    703  5  BU117309                 BU117309 603138889
c 242      144   13.9    511  1  AI415689                 AI415689 mc70a03.x
  243      144   13.9    953  5  BU116264                 BU116264 603139651
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c 244    143.8   13.9    519  1  AA826266               AA826266 od03e04.s
  245    143.4   13.9    878  5  BP165624               BP165624 BP165624
  246    142.2   13.7    535  9  AY409768               AY409768 Pan trogl
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c 248      141   13.6    470  1  AI580850               AI580850 ta33e06.x
  249    140.4   13.6    478  6  CA885050               CA885050 B0115E08-
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  251    139.4   13.5    801  5  BU357013               BU357013 603475462
  252    139.4   13.5    809  2  BF304194               BF304194 601887043
  253    138.4   13.4    402  5  BY289266               BY289266 BY289266
  254    138.2   13.4    914  5  BX843874               BX843874 BX843874
  255      138   13.3    775  4  BI199955               BI199955 602761121
  256    137.8   13.3    718  6  CB460692               CB460692 720592 MA
  257    136.4   13.2    661  6  CA452139               CA452139 UI-M-FZ0-
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  259    135.4   13.1    372  6  BY768835               BY768835 BY768835
  260    134.6   13.0    386  5  BY263646               BY263646 BY263646
  261    134.4   13.0    594  5  BU400899               BU400899 603481850
  262    134.2   13.0    778  7  CK315507               CK315507 SB02026A1
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  266      129   12.5    483  7  CR536826               CR536826 DKFZp459J
  267    128.6   12.4    807  5  BP168056               BP168056 BP168056
  268    128.4   12.4    348  7  R55964                 R55964 yg89e11.r1
  269    128.2   12.4    641  2  AW379374               AW379374 CM2-HT024
  270    126.6   12.2    825  5  BP464677               BP464677 BP464677
  271      125   12.1    646  6  CA334396               CA334396 NISC_ls08
  272    124.4   12.0    377  7  CF977263               CF977263 2-98-A10.
  273    124.2   12.0    868  5  BQ672092               BQ672092 AGENCOURT
  274      124   12.0    870  4  BI913885               BI913885 603183295
  275    123.8   12.0    617  4  BJ622933               BJ622933 BJ622933
  276    123.4   11.9    562  5  BU381982               BU381982 603582664
  277    121.4   11.7    711  7  CO669353               CO669353 DG33-50b1
  278      120   11.6    504  5  BX281785               BX281785 BX281785
  279      120   11.6    729  2  BB585976               BB585976 BB585976
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c 284    115.8   11.2    422  1  AI288864               AI288864 qn24f12.x
c 285    115.8   11.2    737  4  BM679797               BM679797 UI-E-EJ0-
c 286    115.6   11.2    461  2  BF463934               BF463934 UI-M-CG0p
  287    115.6   11.2    790  5  BP141505               BP141505 BP141505
  288    115.4   11.1    336  5  BY134531               BY134531 BY134531
c 289      115   11.1    368  2  BF350775               BF350775 QV0-HT036
  290    113.8   11.0    579  7  CN089828               CN089828 EC2BBA32B
c 291    113.6   11.0    514  1  AI285235               AI285235 qk59h04.x
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c 293    112.4   10.9    582  7  CO626674               CO626674 DG9-278a2
c 294      112   10.8    316  1  AI884993               AI884993 wl88c02.x
c 295    111.2   10.7    446  7  CO352257               CO352257 DR_AOV_SU
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  304    107.8   10.4    422  4  BI390270               BI390270 pgp1c.pk0
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  306    106.8   10.3    434  1  AI279142               AI279142 qm18e02.x
c 307    106.8   10.3    442  5  BX112198               BX112198 BX112198
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  310    106.8   10.3    523  2  BE550993               BE550993 7b67a03.x
  311      106   10.2    705  7  CN108877               CN108877 EC2CAA32D
c 312    105.8   10.2    598  1  AI815935               AI815935 au43g02.x
  313    105.6   10.2    394  9  AY400233               AY400233 Homo sapi
  314    105.6   10.2    394  9  AY400234               AY400234 Pan trogl
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  320    103.8   10.0    761  6  CD755145               CD755145 AGENCOURT
c 321    102.4    9.9    770  2  AW117456               AW117456 xd92a06.x
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  328     98.6    9.5    694  7  CK699353               CK699353 ZF101-P00
  329     98.4    9.5    392  5  BY267956               BY267956 BY267956
  330     97.2    9.4    421  5  BY275639               BY275639 BY275639
  331     97.2    9.4    656  2  BB617916               BB617916 BB617916
  332     95.8    9.3    763  1  AI427225               AI427225 mc70a03.y
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  338     93.4    9.0    683  2  BB318882               BB318882 BB318882
c 339     92.8    9.0    377  2  BF358688               BF358688 QV1-ET000
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  341     91.4    8.8    374  5  BY294857               BY294857 BY294857
c 342     91.4    8.8    452  1  AI262821               AI262821 qk35h10.x
c 343     91.4    8.8    653  7  CF180026               CF180026 815076 MA
  344       91    8.8    656  2  BB645027               BB645027 BB645027
  345       90    8.7    194  4  BI337742               BI337742 361263 MA
  346     88.6    8.6    700  2  BB652926               BB652926 BB652926
c 347     88.4    8.5    733  9  BX190380               BX190380 Danio rer
  348     88.2    8.5    374  2  BE826640               BE826640 QV1-EN004
  349     85.8    8.3    285  7  CN209637               CN209637 4115576 B
c 350     85.6    8.3    332  2  BE826737               BE826737 QV1-EN004
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c 353       84    8.1    723  9  AG035406               AG035406 Pan trogl
  354     83.8    8.1   2594  3  AK047122               AK047122 Mus muscu
c 355     83.4    8.1    479  2  AW524531               AW524531 UI-R-BO0-
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  357       83    8.0    563  5  BQ637244               BQ637244 he07e09.y
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  359       82    7.9    272  2  BB596160               BB596160 BB596160
  360     81.8    7.9    392  2  AW291014               AW291014 UI-H-BI2-
  361     81.6    7.9    586  4  BM696801               BM696801 UI-E-DW0-
c 362     80.6    7.8   1463  8  CC288776               CC288776 CH261-170
  363     80.4    7.8    529  6  CD284927               CD284927 G39161.77
  364     79.4    7.7    583  6  CA353359               CA353359 624860 NC
  365     79.2    7.7    562  5  BX952176               BX952176 DKFZp781K
  366     78.6    7.6    375  5  BY292584               BY292584 BY292584
  367     78.6    7.6    442  7  CN081576               CN081576 EC2BBA19C
  368     78.6    7.6    916  5  BQ672140               BQ672140 AGENCOURT
  369     78.2    7.6    336  4  BG199531               BG199531 RST18822
  370       78    7.5    547  6  BY727136               BY727136 BY727136
  371       78    7.5    660  5  BW337636               BW337636 BW337636
  372       78    7.5    854  3  AK020998               AK020998 Mus muscu
c 373     76.8    7.4    467  4  BI134406               BI134406 UI-M-BH3-
c 374     76.8    7.4    581  8  BH269028               BH269028 CH230-66P
c 375     76.8    7.4    779  8  BH292378               BH292378 CH230-44D
c 376     76.8    7.4   1127  9  GGA200118              AJ231833 Gallus ga
  377     76.6    7.4    411  5  BY276562               BY276562 BY276562
  378     76.6    7.4    418  5  BY278505               BY278505 BY278505
  379     76.6    7.4    483  8  AZ457316               AZ457316 1M0260A07
  380     76.6    7.4    492  4  BI359722               BI359722 384371 MA
  381     76.2    7.4    960  5  BQ933325               BQ933325 AGENCOURT
c 382     75.8    7.3    368  7  CN086072               CN086072 EC2BBA26C
c 383     75.6    7.3    433  1  AL921475               AL921475 AL921475
c 384     75.2    7.3    652  8  BH269030               BH269030 CH230-66P
c 385     74.2    7.2    526  7  CO634943               CO634943 DG9-96n24
  386       74    7.1    457  7  W39242                 W39242 zc16h07.r1
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c   391    72.4    7.0    378  8  AZ089779           AZ089779 RPCI-23-2
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    393    70.8    6.8    474  2  BB682022           BB682022 BB682022
    394    69.6    6.7    742  7  CO395507           CO395507 AGENCOURT
    395    68.2    6.6    313  2  AW430704           AW430704 70599 MAR
    396    67.2    6.5    821  5  BU389844           BU389844 603511165
    397      66    6.4    433  4  BG515406           BG515406 dae04h10.
    398    65.8    6.4    726  5  BU395513           BU395513 603404749
    399      65    6.3    259  2  BB607028           BB607028 BB607028
c   400    64.8    6.3    702  9  CNS02PTU           AL208443 Tetraodon
    401    64.4    6.2    558  7  CK875240           CK875240 SGP136467
c   402    63.4    6.1    527  1  AA741334           AA741334 ob30f08.s
    403    62.6    6.0    226  1  AA776056           AA776056 ae79a07.s
c   404    62.6    6.0    539  1  AL918370           AL918370 AL918370
    405    61.8    6.0    550  7  CR544600           CR544600 DKFZp459F
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    407    60.8    5.9    255  2  BB577810           BB577810 BB577810
c   408    60.4    5.8    484  5  BX099260           BX099260 BX099260
    409    60.2    5.8   1008  9  CL093894           CL093894 ISB1-24C2
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    411    59.6    5.8    420  6  CB798880           CB798880 AMGNNUC:N
c   412    59.6    5.8    845  4  BM042630           BM042630 603615963
    413    59.4    5.7    226  2  AW374585           AW374585 MR1-CT005
c   414    58.6    5.7    426  7  CK776772           CK776772 968132 MA
c   415    58.6    5.7    736  8  AZ989621           AZ989621 2M0273I04
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    417    57.6    5.6    276  2  BB268580           BB268580 BB268580
c   418    57.4    5.5    565  7  CO590783           CO590783 DG2-41k22
    419    56.8    5.5    569  5  BP377634           BP377634 BP377634
    420    56.8    5.5    582  5  BP208357           BP208357 BP208357
c   421    56.6    5.5    964  9  CNS05CLJ           AL331264 Tetraodon
c   422    55.8    5.4    929  9  CNS050XX           AL316158 Tetraodon
c   423    55.6    5.4    502  7  CO691339           CO691339 DG11-30f1
    424    55.4    5.4    311  4  BG193769           BG193769 RST12905
c   425    55.4    5.4    626  8  AZ385580           AZ385580 1M0144G07
    426    54.6    5.3    390  1  AA490022           AA490022 ab02b04.s
    427    54.2    5.2    573  7  CF977921           CF977921 FAR17G1.R
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c   429    53.8    5.2    244  2  BF362751           BF362751 RC1-NN007
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    431    53.8    5.2    582  4  BG219746           BG219746 RST39511
    432    53.4    5.2    254  7  CR774354           CR774354 DKFZp459P
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c   441      52    5.0    590  9  BX240864           BX240864 Danio rer
c   442    51.8    5.0    557  9  CE135710           CE135710 tigr-gss-
    443    51.6    5.0    780  9  CNS04I4Z           AL291788 Tetraodon
    444    51.2    4.9    538  1  AL925790           AL925790 AL925790
    445    51.2    4.9    657  5  BQ078813           BQ078813 fy81c06.y
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c   448    50.8    4.9    996  9  CNS04XL6           AL311811 Tetraodon
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    453    50.6    4.9   1165  9  CL051682           CL051682 CH216-74F
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    455    50.4    4.9    559  5  BY476545           BY476545 BY476545
    456    50.4    4.9    762  7  CK397238           CK397238 AGENCOURT
    457      50    4.8    646  5  BW346790           BW346790 BW346790
    458      50    4.8    765  5  BU247998           BU247998 603591574
c   459    49.8    4.8    544  8  AQ728858           AQ728858 HS_5464_B
    460    49.6    4.8    540  5  BU303720           BU303720 603740472
    461    49.4    4.8   1027  5  BU280790           BU280790 603863275
c   462      49    4.7    873  8  BZ182814           BZ182814 CH230-377

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    466    48.4    4.7    706  2  BB351922           BB351922 BB351922
    467    48.4    4.7   3641  3  AK047548           AK047548 Mus muscu
    468    48.2    4.7    866  5  BQ680977           BQ680977 AGENCOURT
    469      48    4.6    970  5  BU375142           BU375142 603812777
    470    47.6    4.6    652  7  CK689464           CK689464 ZF101-P00
    471    47.4    4.6    405  5  BY441604           BY441604 BY441604
c   472    47.4    4.6    496  4  BF995884           BF995884 QV1-GN020
    473    47.4    4.6    972  9  CNS041CJ           AL270028 Tetraodon
c   474      47    4.5    572  8  AQ680346           AQ680346 HS_2275_B
c   475      47    4.5    575  8  AQ803771           AQ803771 HS_3145_A
c   476      47    4.5    834  8  AQ899706           AQ899706 HS_3145_A
    477    46.6    4.5    216  2  BB054739           BB054739 BB054739
    478    46.4    4.5    603  8  BZ111682           BZ111682 CH230-208
    479    46.4    4.5    781  6  CD348686           CD348686 UI-M-FY0-
    480    46.2    4.5   1261  3  CR724321           CR724321 Tetraodon
    481      46    4.4    382  6  CB809130           CB809130 AMGNNUC:C
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c   483    45.6    4.4    299  2  BE943615           BE943615 UI-M-BH3-
c   484    45.6    4.4    585  6  CB513897           CB513897 ssalrgb54
    485      45    4.3    551  5  BU440266           BU440266 604147091
    486      45    4.3    695  9  AG164478           AG164478 Pan trogl
    487    44.6    4.3   1233  3  CR724192           CR724192 Tetraodon
    488      44    4.3    290  2  BF362977           BF362977 CM4-NN008
    489      44    4.3    600  5  BU922970           BU922970 7042-78 M
    490      44    4.3    614  6  CD351134           CD351134 UI-M-FY0-
    491      44    4.3    740  7  CN531505           CN531505 UI-M-HQ0-
    492      44    4.3    760  7  CN531514           CN531514 UI-M-HQ0-
    493      44    4.3   3037  3  AK052440           AK052440 Mus muscu
    494    43.8    4.2    491  4  BI067139           BI067139 pgf1n.pk0
    495    43.8    4.2    615  4  BI067145           BI067145 pgf1n.pk0
    496    43.6    4.2   1010  1  AL546361           AL546361 AL546361
    497    43.4    4.2    613  7  CF918937           CF918937 Bflor531.
    498    43.4    4.2    651  7  CF919117           CF919117 Bflor531.
    499    43.4    4.2    701  7  CF919027           CF919027 Bflor531.
    500    43.4    4.2    717  5  BU321343           BU321343 603854520
    501    43.4    4.2    841  6  CB999583           CB999583 AGENCOURT
    502    43.4    4.2    883  8  BZ222298           BZ222298 CH230-324
    503    43.4    4.2    892  5  BU135652           BU135652 603124302
c   504    43.2    4.2    623  5  BX924232           BX924232 BX924232
    505    43.2    4.2   3976  3  CR749215           CR749215 Homo sapi
    506      43    4.2    675  7  CN060015           CN060015 Salamande
    507      43    4.2    783  7  CN055172           CN055172 Salamande
    508    42.6    4.1    392  5  BY094706           BY094706 BY094706
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    513    42.4    4.1   1344  3  CR694719           CR694719 Tetraodon
    514    42.4    4.1   1400  3  CR734232           CR734232 Tetraodon
    515    42.4    4.1   5626  3  CR749495           CR749495 Homo sapi
    516    41.8    4.0    388  6  BY655441           BY655441 BY655441
    517    41.8    4.0    593  7  CF919555           CF919555 Bflor531.
    518    41.6    4.0    356  5  BY426574           BY426574 BY426574
    519    41.6    4.0    383  5  BY442078           BY442078 BY442078
    520    41.4    4.0    522  5  BX528198           BX528198 BX528198
c   521    41.4    4.0    549  2  BF465792           BF465792 UI-M-CG0p
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    524    41.4    4.0    693  5  BU707564           BU707564 UI-M-FR0-
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    526    41.4    4.0   1480  3  AK043555           AK043555 Mus muscu
    527    41.4    4.0   1845  3  BC053486           BC053486 Mus muscu
    528    41.4    4.0   1996  1  AL697315           AL697315 AL697315
    529    41.2    4.0    360  6  BY659253           BY659253 BY659253
    530    41.2    4.0    394  5  BY442525           BY442525 BY442525
    531    41.2    4.0    456  5  BX114096           BX114096 BX114096
    532    41.2    4.0    516  4  BM264275           BM264275 ig33c01.y
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   541     41.2    4.0   1871  3  BC029119                          BC029119 Homo sapi
   542     41.2    4.0   1914  3  BC032460                          BC032460 Homo sapi
   543     41.2    4.0   2190  9  AY418857                          AY418857 Homo sapi
   544       41    4.0    384  1  AA967999                          AA967999 uh06g03.r
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 c 556       41    4.0    488  1  AI429407                          AI429407 mn98b02.x
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 c 558       41    4.0    588  1  AI462176                          AI462176 ub70h09.x
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 c 568       41    4.0    846  1  AI746549                          AI746549 ul08d10.x
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 c 573     40.8    3.9    417  1  AI041669                          AI041669 oy33e02.x
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 c 575     40.8    3.9    520  1  AA890428                          AA890428 ak10g03.s
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 c 578     40.8    3.9    589  5  BU072469                          BU072469 im47e01.x
 c 579     40.8    3.9    589  6  CA776810                          CA776810 ip03a07.x
 c 580     40.8    3.9    590  5  BQ631321                          BQ631321 il19f04.x
 c 581     40.8    3.9    590  5  BU951928                          BU951928 in74g09.x
   582     40.8    3.9   1377  3  CR725714                          CR725714 Tetraodon
   583     40.8    3.9   1740  3  CR723886                          CR723886 Tetraodon
   584     40.6    3.9    403  5  BY423102                          BY423102 BY423102
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   586     40.6    3.9    701  7  CO422929                          CO422929 GGEZHT102
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 c 591     40.4    3.9    802  7  CK777862                          CK777862 965008 MA
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   593     40.2    3.9    564  4  BI342191                          BI342191 369892 MA
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 c 605     39.8    3.8    568  4  BM313055                          BM313055 ig82g08.x
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   610     39.8    3.8    968  9  CNS03QY6                          AL256551 Tetraodon
   611     39.6    3.8    372  5  BP112250                          BP112250 BP112250
   612     39.6    3.8    849  6  CD103751                          CD103751 AGENCOURT
   613     39.4    3.8    458  2  BB744766                          BB744766 BB744766
   614     39.4    3.8    472  2  BE405848                          BE405848 WHE0425_A
 c 615     39.4    3.8    582  4  BM232196                          BM232196 K0319G07-
   616     39.4    3.8    661  7  CV333279                          CV333279 IL3-MT026
   617     39.4    3.8    734  7  CF735216                          CF735216 UI-M-HB0-
   618     39.4    3.8    782  2  BE548025                          BE548025 601072053
   619     39.2    3.8    323  2  BF428743                          BF428743 WHE1412_G
   620     39.2    3.8    416  7  CN010218                          CN010218 WHE3868_B
   621     39.2    3.8    424  4  BM352364                          BM352364 ig85g09.y
   622     39.2    3.8    427  5  BQ271919                          BQ271919 ik16b02.y
 c 623     39.2    3.8    430  4  BM352585                          BM352585 ig68f04.x
   624     39.2    3.8    433  6  CA866435                          CA866435 ir63b10.y
 c 625     39.2    3.8    439  1  AI034354                          AI034354 ox20e08.x
   626     39.2    3.8    439  4  BJ282278                          BJ282278 BJ282278
   627     39.2    3.8    439  5  BQ286383                          BQ286383 ik29d06.y
 c 628     39.2    3.8    448  6  CA774485                          CA774485 ip22f06.x
 c 629     39.2    3.8    457  6  CA774738                          CA774738 ip11e06.x
   630     39.2    3.8    463  2  BF473831                          BF473831 WHE0837_H
   631     39.2    3.8    464  6  CA775983                          CA775983 io97b06.y
   632     39.2    3.8    471  7  CN008668                          CN008668 WHE2643_G
   633     39.2    3.8    476  6  CA772586                          CA772586 io82c09.y
   634     39.2    3.8    483  6  CA773899                          CA773899 im58g03.y
   635     39.2    3.8    488  2  BF428626                          BF428626 WHE1411_D
   636     39.2    3.8    493  4  BG909869                          BG909869 TaLr1110B
   637     39.2    3.8    495  6  CA731880                          CA731880 wlp1c.pk0
   638     39.2    3.8    495  6  CD861413                          CD861413 AZ01.002B
   639     39.2    3.8    505  6  CD881005                          CD881005 F1.100K06
   640     39.2    3.8    507  4  BG656094                          BG656094 ib36h11.y
   641     39.2    3.8    519  1  AJ610908                          AJ610908 AJ610908
   642     39.2    3.8    523  5  BQ805985                          BQ805985 WHE3573_D
   643     39.2    3.8    534  1  AJ611394                          AJ611394 AJ611394
   644     39.2    3.8    534  4  BI467039                          BI467039 ic18e10.y
 c 645     39.2    3.8    546  9  FR0026920                         AL019749 F.rubripe
   646     39.2    3.8    565  6  CD102156                          CD102156 AGENCOURT
   647     39.2    3.8    569  5  BU949310                          BU949310 in65d03.y
   648     39.2    3.8    571  5  BU786551                          BU786551 in56c10.y
 c 649     39.2    3.8    573  6  CA867255                          CA867255 ir59f08.x
 c 650     39.2    3.8    576  6  CB067498                          CB067498 iq37f08.x
 c 651     39.2    3.8    577  6  CB068936                          CB068936 is35f02.x
 c 652     39.2    3.8    582  5  BU785471                          BU785471 in46a08.x
 c 653     39.2    3.8    586  4  BM310606                          BM310606 ig50c04.x
 c 654     39.2    3.8    588  4  BM311552                          BM311552 ig66h07.x
 c 655     39.2    3.8    588  6  CB069338                          CB069338 is16h05.x
 c 656     39.2    3.8    589  4  BI713519                          BI713519 ie04a02.x
 c 657     39.2    3.8    590  4  BM352104                          BM352104 ig86e12.x
 c 658     39.2    3.8    601  5  BU077943                          BU077943 im65e04.x
   659     39.2    3.8    617  4  BM264266                          BM264266 ig33b03.y
   660     39.2    3.8    620  6  CD104694                          CD104694 AGENCOURT
   661     39.2    3.8    621  6  CD103792                          CD103792 AGENCOURT
   662     39.2    3.8    625  6  CD103713                          CD103713 AGENCOURT
   663     39.2    3.8    627  6  CD512424                          CD512424 AGENCOURT
   664     39.2    3.8    647  4  BG704056                          BG704056 602687196
   665     39.2    3.8    648  4  BG700455                          BG700455 602680444
   666     39.2    3.8    648  4  BG713927                          BG713927 602674304
   667     39.2    3.8    650  4  BG701218                          BG701218 602680672
   668     39.2    3.8    656  6  CD104701                          CD104701 AGENCOURT
   669     39.2    3.8    664  6  CD102292                          CD102292 AGENCOURT
   670     39.2    3.8    680  1  AV652098                          AV652098 AV652098
   671     39.2    3.8    693  7  CK781175                          CK781175 UI-M-GV0-
   672     39.2    3.8    738  6  CD103461                          CD103461 AGENCOURT
   673     39.2    3.8    749  6  CD104003                          CD104003 AGENCOURT
   674     39.2    3.8    763  6  CD102386                          CD102386 AGENCOURT
   675     39.2    3.8    763  6  CD104349                          CD104349 AGENCOURT
   676     39.2    3.8    781  6  CD000264                          CD000264 AGENCOURT
   677     39.2    3.8    782  6  CD512365                          CD512365 AGENCOURT
   678     39.2    3.8    791  6  CD104786                          CD104786 AGENCOURT
   679     39.2    3.8    792  6  CD102761                          CD102761 AGENCOURT
   680     39.2    3.8    795  6  CD512411                          CD512411 AGENCOURT
   681     39.2    3.8    799  6  CD102757                          CD102757 AGENCOURT
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  682    39.2    3.8    800  6  CD103030            CD103030 AGENCOURT
  683    39.2    3.8    804  6  CD512491            CD512491 AGENCOURT
  684    39.2    3.8    811  6  CD000531            CD000531 AGENCOURT
  685    39.2    3.8    813  6  CB999989            CB999989 AGENCOURT
  686    39.2    3.8    814  6  CD103471            CD103471 AGENCOURT
  687    39.2    3.8    838  6  CD001024            CD001024 AGENCOURT
  688    39.2    3.8    842  6  CD104017            CD104017 AGENCOURT
  689    39.2    3.8    845  6  CB998993            CB998993 AGENCOURT
  690    39.2    3.8    878  6  CD512192            CD512192 AGENCOURT
  691    39.2    3.8    904  5  BU144883            BU144883 603229681
  692      39    3.8    401  2  BB804414            BB804414 BB804414
  693      39    3.8    414  5  BY421952            BY421952 BY421952
  694      39    3.8    427  7  CO436236            CO436236 ddPCR2_17
  695      39    3.8    445  1  AA698719            AA698719 HL05552.5
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  697      39    3.8    545  4  BM440456            BM440456 pgr1n.pk0
  698      39    3.8    548  1  AA567371            AA567371 HL01080.5
  699      39    3.8    582  5  BP354326            BP354326 BP354326
  700      39    3.8    600  4  BM147637            BM147637 TCAAP1Q13
  701      39    3.8    719  4  BG775252            BG775252 602650266
  702      39    3.8    782  4  BG490422            BG490422 602519448
  703      39    3.8    832  4  BM048129            BM048129 603620480
  704      39    3.8    879  5  BU502483            BU502483 AGENCOURT
  705      39    3.8    951  5  BQ944019            BQ944019 AGENCOURT
  706      39    3.8   1005  5  BQ944936            BQ944936 AGENCOURT
  707      39    3.8   1011  4  BM554297            BM554297 AGENCOURT
  708      39    3.8   1044  5  BM925155            BM925155 AGENCOURT
  709    38.8    3.7    269  1  AA365469            AA365469 EST76250
  710    38.8    3.7    655  5  BX422176            BX422176 BX422176
  711    38.8    3.7    673  4  BM791148            BM791148 K-EST0071
  712    38.8    3.7    862  6  CD357832            CD357832 AGENCOURT
  713    38.8    3.7    931  6  CB999539            CB999539 AGENCOURT
  714    38.8    3.7   1104  6  CB999061            CB999061 AGENCOURT
  715    38.8    3.7   1198  5  BQ955992            BQ955992 AGENCOURT
  716    38.6    3.7    505  4  BM253186            BM253186 512568 MA
  717    38.6    3.7    527  8  AQ457532            AQ457532 HS_5087_A
  718    38.6    3.7    565  5  BQ239435            BQ239435 TaE05031A
c 719    38.6    3.7    596  7  CO288202            CO288202 EK067954.
  720    38.6    3.7    940  5  BX369835            BX369835 BX369835
  721    38.6    3.7   4919  3  BC040674            BC040674 Homo sapi
  722    38.4    3.7    402  1  AA776183            AA776183 ae80d06.s
  723    38.4    3.7    532  4  BM152584            BM152584 TCBAP1E93
  724    38.4    3.7    592  6  CA384192            CA384192 664641 NC
  725    38.4    3.7    609  6  CD103749            CD103749 AGENCOURT
  726    38.4    3.7    619  9  CR842092            CR842092 GR0AAA76C
  727    38.4    3.7    620  7  CV086415            CV086415 CS_gil_42
  728    38.4    3.7    832  7  CN047600            CN047600 V2_p13_P8
c 729    38.4    3.7    910  9  CNS006ON            AL065629 Drosophil
  730    38.4    3.7   1064  5  BU174116            BU174116 AGENCOURT
  731    38.4    3.7   1066  4  BM808284            BM808284 AGENCOURT
  732    38.4    3.7   1178  8  BZ553247            BZ553247 pacs1-60_
  733    38.4    3.7   1201  4  BM423379            BM423379 AGENCOURT
  734    38.2    3.7    274  1  AA364433            AA364433 EST75052
  735    38.2    3.7    319  1  AA364219            AA364219 EST74757
  736    38.2    3.7    336  1  AA364221            AA364221 EST74759
  737    38.2    3.7    349  6  CA652911            CA652911 wre1n.pk1
  738    38.2    3.7    435  7  T60289              T60289 yb87e10.r1
  739    38.2    3.7    447  6  CD102287            CD102287 AGENCOURT
  740    38.2    3.7    467  4  BG322727            BG322727 EM1_13_E0
c 741    38.2    3.7    504  8  AZ699074            AZ699074 RPCI-23-2
c 742    38.2    3.7    520  2  BE466906            BE466906 hz28f07.x
  743    38.2    3.7    531  4  BG654779            BG654779 ib44d10.x
c 744    38.2    3.7    543  8  AZ620467            AZ620467 1M0453O07
c 745    38.2    3.7    572  5  BQ632353            BQ632353 il25h10.x
c 746    38.2    3.7    579  6  CB068001            CB068001 ip39b08.x
c 747    38.2    3.7    622  6  CA088065            CA088065 SCQSAM210
c 748    38.2    3.7    796  2  BE397301            BE397301 601288632
  749    38.2    3.7    799  6  CD512408            CD512408 AGENCOURT
c 750    38.2    3.7    947  5  BX361563            BX361563 BX361563
  751    38.2    3.7    999  6  CD000244            CD000244 AGENCOURT
  752      38    3.7    471  4  BM690353            BM690353 UI-E-CI0-
  753      38    3.7    529  7  CK822554            CK822554 ig92b01.x
  754      38    3.7    624  6  CD000819            CD000819 AGENCOURT

  755      38    3.7    667  2  BB659444            BB659444 BB659444
  756      38    3.7    686  6  CD103837            CD103837 AGENCOURT
  757      38    3.7    773  6  CB999985            CB999985 AGENCOURT
  758      38    3.7    779  6  CD000450            CD000450 AGENCOURT
  759      38    3.7    816  1  AU117395            AU117395 AU117395
  760      38    3.7    832  6  CB999251            CB999251 AGENCOURT
  761      38    3.7    851  6  CD000325            CD000325 AGENCOURT
  762      38    3.7    878  6  CB999408            CB999408 AGENCOURT
  763      38    3.7    893  5  BU523040            BU523040 AGENCOURT
  764      38    3.7   1098  6  CB999002            CB999002 AGENCOURT
  765      38    3.7   1863  9  CL960212            CL960212 OsIFCC003
  766      38    3.7   3651  3  AK084752            AK084752 Mus muscu
  767      38    3.7   3869  3  AK031112            AK031112 Mus muscu
  768      38    3.7   3924  3  AK083538            AK083538 Mus muscu
  769    37.8    3.7    437  7  CN391010            CN391010 170005322
  770    37.8    3.7    479  1  AA688911            AA688911 vs05g09.r
c 771    37.8    3.7    493  6  CA943388            CA943388 ip40f03.x
  772    37.8    3.7    499  7  CV336344            CV336344 IL5-EN008
  773    37.8    3.7    500  4  BM146494            BM146494 TCAAP1E49
  774    37.8    3.7    546  7  CN391011            CN391011 170004247
  775    37.8    3.7    551  4  BM147912            BM147912 TCAAP1Q15
  776    37.8    3.7    558  7  CN391008            CN391008 170005325
  777    37.8    3.7    565  2  BE264631            BE264631 601192423
  778    37.8    3.7    569  4  BM759253            BM759253 K-EST0039
  779    37.8    3.7    581  5  BP356172            BP356172 BP356172
  780    37.8    3.7    582  5  BP286742            BP286742 BP286742
  781    37.8    3.7    582  7  CN483145            CN483145 hw28h07.y
  782    37.8    3.7    583  5  BP284410            BP284410 BP284410
  783    37.8    3.7    584  5  BP336907            BP336907 BP336907
  784    37.8    3.7    584  7  CN391006            CN391006 170005977
  785    37.8    3.7    587  2  BE894869            BE894869 601434053
  786    37.8    3.7    595  2  BE276689            BE276689 601144787
  787    37.8    3.7    595  7  CN391009            CN391009 170005326
  788    37.8    3.7    597  5  BP366089            BP366089 BP366089
  789    37.8    3.7    603  5  BP277914            BP277914 BP277914
c 790    37.8    3.7    605  2  AW236141            AW236141 xn25g02.x
  791    37.8    3.7    608  1  AL527352            AL527352 AL527352
  792    37.8    3.7    609  7  CF132379            CF132379 UI-HF-FQ0
  793    37.8    3.7    622  7  CN485198            CN485198 hx24e03.y
  794    37.8    3.7    633  7  CV026154            CV026154 4006 Full
  795    37.8    3.7    634  1  AV649762            AV649762 AV649762
  796    37.8    3.7    638  2  BF219760            BF219760 601296685
  797    37.8    3.7    661  4  BI826255            BI826255 603075955
  798    37.8    3.7    670  4  BI829519            BI829519 603080349
  799    37.8    3.7    672  2  BE894852            BE894852 601434034
  800    37.8    3.7    672  7  CN391003            CN391003 170004179
  801    37.8    3.7    675  4  BG490460            BG490460 602519478
  802    37.8    3.7    677  4  BI090613            BI090613 602853839
  803    37.8    3.7    695  4  BM046512            BM046512 603626562
  804    37.8    3.7    697  2  BE280160            BE280160 601158361
  805    37.8    3.7    706  2  BE409866            BE409866 601299635
  806    37.8    3.7    711  2  BE410468            BE410468 601302071
  807    37.8    3.7    712  2  BE262862            BE262862 601147956
  808    37.8    3.7    721  4  BI823887            BI823887 603039054
  809    37.8    3.7    737  4  BG822539            BG822539 602725624
  810    37.8    3.7    748  4  BI912207            BI912207 603069405
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  812    37.8    3.7    753  4  BG718997            BG718997 602699109
  813    37.8    3.7    756  4  BG771599            BG771599 602719929
  814    37.8    3.7    771  4  BI829464            BI829464 603080487
  815    37.8    3.7    776  5  BQ226952            BQ226952 AGENCOURT
  816    37.8    3.7    782  4  BI518856            BI518856 603061766
  817    37.8    3.7    788  4  BI667679            BI667679 603293027
  818    37.8    3.7    799  4  BM045780            BM045780 603624747
  819    37.8    3.7    808  4  BG740654            BG740654 602631089
  820    37.8    3.7    810  4  BG252525            BG252525 602366045
  821    37.8    3.7    815  4  BG743989            BG743989 602722761
  822    37.8    3.7    819  4  BI836599            BI836599 603089580
  823    37.8    3.7    825  4  BI862467            BI862467 603391384
  824    37.8    3.7    832  4  BI461274            BI461274 603207211
  825    37.8    3.7    844  4  BG327069            BG327069 602426277
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  829    37.8    3.7    851  5  BU956865            BU956865 AGENCOURT
  830    37.8    3.7    855  2  BE871126            BE871126 601447382
  831    37.8    3.7    856  1  AL546240            AL546240 AL546240
  832    37.8    3.7    863  4  BI828042            BI828042 603073787
  833    37.8    3.7    868  6  CA488022            CA488022 AGENCOURT
  834    37.8    3.7    871  5  BU542727            BU542727 AGENCOURT
  835    37.8    3.7    889  5  BQ954497            BQ954497 AGENCOURT
  836    37.8    3.7    889  7  CF272496            CF272496 AGENCOURT
  837    37.8    3.7    890  4  BG287979            BG287979 602387754
  838    37.8    3.7    893  4  BG747004            BG747004 602704582
  839    37.8    3.7    895  5  BQ941900            BQ941900 AGENCOURT
  840    37.8    3.7    896  5  BQ216489            BQ216489 AGENCOURT
  841    37.8    3.7    897  5  BU957145            BU957145 AGENCOURT
  842    37.8    3.7    900  5  BQ934527            BQ934527 AGENCOURT
  843    37.8    3.7    900  5  BQ958970            BQ958970 AGENCOURT
  844    37.8    3.7    902  2  BE619521            BE619521 601473077
  845    37.8    3.7    906  5  BU944646            BU944646 AGENCOURT
  846    37.8    3.7    914  5  BQ944028            BQ944028 AGENCOURT
  847    37.8    3.7    915  5  BQ955025            BQ955025 AGENCOURT
  848    37.8    3.7    918  5  BU175422            BU175422 AGENCOURT
  849    37.8    3.7    926  6  CD243465            CD243465 AGENCOURT
  850    37.8    3.7    929  5  BQ227659            BQ227659 AGENCOURT
  851    37.8    3.7    936  4  BG326662            BG326662 602425515
  852    37.8    3.7    942  5  BU542588            BU542588 AGENCOURT
  853    37.8    3.7    945  5  BQ934742            BQ934742 AGENCOURT
  854    37.8    3.7    947  4  BG331675            BG331675 602432685
  855    37.8    3.7    949  5  BQ889036            BQ889036 AGENCOURT
  856    37.8    3.7    949  5  BQ958647            BQ958647 AGENCOURT
  857    37.8    3.7    954  4  BM424036            BM424036 AGENCOURT
  858    37.8    3.7    954  5  BQ919599            BQ919599 AGENCOURT
  859    37.8    3.7    971  5  BX400451            BX400451 BX400451
  860    37.8    3.7    972  5  BQ952738            BQ952738 AGENCOURT
  861    37.8    3.7    978  5  BQ943836            BQ943836 AGENCOURT
  862    37.8    3.7    986  5  BQ954806            BQ954806 AGENCOURT
  863    37.8    3.7    992  2  BE736855            BE736855 601306682
  864    37.8    3.7   1009  5  BM917953            BM917953 AGENCOURT
  865    37.8    3.7   1011  1  AL539344            AL539344 AL539344
  866    37.8    3.7   1018  2  BE790356            BE790356 601480536
  867    37.8    3.7   1018  2  BE902991            BE902991 601676948
  868    37.8    3.7   1038  2  BE733347            BE733347 601570567
  869    37.8    3.7   1041  4  BG331618            BG331618 602432618
  870    37.8    3.7   1041  5  BQ073173            BQ073173 AGENCOURT
  871    37.8    3.7   1044  4  BG342082            BG342082 602463028
  872    37.8    3.7   1055  2  BE778041            BE778041 601463144
  873    37.8    3.7   1066  5  BQ052829            BQ052829 AGENCOURT
  874    37.8    3.7   1124  4  BM810321            BM810321 AGENCOURT
  875    37.8    3.7   1129  2  BE729283            BE729283 601561645
  876    37.8    3.7   1130  4  BM462207            BM462207 AGENCOURT
  877    37.8    3.7   1158  5  BU902073            BU902073 AGENCOURT
c 878    37.8    3.7   1172  9  CNS02QMV            AL209488 Tetraodon
  879    37.8    3.7   2167  3  CR624380            CR624380 full-leng
  880    37.6    3.6    226  1  AA365847            AA365847 EST76701
  881    37.6    3.6    319  5  BU078232            BU078232 im66b01.y
  882    37.6    3.6    342  6  CA843160            CA843160 ir54d02.y
  883    37.6    3.6    342  6  CA941507            CA941507 ir32b01.y
  884    37.6    3.6    342  6  CA947024            CA947024 is10b12.y
  885    37.6    3.6    342  6  CA947074            CA947074 is10h05.y
  886    37.6    3.6    342  6  CA948274            CA948274 iq20b04.y
  887    37.6    3.6    360  6  CA950974            CA950974 ir93a08.y
  888    37.6    3.6    367  6  CA946943            CA946943 is09b04.y
  889    37.6    3.6    369  4  BM312077            BM312077 ig65h10.y
  890    37.6    3.6    369  6  CA841363            CA841363 ip33d05.y
  891    37.6    3.6    369  6  CA942296            CA942296 ir56a01.y
  892    37.6    3.6    369  6  CA948215            CA948215 iq19d04.y
  893    37.6    3.6    369  6  CB067182            CB067182 iq33c02.y
  894    37.6    3.6    370  6  CA946979            CA946979 is09e11.y
  895    37.6    3.6    377  6  CA394022            CA394022 cs46b11.y
  896    37.6    3.6    379  6  CB178027            CB178027 is24b08.x
  897    37.6    3.6    381  6  CA867987            CA867987 ir83h12.y
  898    37.6    3.6    386  6  CA946938            CA946938 is09a07.y
  899    37.6    3.6    387  6  CA775628            CA775628 io88c03.y
  900    37.6    3.6    389  5  BU072158            BU072158 im55a05.y
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c 901    37.6    3.6    391  6  CA847779            CA847779 iq42a09.x
  902    37.6    3.6    396  6  CA941077            CA941077 ir38b10.y
  903    37.6    3.6    396  6  CA952703            CA952703 iq12b06.y
  904    37.6    3.6    397  4  BM312530            BM312530 ig75g03.y
  905    37.6    3.6    397  6  CA950923            CA950923 ir92c08.y
  906    37.6    3.6    398  6  CA771267            CA771267 io69a06.y
  907    37.6    3.6    398  6  CA948194            CA948194 iq19a10.y
c 908    37.6    3.6    399  6  CA840975            CA840975 ip31d09.x
  909    37.6    3.6    400  4  BM313334            BM313334 ig82g08.y
  910    37.6    3.6    400  5  BQ631989            BQ631989 il24h11.y
  911    37.6    3.6    400  6  CA943302            CA943302 ip41e03.y
  912    37.6    3.6    400  6  CB067746            CB067746 iq37a08.y
  913    37.6    3.6    402  6  CA947019            CA947019 is10b06.y
c 914    37.6    3.6    403  4  BM663400            BM663400 UI-E-CI0-
  915    37.6    3.6    403  5  BQ272140            BQ272140 ik18h01.y
  916    37.6    3.6    403  6  CD104992            CD104992 AGENCOURT
  917    37.6    3.6    403  7  CF534956            CF534956 UI-M-GH0-
  918    37.6    3.6    404  6  CA847866            CA847866 iq39d07.y
  919    37.6    3.6    408  5  BU072900            BU072900 il36b05.y
  920    37.6    3.6    408  6  CA848527            CA848527 ip35h06.y
c 921    37.6    3.6    411  4  BI711815            BI711815 id91b01.x
c 922    37.6    3.6    411  5  BQ478091            BQ478091 ik80c03.x
  923    37.6    3.6    414  6  CA867768            CA867768 ir80h09.y
  924    37.6    3.6    414  6  CD102656            CD102656 AGENCOURT
  925    37.6    3.6    414  7  W67833              W67833 zd39f08.r1
  926    37.6    3.6    415  4  BI711532            BI711532 id91b01.y
  927    37.6    3.6    416  6  CA841844            CA841844 ip28h01.x
  928    37.6    3.6    417  6  CA843168            CA843168 ir54d12.y
  929    37.6    3.6    419  5  BU949461            BU949461 in67g05.y
  930    37.6    3.6    419  6  CB067105            CB067105 iq32b04.y
  931    37.6    3.6    420  6  CA774942            CA774942 ip10g11.y
  932    37.6    3.6    422  6  CA775577            CA775577 io87e08.y
  933    37.6    3.6    422  6  CD104022            CD104022 AGENCOURT
c 934    37.6    3.6    423  4  BM663222            BM663222 UI-E-CI0-
  935    37.6    3.6    423  6  CA773973            CA773973 im59h05.y
  936    37.6    3.6    424  5  BU072096            BU072096 im54c01.y
c 937    37.6    3.6    424  5  BU074641            BU074641 im78f05.x
  938    37.6    3.6    424  6  CA777040            CA777040 ip02d02.y
  939    37.6    3.6    425  4  BM310977            BM310977 ig59b08.y
  940    37.6    3.6    425  4  BM352914            BM352914 ig68h09.y
  941    37.6    3.6    425  5  BQ269014            BQ269014 ik19h04.y
  942    37.6    3.6    425  6  CD102521            CD102521 AGENCOURT
  943    37.6    3.6    426  1  AV647145            AV647145 AV647145
  944    37.6    3.6    427  4  BG656273            BG656273 ib35c02.x
c 945    37.6    3.6    428  6  CA842802            CA842802 ir24h09.x
c 946    37.6    3.6    428  6  CA868528            CA868528 ir80h09.x
  947    37.6    3.6    428  6  CD105140            CD105140 AGENCOURT
  948    37.6    3.6    429  5  BQ286494            BQ286494 ik30g04.y
c 949    37.6    3.6    429  6  CA950242            CA950242 ir89a03.x
  950    37.6    3.6    429  6  CB070396            CB070396 is36f07.y
  951    37.6    3.6    429  6  CB178556            CB178556 is40f07.y
  952    37.6    3.6    429  6  CD000232            CD000232 AGENCOURT
  953    37.6    3.6    430  6  CA947190            CA947190 is12d07.y
c 954    37.6    3.6    431  5  BQ287841            BQ287841 ik36b09.x
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c 956    37.6    3.6    432  6  CA848213            CA848213 ip35e06.x
c 957    37.6    3.6    434  6  CA941881            CA941881 ir47a09.x
  958    37.6    3.6    435  4  BI712910            BI712910 id98g09.y
c 959    37.6    3.6    436  1  AI635292            AI635292 tz80c11.x
  960    37.6    3.6    436  4  BM314673            BM314673 ig53f11.y
c 961    37.6    3.6    438  6  CA774730            CA774730 ip11d02.x
  962    37.6    3.6    439  5  BU071699            BU071699 im32f01.y
  963    37.6    3.6    440  6  CD104454            CD104454 AGENCOURT
  964    37.6    3.6    441  4  BM353023            BM353023 ig70e09.y
  965    37.6    3.6    441  5  BU078941            BU078941 im68d10.y
  966    37.6    3.6    442  6  CB069653            CB069653 is26d12.x
  967    37.6    3.6    442  6  CD000564            CD000564 AGENCOURT
  968    37.6    3.6    443  4  BI438421            BI438421 ic23c02.y
  969    37.6    3.6    443  5  BQ269877            BQ269877 ik31c03.y
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  971    37.6    3.6    444  5  BU951035            BU951035 io75a10.y
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c 973    37.6    3.6    444  6  CA867251            CA867251 ir59f02.x
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  974    37.6    3.6    444  6  CA867536          CA867536 ir29f03.y
  975    37.6    3.6    444  9  AY412722          AY412722 Homo sapi
  976    37.6    3.6    445  4  BM353367          BM353367 ig46b04.y
c 977    37.6    3.6    445  5  BQ271813          BQ271813 ik18h01.x
  978    37.6    3.6    445  5  BQ777123          BQ777123 il43f06.y
  979    37.6    3.6    445  6  CA948857          CA948857 iq28g04.y
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  981    37.6    3.6    445  6  CD103969          CD103969 AGENCOURT
  982    37.6    3.6    446  5  BQ417393          BQ417393 ik37d05.y
  983    37.6    3.6    446  5  BQ778637          BQ778637 il30g01.y
c 984    37.6    3.6    446  5  BU069246          BU069246 im59g11.x
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c 986    37.6    3.6    447  6  CA841741          CA841741 ip27d06.x
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  988    37.6    3.6    448  7  N72965            N72965 yv48h10.r1
c 989    37.6    3.6    449  1  AI640312          AI640312 wa16g04.x
  990    37.6    3.6    449  4  BM311107          BM311107 ig60h04.y
  991    37.6    3.6    449  6  CA388990          CA388990 cs04e12.y
  992    37.6    3.6    450  5  BU785777          BU785777 in46a08.y
  993    37.6    3.6    450  6  CA842422          CA842422 ir26h08.y
  994    37.6    3.6    451  6  CA866270          CA866270 ir36e02.y
  995    37.6    3.6    451  6  CB177238          CB177238 is18b03.y
  996    37.6    3.6    451  6  CB177488          CB177488 is22a03.y
  997    37.6    3.6    452  5  BQ632610          BQ632610 il25e05.y
c 998    37.6    3.6    452  6  CA866104          CA866104 ir38b10.x
  999    37.6    3.6    452  6  CD104127          CD104127 AGENCOURT
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 1001    37.6    3.6    453  6  CA843373          CA843373 ir49h01.y
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 1006    37.6    3.6    455  6  CB067044          CB067044 iq31d04.y
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 1010    37.6    3.6    456  5  BU072068          BU072068 im53h03.y
 1011    37.6    3.6    457  5  BU790328          BU790328 in49f12.y
c1012    37.6    3.6    457  6  CA771783          CA771783 io82h02.x
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 1021    37.6    3.6    458  6  CA948436          CA948436 iq22e11.y
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 1023    37.6    3.6    459  5  BU071927          BU071927 im52a12.y
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 1051    37.6    3.6    464  6  CA848746          CA848746 ir24h09.y
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 1054    37.6    3.6    464  6  CD103677          CD103677 AGENCOURT
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 1072    37.6    3.6    471  5  BU786011          BU786011 in48h12.y
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 1106    37.6    3.6    479  5  BU952695          BU952695 io73g07.y
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 1109    37.6    3.6    480  6  CA774975          CA774975 ip11d02.y
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 1116    37.6    3.6    481  6  CB178473          CB178473 is39c04.y
c1117    37.6    3.6    481  6  CD608274          CD608274 56098855H
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 1119    37.6    3.6    482  4  BM314634          BM314634 ig53b01.y
 1120   37.6   3.6   482  5  BU072878             BU072878 il35h05.y
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 1128   37.6   3.6   484  6  CA777179             CA777179 ip04c02.y
 1129   37.6   3.6   484  6  CD102603             CD102603 AGENCOURT
 1130   37.6   3.6   484  6  CD512027             CD512027 AGENCOURT
 1131   37.6   3.6   485  5  BQ416997             BQ416997 ik40d10.y
 1132   37.6   3.6   485  6  CA777020             CA777020 ip02a09.y
 1133   37.6   3.6   485  6  CA777689             CA777689 ip19h04.y
 1134   37.6   3.6   485  6  CA952306             CA952306 iq18a04.y
 1135   37.6   3.6   486  4  BM313506             BM313506 ig71a01.y
 1136   37.6   3.6   486  6  CA943144             CA943144 ip39b08.y
 1137   37.6   3.6   486  6  CA946958             CA946958 is09c11.y
 1138   37.6   3.6   487  6  CA776566             CA776566 ip06g06.y
 1139   37.6   3.6   487  6  CA865916             CA865916 ir43e03.y
 1140   37.6   3.6   487  6  CB067623             CB067623 iq35c12.y
 1141   37.6   3.6   488  5  BQ778075             BQ778075 il40f08.y
 1142   37.6   3.6   488  5  BU948942             BU948942 in71b02.y
 1143   37.6   3.6   488  5  BU952169             BU952169 in74e09.y
 1144   37.6   3.6   488  6  CA842680             CA842680 iq45h05.y
 1145   37.6   3.6   488  6  CD109299             CD109299 AGENCOURT
 1146   37.6   3.6   489  4  BI438478             BI438478 ic23h12.y
 1147   37.6   3.6   489  4  BI467014             BI467014 ic18c07.y
 1148   37.6   3.6   489  6  CA941027             CA941027 ir37e05.y
 1149   37.6   3.6   489  6  CA948422             CA948422 iq22c11.y
c1150   37.6   3.6   489  6  CB066970             CB066970 iq34b08.x
 1151   37.6   3.6   490  4  BM263775             BM263775 ig30d05.y
 1152   37.6   3.6   491  6  CA843153             CA843153 ir54c05.y
 1153   37.6   3.6   491  6  CA868042             CA868042 ir76g11.y
 1154   37.6   3.6   491  6  CA868527             CA868527 ir80h05.x
 1155   37.6   3.6   491  6  CA948811             CA948811 iq28b06.y
 1156   37.6   3.6   491  6  CD109323             CD109323 AGENCOURT
 1157   37.6   3.6   492  6  CA866718             CA866718 ir75e02.y
 1158   37.6   3.6   493  4  BM263510             BM263510 ig27a02.y
 1159   37.6   3.6   493  4  BM312122             BM312122 ig66e09.y
 1160   37.6   3.6   493  5  BQ269513             BQ269513 ik26e05.y
c1161   37.6   3.6   493  5  BU783912             BU783912 in11d10.x
 1162   37.6   3.6   493  6  CA772629             CA772629 io82h02.y
 1163   37.6   3.6   493  6  CA772697             CA772697 io83f12.y
 1164   37.6   3.6   493  6  CA772773             CA772773 io84g06.y
 1165   37.6   3.6   493  6  CA777594             CA777594 ip18e03.y
 1166   37.6   3.6   493  6  CA842500             CA842500 iq43a11.y
c1167   37.6   3.6   494  5  BU784703             BU784703 in55f02.x
 1168   37.6   3.6   494  6  CA775609             CA775609 io88a02.y
 1169   37.6   3.6   494  6  CB999190             CB999190 AGENCOURT
 1170   37.6   3.6   495  5  BQ268058             BQ268058 ij94e05.y
 1171   37.6   3.6   495  6  CA774988             CA774988 ip11e06.y
c1172   37.6   3.6   496  4  BM663306             BM663306 UI-E-CI0-
 1173   37.6   3.6   497  6  CA842181             CA842181 ip29d04.y
c1174   37.6   3.6   498  1  AA707911             AA707911 zg04d03.s
 1175   37.6   3.6   498  5  BQ777929             BQ777929 il38g12.y
 1176   37.6   3.6   498  6  CA772241             CA772241 io93f05.y
 1177   37.6   3.6   498  6  CA848050             CA848050 iq42a09.y
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 1179   37.6   3.6   499  6  CA774931             CA774931 ip10f05.y
 1180   37.6   3.6   499  6  CA867603             CA867603 ir30f02.y
 1181   37.6   3.6   500  4  BM510422             BM510422 ij41d04.y
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 1183   37.6   3.6   500  6  CA865730             CA865730 ir40h01.y
c1184   37.6   3.6   500  6  CA866758             CA866758 ir72b01.x
 1185   37.6   3.6   500  6  CB153862             CB153862 K-EST0211
c1186   37.6   3.6   501  4  BI522078             BI522078 603081801
 1187   37.6   3.6   501  4  BM312144             BM312144 ig66g09.y
 1188   37.6   3.6   501  5  BU951702             BU951702 in59e12.y
 1189   37.6   3.6   501  6  CA775505             CA775505 io86e08.y
 1190   37.6   3.6   502  5  BQ286193             BQ286193 ik27b01.y
 1191   37.6   3.6   502  5  BU951052             BU951052 io75c04.y
 1192   37.6   3.6   503  4  BM263800             BM263800 ig30f12.y
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 1193   37.6   3.6   503  4  BM313560             BM313560 ig71g03.y
 1194   37.6   3.6   504  4  BM504034             BM504034 ig98h07.y
 1195   37.6   3.6   504  6  CA847987             CA847987 iq41b07.y
 1196   37.6   3.6   504  6  CD102368             CD102368 AGENCOURT
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 1198   37.6   3.6   505  4  BM505147             BM505147 ig90h11.y
 1199   37.6   3.6   505  5  BQ417442             BQ417442 ik38a09.y
 1200   37.6   3.6   505  5  BU951073             BU951073 io75e04.y
 1201   37.6   3.6   505  6  CA842373             CA842373 ir26c02.y
c1202   37.6   3.6   506  1  AA719616             AA719616 zh37b11.s
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 1205   37.6   3.6   506  4  BM263570             BM263570 ig27g03.y
 1206   37.6   3.6   506  4  BM313577             BM313577 ig71h10.y
 1207   37.6   3.6   506  5  BU949483             BU949483 in68a10.y
 1208   37.6   3.6   506  6  CA843196             CA843196 ir55a02.y
 1209   37.6   3.6   507  4  BM312299             BM312299 ig41f09.y
 1210   37.6   3.6   507  5  BQ477906             BQ477906 ik87e12.y
 1211   37.6   3.6   508  5  BU951671             BU951671 in59a12.y
 1212   37.6   3.6   508  6  CA947221             CA947221 is12g11.y
 1213   37.6   3.6   509  5  BQ776769             BQ776769 il33a04.y
 1214   37.6   3.6   509  6  CA946968             CA946968 is09d12.y
 1215   37.6   3.6   510  5  BU952185             BU952185 in74g09.y
 1216   37.6   3.6   510  6  CA847891             CA847891 iq39g03.y
c1217   37.6   3.6   510  6  CB070342             CB070342 is36f07.x
 1218   37.6   3.6   510  6  CD103048             CD103048 AGENCOURT
 1219   37.6   3.6   511  6  CA866243             CA866243 ir36a12.y
 1220   37.6   3.6   511  6  CA942950             CA942950 ir66b03.y
 1221   37.6   3.6   512  4  BM352814             BM352814 ig67e04.y
 1222   37.6   3.6   512  4  BM505043             BM505043 ig89f03.y
 1223   37.6   3.6   512  6  CA773211             CA773211 im61b01.y
 1224   37.6   3.6   512  6  CA776636             CA776636 ip08g03.y
 1225   37.6   3.6   512  6  CA842213             CA842213 ip29g11.y
 1226   37.6   3.6   512  6  CA848014             CA848014 iq41e06.y
 1227   37.6   3.6   513  6  CA941539             CA941539 ir32f03.y
 1228   37.6   3.6   515  4  BI712659             BI712659 ie07f04.y
 1229   37.6   3.6   515  6  CA942222             CA942222 ir47h03.y
 1230   37.6   3.6   515  6  CB069531             CB069531 is16d09.y
 1231   37.6   3.6   516  5  BP216474             BP216474 BP216474
 1232   37.6   3.6   516  5  BP216509             BP216509 BP216509
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 1234   37.6   3.6   517  5  BP201090             BP201090 BP201090
 1235   37.6   3.6   517  5  BU074680             BU074680 im75b10.y
 1236   37.6   3.6   519  6  CA773126             CA773126 im60a03.y
c1237   37.6   3.6   519  6  CB178713             CB178713 is39c04.x
 1238   37.6   3.6   520  5  BU949872             BU949872 in61f02.y
 1239   37.6   3.6   520  6  CB115409             CB115409 K-EST0159
c1240   37.6   3.6   521  1  AA757575             AA757575 zg38a06.s
 1241   37.6   3.6   521  1  AI114753             AI114753 HA1357 Hu
c1242   37.6   3.6   522  6  CA943549             CA943549 ir29f03.x
 1243   37.6   3.6   523  6  CA941182             CA941182 ir39f11.y
 1244   37.6   3.6   524  4  BM503363             BM503363 ig73a07.y
 1245   37.6   3.6   524  4  BM505091             BM505091 ig90c03.y
 1246   37.6   3.6   524  5  BQ631718             BQ631718 il21c10.y
 1247   37.6   3.6   524  5  BQ776788             BQ776788 il33c04.y
c1248   37.6   3.6   524  5  BU077981             BU077981 im66b01.x
 1249   37.6   3.6   524  6  CA942423             CA942423 ir57g07.y
c1250   37.6   3.6   524  6  CB067481             CB067481 iq37d12.x
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 1252   37.6   3.6   525  4  BM310883             BM310883 ig50a03.y
 1253   37.6   3.6   525  4  BM313073             BM313073 ig79a10.y
c1254   37.6   3.6   525  5  BU948757             BU948757 in72b10.x
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c1256   37.6   3.6   525  6  CA948579             CA948579 iq28g04.x
 1257   37.6   3.6   525  6  CA949665             CA949665 iq23e09.y
 1258   37.6   3.6   525  6  CD511976             CD511976 AGENCOURT
c1259   37.6   3.6   526  4  BG656461             BG656461 ib37f08.x
 1260   37.6   3.6   527  4  BM509683             BM509683 ig92g03.y
 1261   37.6   3.6   527  7  CK821249             CK821249 ig50c04.x
c1262   37.6   3.6   528  5  BQ286058             BQ286058 ik25c12.x
 1263   37.6   3.6   528  6  CA947125             CA947125 is11e09.y
c1264   37.6   3.6   529  4  BG656314             BG656314 ib35h01.x
 1265   37.6   3.6   530  4  BM310904             BM310904 ig50c04.y
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c1266   37.6   3.6   530  5  BQ286698          BQ286698 ik33b10.x
c1267   37.6   3.6   531  4  BG656315          BG656315 ib35h02.x
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 1269   37.6   3.6   531  5  BQ268977          BQ268977 ik19c02.y
 1270   37.6   3.6   531  5  BQ269048          BQ269048 ik20d02.y
 1271   37.6   3.6   531  5  BQ417218          BQ417218 ik35b12.y
 1272   37.6   3.6   531  5  BQ778570          BQ778570 il29e09.y
 1273   37.6   3.6   531  5  BU949436          BU949436 in67d04.y
 1274   37.6   3.6   531  6  CD103198          CD103198 AGENCOURT
 1275   37.6   3.6   532  4  BI553573          BI553573 603197581
 1276   37.6   3.6   532  6  CA949677          CA949677 iq23f12.y
 1277   37.6   3.6   532  6  CD000609          CD000609 AGENCOURT
 1278   37.6   3.6   533  6  CD102975          CD102975 AGENCOURT
 1279   37.6   3.6   533  6  CD512320          CD512320 AGENCOURT
 1280   37.6   3.6   534  4  BM263634          BM263634 ig28e12.y
 1281   37.6   3.6   534  4  BM353212          BM353212 ig44b04.y
c1282   37.6   3.6   534  6  CA771769          CA771769 io82f08.x
 1283   37.6   3.6   534  6  CB067778          CB067778 iq37d12.y
 1284   37.6   3.6   535  4  BI791743          BI791743 ie04a02.y
 1285   37.6   3.6   535  4  BM353765          BM353765 ig55h04.y
 1286   37.6   3.6   535  5  BQ286186          BQ286186 ik27a06.y
 1287   37.6   3.6   535  6  CA865702          CA865702 ir40d04.y
 1288   37.6   3.6   535  6  CB147237          CB147237 K-EST0203
 1289   37.6   3.6   536  6  CA866716          CA866716 ir75d11.y
 1290   37.6   3.6   537  4  BM504994          BM504994 ig89a10.y
 1291   37.6   3.6   537  5  BU069227          BU069227 im59e11.x
 1292   37.6   3.6   538  4  BI438477          BI438477 ic23h11.y
 1293   37.6   3.6   538  4  BM312100          BM312100 ig66c03.y
 1294   37.6   3.6   538  6  CA773424          CA773424 im63h12.y
 1295   37.6   3.6   538  6  CB177325          CB177325 is19c12.y
 1296   37.6   3.6   539  6  CA950020          CA950020 ir85f11.y
 1297   37.6   3.6   539  6  CA952700          CA952700 iq12b02.y
 1298   37.6   3.6   540  4  BI712906          BI712906 id98g05.y
c1299   37.6   3.6   540  4  BM672301          BM672301 UI-E-CL1-
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 1301   37.6   3.6   540  6  CD102288          CD102288 AGENCOURT
 1302   37.6   3.6   541  6  CA841887          CA841887 ip29d07.x
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 1304   37.6   3.6   542  5  BQ416863          BQ416863 ik42f03.x
 1305   37.6   3.6   542  6  CA942551          CA942551 ir59f02.y
 1306   37.6   3.6   543  4  BM310805          BM310805 ig48g09.y
 1307   37.6   3.6   543  4  BM314706          BM314706 ig54a07.y
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 1310   37.6   3.6   544  6  CA842172          CA842172 ip29c06.y
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 1312   37.6   3.6   544  6  CD102796          CD102796 AGENCOURT
c1313   37.6   3.6   545  1  AI144441          AI144441 qc07a12.x
c1314   37.6   3.6   545  1  AI261783          AI261783 qk10d04.x
c1315   37.6   3.6   545  4  BG655815          BG655815 ib40d04.x
 1316   37.6   3.6   545  5  BQ777915          BQ777915 il38f08.y
 1317   37.6   3.6   545  6  CD000917          CD000917 AGENCOURT
 1318   37.6   3.6   545  6  CD102165          CD102165 AGENCOURT
 1319   37.6   3.6   545  6  CD103787          CD103787 AGENCOURT
 1320   37.6   3.6   546  4  BM700961          BM700961 UI-E-CL1-
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 1322   37.6   3.6   546  6  CB177810          CB177810 is21b06.x
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c1324   37.6   3.6   547  4  BI467348          BI467348 ic23c02.x
 1325   37.6   3.6   547  4  BM271901          BM271901 ig36e10.y
c1326   37.6   3.6   548  4  BG656466          BG656466 ib37g02.x
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 1329   37.6   3.6   548  5  BU078165          BU078165 im65a11.y
 1330   37.6   3.6   548  6  CA842010          CA842010 ip27a10.y
 1331   37.6   3.6   548  6  CA942926          CA942926 ir65f06.y
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 1334   37.6   3.6   549  4  BM503898          BM503898 ig97b08.y
 1335   37.6   3.6   549  5  BQ631127          BQ631127 il16h06.y
 1336   37.6   3.6   549  5  BQ631695          BQ631695 il21a09.y
 1337   37.6   3.6   549  7  CK825897          CK825897 ik34d01.x
 1338   37.6   3.6   550  4  BI467022          BI467022 ic18d03.y

 1339   37.6   3.6   550  4  BM352286          BM352286 ig84g11.y
 1340   37.6   3.6   550  9  CL723170          CL723170 OR_BBa005
 1341   37.6   3.6   551  4  BM314579          BM314579 ig52d09.y
 1342   37.6   3.6   551  5  BU078104          BU078104 im64a12.y
 1343   37.6   3.6   551  6  CA848593          CA848593 ip36g05.y
 1344   37.6   3.6   551  6  CA941609          CA941609 ir33f03.y
 1345   37.6   3.6   551  6  CA942163          CA942163 ir47a09.y
 1346   37.6   3.6   551  6  CA942307          CA942307 ir56b04.y
 1347   37.6   3.6   551  6  CA950002          CA950002 ir85e04.y
 1348   37.6   3.6   551  6  CD104979          CD104979 AGENCOURT
 1349   37.6   3.6   553  4  BM311253          BM311253 ig62g10.y
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 1355   37.6   3.6   554  6  CD104822          CD104822 AGENCOURT
 1356   37.6   3.6   555  4  BM313203          BM313203 ig80g12.y
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 1359   37.6   3.6   555  6  CA867809          CA867809 ir81e05.y
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 1362   37.6   3.6   556  6  CD102793          CD102793 AGENCOURT
 1363   37.6   3.6   557  5  BQ635884          BQ635884 hd01e01.y
 1364   37.6   3.6   558  4  BM509718          BM509718 ig93b07.y
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c1367   37.6   3.6   559  4  BI467405          BI467405 ic23h12.x
 1368   37.6   3.6   559  4  BM272504          BM272504 ig42g04.y
c1369   37.6   3.6   559  5  BU077852          BU077852 im64a12.x
 1370   37.6   3.6   559  5  BU950967          BU950967 io74c05.y
 1371   37.6   3.6   559  6  CA773284          CA773284 im62a10.y
 1372   37.6   3.6   559  6  CA841179          CA841179 ip30f05.y
 1373   37.6   3.6   560  4  BM272397          BM272397 ig40d04.y
 1374   37.6   3.6   560  4  BM352936          BM352936 ig69b11.y
 1375   37.6   3.6   560  5  BU948658          BU948658 in70f04.x
c1376   37.6   3.6   560  6  CA865484          CA865484 ir40h01.x
c1377   37.6   3.6   561  4  BI438624          BI438624 ic24g02.x
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 1381   37.6   3.6   562  5  BQ130238          BQ130238 ij82g07.y
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 1384   37.6   3.6   563  4  BM352931          BM352931 ig69b04.y
 1385   37.6   3.6   563  4  BM690536          BM690536 UI-E-CI0-
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 1387   37.6   3.6   563  5  BU947879          BU947879 io54h08.y
c1388   37.6   3.6   563  6  CA946750          CA946750 is10b12.x
 1389   37.6   3.6   563  6  CB163272          CB163272 K-EST0224
 1390   37.6   3.6   563  7  CK821353          CK821353 ig53b01.x
 1391   37.6   3.6   564  4  BI712962          BI712962 id99d07.y
 1392   37.6   3.6   564  5  BQ417319          BQ417319 ik36e01.y
 1393   37.6   3.6   564  5  BU947260          BU947260 io45f08.y
 1394   37.6   3.6   564  5  BU951722          BU951722 in59g12.y
 1395   37.6   3.6   565  4  BM264215          BM264215 ig32d06.y
 1396   37.6   3.6   565  4  BM315084          BM315084 ig43c07.y
 1397   37.6   3.6   565  4  BM690602          BM690602 UI-E-CI0-
 1398   37.6   3.6   565  5  BQ777391          BQ777391 il47e05.y
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 1400   37.6   3.6   565  5  BU950100          BU950100 in64e07.y
 1401   37.6   3.6   566  5  BU949004          BU949004 in72b10.y
 1402   37.6   3.6   567  4  BI713714          BI713714 ie03a12.y
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 1404   37.6   3.6   567  5  BQ417187          BQ417187 ik42g11.y
c1405   37.6   3.6   567  5  BU951519          BU951519 in60h03.x
c1406   37.6   3.6   567  6  CA847718          CA847718 iq41b07.x
 1407   37.6   3.6   568  4  BI713711          BI713711 ie03a09.y
 1408   37.6   3.6   568  4  BM313590          BM313590 ig72d03.y
 1409   37.6   3.6   568  4  BM352866          BM352866 ig68c03.y
 1410   37.6   3.6   568  4  BM503450          BM503450 ig74b05.y
 1411   37.6   3.6   568  5  BQ778563          BQ778563 il29d09.y
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  1416    37.6    3.6    568  6  CD104431                 CD104431 AGENCOURT
 c1417    37.6    3.6    569  1  AI093602                 AI093602 ou82a12.s
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  1419    37.6    3.6    569  4  BM352780                 BM352780 ig67a08.y
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 c1424    37.6    3.6    569  6  CA941296                 CA941296 ir33c06.x
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  1438    37.6    3.6    572  6  CA848605                 CA848605 ip36h09.y
 c1439    37.6    3.6    573  4  BI467266                 BI467266 ic22b07.x
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  1450    37.6    3.6    575  6  CA842083                 CA842083 ip28a09.y
  1451    37.6    3.6    576  5  BQ269252                 BQ269252 ik23c03.y
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 c1454    37.6    3.6    576  5  BQ416869                 BQ416869 ik42f10.x
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  1456    37.6    3.6    577  4  BI439204                 BI439204 ic27g05.y
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  1458    37.6    3.6    577  4  BM353029                 BM353029 ig70f04.y
 c1459    37.6    3.6    578  5  BQ271550                 BQ271550 ik15d01.x
  1460    37.6    3.6    578  5  BU076667                 BU076667 im50g12.y
 c1461    37.6    3.6    578  6  CA952835                 CA952835 ir45a06.x
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                                   ALIGNMENTS


RESULT 1
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LOCUS       AK045973                1808 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male corpora quadrigemina cDNA, RIKEN
            full-length enriched library, clone:B230328N06 product:NEUROTRIMIN
            PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
ACCESSION   AK045973
VERSION     AK045973.1  GI:26337738
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1808)
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  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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                     /db_xref="GI:26337739"
                     /translation="MKTIQAKMHNSISWAIFTGLAALCLFQGVPVRSGDATFPKAMDN
                     VTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEI
                     QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIAT
                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGEYECSASNDVAAPVVRRVKVT
                     VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWFKDDKRLVEGKKGVKVENRPF
                     LSKLTFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVNNGTSRRAGCIWLLP
                     LLVLHLLLKF"
ORIGIN

  Query Match            84.9%;  Score 878.2;  DB 3;  Length 1808;
  Best Local Similarity  90.5%;  Pred. No. 5.4e-244;
  Matches  937;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy          1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60
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Db        204 ATGAAAACCATCCAGGCAAAAATGCACAATTCTATCTCGTGGGCAATCTTCACGGGGCTG 263

Qy         61 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
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Qy        301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
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Qy        481 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 540
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Qy        721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780
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Db        924 CTGCAGTGTGAAGCTTCCGCAGTCCCTTCAGCAGAATTTCAATGGTTCAAGGATGACAAA 983

Qy        781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840
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RESULT 2
AK046377
LOCUS       AK046377                1808 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male corpora quadrigemina cDNA, RIKEN
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            PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
ACCESSION   AK046377
VERSION     AK046377.1  GI:26338018
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1808)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
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ORIGIN

  Query Match             84.9%;  Score 878.2;  DB 3;  Length 1808;
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  Matches  937;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

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Qy         61 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
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Qy        121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180
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RESULT 3
AY406347
LOCUS       AY406347                 874 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406347
VERSION     AY406347.1  GI:39762321
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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RESULT 4
AY406348
LOCUS       AY406348                 773 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Pan troglodytes HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY406348
VERSION     AY406348.1  GI:39762322
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 773)
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  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 773)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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ORIGIN

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  Matches  761;  Conservative    0;  Mismatches    6;  Indels    6;  Gaps    1;

Qy        168 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 227
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Qy        228 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 287
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Db         61 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 120

Qy        288 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 347
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Db        241 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAACGAAGGGAACAATATCAGCCTCAC 300

Qy        468 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAA--- 524
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Db        301 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCCCCCAAACC 360

Qy        525 ---AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA 581
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Db        361 CGCAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA 420

Qy        582 GCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAG 641
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Db        421 GCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAG 480

Qy        642 AGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCC 701
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Db        481 AGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCC 540

Qy        702 CGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCA 761
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Qy        762 GTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAG 821
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Qy        822 ACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACAC 881
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Db        661 ACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACAC 720

Qy        882 TTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTG 934
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Db        721 TTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTG 773


RESULT 5
AY406349
LOCUS       AY406349                 874 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406349
VERSION     AY406349.1  GI:39762323
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .874
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>874
                     /locus_tag="HCM2527"
ORIGIN

  Query Match             68.6%;  Score 709.6;  DB 9;  Length 874;
  Best Local Similarity   89.1%;  Pred. No. 5.6e-195;
  Matches  779;  Conservative    0;  Mismatches   89;  Indels    6;  Gaps    1;

Qy        168 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA 227
              |||||| ||||||||||| ||||||||||||||||||||||||||||| |||||||||||
Db          1 GTGCACAATTGACAACCGAGTCACCCGGGTGGCCTGGCTAAACCGCAGTACCATCCTCTA 60

Qy        228 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAAC 287
              |||||| ||||||||||||||||| |||||||| |||||||| ||||| |||||||| ||
Db         61 TGCTGGAAATGACAAGTGGTGCCTAGATCCTCGTGTGGTCCTCCTGAGTAACACCCAGAC 120

Qy        288 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 347
               ||||||||||| ||||||||||| ||||||||||| || ||||||||||| ||||||||
Db        121 CCAGTACAGCATTGAGATCCAGAATGTGGATGTGTACGATGAGGGCCCTTATACCTGCTC 180

Qy        348 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 407
              ||| ||||||||||||||||| |||||||| ||||||||||||||||| |||||||||||
Db        181 GGTACAGACAGACAACCACCCTAAGACCTCCAGGGTCCACCTCATTGTACAAGTATCTCC 240

Qy        408 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 467
              |||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||
Db       241 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAACATCAGCCTCAC 300

Qy       468 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAA--- 524
              |||||||| || |||||||| |||||||| || || |||||||| || ||||||||
Db       301 TTGCATAGCCACAGGTAGACCGGAGCCTACAGTAACCTGGAGACATATTTCTCCCAAGCC 360

Qy       525 ---AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA 581
                ||| ||||||||||||||||| || || ||| |||| || ||||||||||| |||||
Db       361 CGCAGCCGTTGGCTTTGTGAGTGAGGATGAGTACCTGGAGATCCAGGGCATCACTCGGGA 420

Qy       582 GCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAG 641
              |||||||| || ||||||||||| |||||||| |||||||| || || |||||||| ||
Db       421 ACAGTCAGGCGAGTACGAGTGCAGCGCCTCCAACGACGTGGCGGCACCAGTGGTACGAAG 480

Qy       642 AGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCC 701
             ||| ||||||||||||||||||||||||||||| |||||||| ||||| |||||||||||
Db       481 AGTGAAGGTCACCGTGAACTATCCACCATACATCTCAGAAGCTAAGGGCACAGGTGTCCC 540

Qy       702 CGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCA 761
             |||||| || |||||||| |||||||||||||| || |||||||| ||||||||||| ||
Db       541 CGTGGGGCAGAAGGGGACTCTGCAGTGTGAAGCTTCCGCAGTCCCTTCAGCAGAATTTCA 600

Qy       762 GTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAG 821
              |||| ||||||||||||||||||| | ||||||||||| || || ||||||||||||||
Db       601 ATGGTTCAAGGATGACAAAAGACTGGTCGAAGGAAAGAAGGGAGTCAAAGTGGAAAACAG 660

Qy       822 ACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACAC 881
             ||||||||| |||||||||| ||| ||||| |||||||||||||||||||||||||||||
Db       661 ACCTTTCCTTTCAAAACTCACCTTTTTCAACGTCTCTGAACATGACTATGGGAACTACAC 720

Qy       882 TTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGG 941
              || |||||||||||||||||||| |||||||| ||||||||||||||||||||||| ||
Db       721 ATGTGTGGCCTCCAACAAGCTGGGTCACACCAACGCCAGCATCATGCTATTTGGTCCCGG 780

Qy       942 CGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC 1001
              || ||||| ||||| | ||| || || || ||||||||||||||| | ||||| || ||
Db       781 TGCTGTCAGTGAGGTCAACAATGGGACATCAAGGAGGGCAGGCTGCATTTGGCTCCTCCC 840

Qy      1002 TCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGA 1035
             |||||||||||| |||||||| ||||||||||||
Db       841 TCTTCTGGTCTTACACCTGCTCCTCAAATTTTGA 874


RESULT 6
BU155617
LOCUS       BU155617                 856 bp    mRNA    linear   EST 03-SEP-2002
DEFINITION  AGENCOURT_7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839
            5', mRNA sequence.
ACCESSION   BU155617
VERSION     BU155617.1  GI:22669149
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13527  row: m  column: 16
            High quality sequence stop: 593.
FEATURES             Location/Qualifiers
     source          1..856
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6166839"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             64.2%;  Score 664.8;  DB 5;  Length 856;
  Best Local Similarity   97.6%;  Pred. No. 6.3e-182;
  Matches  728;  Conservative    0;  Mismatches   12;  Indels    6;  Gaps    5;

Qy        81 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        94 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 153

Qy       141 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       154 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 213

Qy       201 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       214 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 273

Qy       261 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       274 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 333

Qy       321 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       334 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 393

Qy       381 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       394 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 453

Qy       441 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       454 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 513

Qy       501 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       514 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 573

Qy       561 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       574 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 633

Qy       621 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       634 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 693

Qy       681 AGCCAAGGGTACAGGTGT-CCCCGTGGGACAAAAGGGGACACTGCAG-TGTGAAGCCTCA 738
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Db       694 AGCCAAGGGTACAGGTGTCCCCCGTGGGACAAAAGGGGACACTGCAGTTGTGAAACCTCA 753

Qy       739 GCAGTCCCCTCAGCAG-AATTCCAGTGGTACAAGGATG-ACAAAAGACTGATT--GAAGG 794
             |||||||||||||||| ||||||||||||||| ||||| || |||||||||||   | ||
Db       754 GCAGTCCCCTCAGCAGAAATTCCAGTGGTACAGGGATGAACCAAAGACTGATTTGAAGGG 813

Qy       795 AAAGAAAGGGGTGAAAGTGGAAAACA 820
             ||| ||||||||| ||  ||  || |
Db       814 AAAAAAAGGGGTGGAAAGGGGGAAAA 839


RESULT 7
CN362539
LOCUS       CN362539                 748 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000470517655 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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ACCESSION   CN362539
VERSION     CN362539.1  GI:47362473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 748)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 748   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .748
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, embryoid bodies
                     derived from H1, H7 and H9 cells"
                     /clone_lib="GRN_EB"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from embryoid body outgrowths derived from hES cell lines
                     H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                     conditions."
ORIGIN

  Query Match             61.8%;  Score 640;  DB 7;  Length 748;
  Best Local Similarity   100.0%;  Pred. No. 1e-174;
  Matches  640;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         81 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 140
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Db        109 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 168

Qy        141 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 200
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Db        169 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 228

Qy        201 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 288

Qy        261 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 348

Qy        321 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 408

Qy        381 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 468

Qy        441 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 528

Qy        501 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 588

Qy        561 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 620
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 648

Qy        621 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 708

Qy        681 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720
              ||||||||||||||||||||||||||||||||||||||||
Db        709 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 748


RESULT 8
BE798585
LOCUS       BE798585                1039 bp    mRNA    linear   EST 20-SEP-2000
DEFINITION  601581610F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935955 5',
            mRNA sequence.
ACCESSION   BE798585
VERSION     BE798585.1  GI:10219783
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1039)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM779  row: d  column: 04
            High quality sequence stop: 849.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3935955"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match             61.4%;  Score 635.2;  DB 2;  Length 1039;
  Best Local Similarity   97.6%;  Pred. No. 2.8e-173;
  Matches  656;  Conservative    0;  Mismatches   13;  Indels    3;  Gaps    1;

Qy        165 CAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCT 224
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         65 CAGGTGCACTATTGACAACCGGGTCGCCCGGGTGGCCTGGCTAAACCGCAGCACCATCCT 124

Qy        225 CTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCA 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCA 184

Qy        285 AACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTG 344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTG 244
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Qy        345 CTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATC 404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATC 304

Qy        405 TCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCT 464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 TCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCT 364

Qy        465 CACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAA 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 CACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAA 424

Qy        525 AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCA 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCA 484

Qy        585 GTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGT 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 GTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGT 544

Qy        645 AAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGT 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 AAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGT 604

Qy        705 GGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTG 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 GGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTG 664

Qy        765 GTACAAGGATGACAAAAGACTGATTGAAGGAA---AGAAAGGGGTGAAAGTGGAAAACAG 821
              ||||||||||||||||||||||||||||||||   | |  || |   |  ||||||||||
Db        665 GTACAAGGATGACAAAAGACTGATTGAAGGAACAGACAGGGGTGAACAGTTGGAAAACAG 724

Qy        822 ACCTTTCCTCTC 833
              ||||||   |||
Db        725 ACCTTTTTCCTC 736


RESULT 9
CD354474
LOCUS       CD354474                 765 bp    mRNA    linear   EST 15-JUL-2003
DEFINITION  UI-M-GM0-cgd-g-16-0-UI.r1 NIH_BMAP_GM0 Mus musculus cDNA clone
            IMAGE:30361215 5', mRNA sequence.
ACCESSION   CD354474
VERSION     CD354474.1  GI:31146975
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 765)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1..765
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30361215"
                     /tissue_type="whole brain"
                     /dev_stage="1, 5 and 15 days newborn"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_GM0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel.First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site.Double strand cDNA was size
                     selected according to mRNA size fraction,ligated with EcoR
                     I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is CGAACTGAAT. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
ORIGIN

  Query Match             59.9%;  Score 619.6;  DB 6;  Length 765;
  Best Local Similarity   91.0%;  Pred. No. 8.9e-169;
  Matches  658;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy         15 GCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTGGCTGCTCTGTGTCT 74
              | |||||||||||||||||||||| ||||||||||||||||||||||| |||||||| ||
Db          1 GGCAAAAATGCACAATTCTATCTCGTGGGCAATCTTCACGGGGCTGGCGGCTCTGTGCCT 60

Qy         75 CTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGT 134
              ||||||||||||||| ||||| ||||||||||||||||| ||||||||||||||||||||
Db         61 CTTCCAAGGAGTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAACGT 120

Qy        135 GACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCG 194
              ||||||| ||||||||||||||||||||||||||||||| ||||||||||| ||||||||
Db        121 GACGGTCAGGCAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCG 180

Qy        195 GGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGA 254
              ||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||| ||
Db        181 GGTGGCCTGGCTAAACCGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGA 240

Qy        255 TCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGT 314
              |||||| |||||||| ||||| |||||||| || ||||||||||| ||||||||||| ||
Db        241 TCCTCGTGTGGTCCTCCTGAGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGT 300

Qy        315 GGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGAC 374
              ||||||||| || ||||||||||| ||||||||||| ||||||||||||||||| |||||
Db        301 GGATGTGTACGATGAGGGCCCTTATACCTGCTCGGTACAGACAGACAACCACCCTAAGAC 360

Qy        375 CTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATAT 434
              ||| ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        361 CTCCAGGGTCCACCTCATTGTACAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATAT 420

Qy        435 CTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCC 494
              ||||||||||||||||||||| || |||||||| |||||||| || |||||||| |||||
Db        421 CTCCATTAATGAAGGGAACAACATCAGCCTCACTTGCATAGCCACAGGTAGACCGGAGCC 480

Qy        495 TACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATA 554
              ||| || || |||||||| || |||||||| || ||||||||||||||||| || || ||
Db        481 TACAGTAACCTGGAGACATATTTCTCCCAAGGCCGTTGGCTTTGTGAGTGAGGATGAGTA 540

Qy        555 CTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAA 614
              | |||| || ||||||||||| ||||| |||||||| || ||||||||||| ||||||||
Db        541 CCTGGAGATCCAGGGCATCACTCGGGAACAGTCAGGCGAGTACGAGTGCAGCGCCTCCAA 600

Qy        615 TGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACAT 674
               |||||||| || || |||||||| ||||| |||||||||||||||||||||||||||||
Db        601 CGACGTGGCGGCACCAGTGGTACGAAGAGTGAAGGTCACCGTGAACTATCCACCATACAT 660

Qy        675 TTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGC 734
               |||||||| ||||| ||| ||||||||||||| || |||||||| ||||||||||||||
Db        661 CTCAGAAGCTAAGGGCACANGTGTCCCCGTGGGGCAGAAGGGGACTCTGCAGTGTGAAGC 720

Qy        735 CTC 737
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                ||
Db          721 TTC 723

RESULT 10
CO635648
LOCUS       CO635648                1450 bp    mRNA    linear   EST 22-JUL-2004
DEFINITION  Contig2663 WL/RJ Phraped ESTs Gallus gallus cDNA 5', mRNA sequence.
ACCESSION   CO635648
VERSION     CO635648.1  GI:50538871
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1450)
  AUTHORS   Fitzsimmons,C.J., Savolainen,P., Amini,B., Hjalm,G., Lundeberg,J.
            and Andersson,L.
  TITLE     Detection of sequence polymorphisms in red junglefowl and White
            Leghorn ESTs
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Carolyn Fitzsimmons
            Leif Andersson IMBIM/Dept. Animal Breeding and Genetics
            Uppsala University/Swedish University of Agricultural Sciences
            Box 597, SE-751 24 Uppsala, SWEDEN
            Tel: 00 46 (0)18 471 4593
            Fax: 00 46 (0)18 471 4833
            Email: Carolyn.Fitzsimmons@bmc.uu.se
            This EST is a consensus sequence obtained from a Phrap assembly of
            4 cDNA libraries. The consensus sequence is submitted because SNP
            data in the publication 'Detection of sequence polymorphisms in red
            junglefowl and White Leghorn ESTs', is reported with reference to
            positions in the Phrap consensus sequence.
            Seq primer: (5'-end) M13 reverse.
FEATURES             Location/Qualifiers
     source          1..1450
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Red junglefowl/White Leghorn"
                     /db_xref="taxon:9031"
                     /sex="female/male"
                     /lab_host="ElectroMAX DH10B (Invitrogen)"
                     /clone_lib="WL/RJ Phraped ESTs"
                     /note="Organ: brain/testis; Vector: pSPORT-1; Site_1: Hind
                     III; Site_2: EcoRI; The cDNA libraries were created with
                     the Superscript Plasmid System (Invitrogen)."
ORIGIN

  Query Match             54.6%;  Score 564.8;  DB 7;  Length 1450;
  Best Local Similarity   75.6%;  Pred. No. 9.8e-153;
  Matches  726;  Conservative    0;  Mismatches  232;  Indels    2;  Gaps    2;

Qy           78 CCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGAC 137
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          307 CCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGAC 366

Qy          138 GGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGT 197
                 || ||||| |||||||| ||||| ||||||||| |  | |||||||| |||||||| ||
Db          367 TGTGCGGCAAGGGGAGAGTGCCACGCTCAGGTGCTCCGTGGACAACCGCGTCACCCGCGT 426

Qy          198 GGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCC 257
                ||||||||| |||||||||| |||||||||||| || ||||||||||||||| |||| ||
Db          427 GGCCTGGCTGAACCGCAGCAGCATCCTCTATGCCGGCAATGACAAGTGGTGCTTGGACCC 486

Qy          258 TCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGA 317
                  | ||||| || |||  ||||||| |||| |||||||||||| |||||||  |||||||
Db          487 GAGGGTGGTGCTCCTGGCCAACACCAAAACCCAGTACAGCATCCAGATCCACGACGTGGA 546

Qy          318 TGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTC 377
                 ||||| || || || || ||||||||||| |||||||||||||| ||||| ||||| ||
Db          547 CGTGTACGATGAAGGGCCCTACACCTGCTCCGTGCAGACAGACAATCACCCCAAGACATC 606
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Qy          378 TAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTC 437
                | | || ||||||||||||||||| || || ||||||   ||||| ||||| || |||||
Db          607 TCGCGTGCACCTCATTGTGCAAGTGTCGCCGAAAATTACCGAGATCTCTTCTGACATCTC 666

Qy          438 CATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC 497
                ||| ||||||||   |||  | ||||||||||||||||| || || || ||||| || ||
Db          667 CATCAATGAAGGTGGCAACGTCAGCCTCACCTGCATAGCCACGGGCAGGCCAGACCCCAC 726

Qy          498 GGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGG-CTTTGTGAGTGAAGACGAATACT 556
                  | || |||||||||||||| |||||||| || || |||  | || || || || |||
Db          727 AATCACCTGGAGACACATCTCGCCCAAAGCTGTGGGCCTTCATCAGCGAGGATGAGTACC 786

Qy          557 TGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATG 616
                |||| ||   ||||||||| ||||||||||| || || || |||||||||||   |||||
Db          787 TGGAGATCACGGGCATCACACGGGAGCAGTCGGGCGAGTATGAGTGCAGTGCTGTCAATG 846

Qy          617 ACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTT 676
                | ||||| |  || |  || |||| ||| || ||||| || ||||| || || ||||| |
Db          847 ATGTGGCTGTCCCAGATGTCCGGAAAGTCAAAGTCACTGTCAACTACCCGCCGTACATCT 906

Qy          677 CAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCT 736
                |  | ||||||   ||||| | | | ||||| || ||||| |  |||||||| || ||||
Db          907 CCAATGCCAAGAACACAGGCGCCTCAGTGGGCCAGAAGGGCATCCTGCAGTGCGAGGCCT 966

Qy          737 CAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAA 796
                | || || |||   ||||| || ||||||| |||||| ||||  ||  |     | ||
Db          967 CGGCTGTTCCCGTGGCAGAGTTTCAGTGGTTCAAGGAGGACACCAGGTTAGCAAATGGGC 1026

Qy          797 AGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCT 856
                 | | || |||    | || | ||       |||||| |  || | |||||||||||| |
Db         1027 TGGAGGGCGTGCGGATCGAGAGCAAGGGCCGCCTCTCGACGCTGACCTTCTTCAATGTGT 1086

Qy          857 CTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATG 916
                | ||  | |||||||| |||||||| || |||||| | |||||| ||||| |||||||||
Db         1087 CGGAGAAGGACTATGGCAACTACACGTGTGTGGCCACAAACAAGTTGGGCAACACCAATG 1146

Qy          917 CCAGCATCATGCTAT-TTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGG 975
                |||||||||| || |   || || || || ||   |||     |||| |   | ||  ||
Db         1147 CCAGCATCATCCTGTACGGGCCCCGGAGCGGTGCACGACAGTGGCAATGCAGCCTCCCGG 1206

Qy          976 AGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGA 1035
                   || |   || |||| ||   | |    ||  ||   | ||| || ||| | ||||||
Db         1207 GCAGCCGCTGGCCTCTGCCTCTGGGCCACCCTCCTCGCTCGCCTCCTCCTCGACTTTTGA 1266


RESULT 11
CR548212
LOCUS       CR548212                 600 bp    mRNA    linear   EST 12-JUL-2004
DEFINITION  DKFZp459M1538_r1 459 (synonym: pcor1) Pongo pygmaeus cDNA clone
            DKFZp459M1538 5', mRNA sequence.
ACCESSION   CR548212
VERSION     CR548212.1  GI:50241868
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical
            Research Center at the Heinrich-Heine-University,
            Duesseldorf/Germany) within the cDNA sequencing consortium of the
            German Genome Project. This clone (DKFZp459M1538) is available at
            the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum,
            Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email:
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            clone@rzpd.de Further information about the clone and the
            sequencing project is available at
            http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1..600
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp459M1538"
                     /tissue_type="cortex"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="459 (synonym: pcor1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
ORIGIN

  Query Match             52.6%;  Score 544;  DB 7;  Length 600;
  Best Local Similarity   99.1%;  Pred. No. 8.7e-147;
  Matches  547;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        395 TGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACA 454
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         49 TTCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACA 108

Qy        455 ATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACA 514
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 ATATCAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACA 168

Qy        515 TCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCA 574
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 TCTCCCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCA 228

Qy        575 CCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGG 634
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 CCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGG 288

Qy        635 TACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAG 694
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 TACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAG 348

Qy        695 GTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAG 754
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAG 408

Qy        755 AATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGG 814
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        409 AATTCCAGTGGTGCAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGG 468

Qy        815 AAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGA 874
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 AAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGA 528

Qy        875 ACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTG 934
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        529 ACTACACTTGCGTGGCCTCCAACAAACTGGGCCACACCAATGCCAGCATCATGCTATTTG 588

Qy        935 GTCCAGGCGCCG 946
              ||||||||||||
Db        589 GTCCAGGCGCCG 600


RESULT 12
CF737474
LOCUS       CF737474                 759 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  UI-M-HD0-cks-o-09-0-UI.r1 NIH_BMAP_HD0 Mus musculus cDNA clone
            IMAGE:30614264 5', mRNA sequence.
ACCESSION   CF737474
VERSION     CF737474.1  GI:37633810
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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REFERENCE   1  (bases 1 to 759)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1..759
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30614264"
                     /tissue_type="whole eye"
                     /dev_stage="embryo 12.5,13.5,14.5 dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_HD0"
                     /note="Organ: Eye; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I;  The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel.First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site .Double strand cDNA was
                     size selected according to mRNA size fraction ,ligated
                     with EcoR I adaptor , digested with NotI and then cloned
                     directionally into pYX-Asc vector . The library tag
                     sequence located between the Not I site and the polyA tail
                     is TTATTGAAGT. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH)."
ORIGIN

  Query Match             52.4%;  Score 542.4;  DB 7;  Length 759;
  Best Local Similarity   90.2%;  Pred. No. 2.7e-146;
  Matches  590;  Conservative    0;  Mismatches   63;  Indels    1;  Gaps    1;

Qy         81 AGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGT 140
              ||||||||| ||||| ||||||||||||||||| ||||||||||||||||||||||||||
Db        101 AGGAGTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAACGTGACGGT 160

Qy        141 CCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGC 200
              | ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||
Db        161 CAGGCAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCGGGTGGC 220

Qy        201 CTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCG 260
              ||||||||||||||| ||||||||||||||||| ||||||||||||||||| ||||||||
Db        221 CTGGCTAAACCGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGATCCTCG 280

Qy        261 CGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGT 320
               |||||||| ||||| |||||||| || ||||||||||| ||||||||||| ||||||||
Db        281 TGTGGTCCTCCTGAGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGTGGATGT 340

Qy        321 GTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAG 380
              ||| || ||||||||||| ||||||||||| ||||||||||||||||| |||||||| ||
Db        341 GTACGATGAGGGCCCTTATACCTGCTCGGTACAGACAGACAACCACCCTAAGACCTCCAG 400

Qy        381 GGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 440
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        401 GGTCCACCTCATTGTACAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCAT 460

Qy        441 TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGT 500
              ||||||||||||||| || |||||||| |||||||| || |||||||| |||||||| ||
Db        461 TAATGAAGGGAACAACATCAGCCTCACTTGCATAGCCACAGGTAGACCGGAGCCTACAGT 520
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Qy        501 TACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA 560
               || |||||||| || |||||||| || ||||||||||||||||| || || ||| ||||
Db        521 AACCTGGAGACATATTTCTCCCAAGGCCGTTGGCTTTGTGAGTGAGGATGAGTACCTGGA 580

Qy        561 AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGT 620
               || ||||||||||| ||||| |||||||| || ||||||||||| |||||||| |||||
Db        581 GATCCAGGGCATCACTCGGGAACAGTCAGGCGAGTACGAGTGCAGCGCCTCCAACGACGT 640

Qy        621 GGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGA 680
              ||| || || |||||||| ||||| |||||||||||| |||||||||||||||| |||
Db        641 GGCGGCACCAGTGGTACGAAGAGTGAAGGTCACCGTGNACTATCCACCATACATCTCAAG 700

Qy        681 AGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGC 734
              ||| ||||| ||||||||||||||||| ||| |  |||| ||||||||||||||
Db        701 AGCTAAGGGCACAGGTGTCCCCGTGGGGCAAGA-NGGACTCTGCAGTGTGAAGC 753


RESULT 13
BI666583
LOCUS       BI666583                 865 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603291469F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310833 5',
            mRNA sequence.
ACCESSION   BI666583
VERSION     BI666583.1  GI:15580816
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 865)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11787  row: j  column: 18
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FEATURES             Location/Qualifiers
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                     /note="Organ: brain; Vector: pBluescriptR (modified
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                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length  clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

  Query Match             52.3%;  Score 541;  DB 4;  Length 865;
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  Matches  552;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 60
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Db        183 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 242

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Qy        121 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 180
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Qy        421 ATTTCTTCAGATATCTCCATTAATGAAGGGAAC-AATATTAGCCTCACCTGCATAGCAAC 479
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Qy        480 TGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGT 539
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Qy        540 GAGTGAAGACGAA 552
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RESULT 14
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LOCUS       BE263639                 545 bp    mRNA    linear   EST 13-JUL-2000
DEFINITION  601192064F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536127 5',
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ACCESSION   BE263639
VERSION     BE263639.1  GI:9137183
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 545)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Plate: LLCM217  row: p  column: 16
            High quality sequence stop: 545.
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                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
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                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
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                  insert size 1.8kb.  Library constructed by Ling Hong in
                  the laboratory of Gerald M. Rubin (University of
                  California, Berkeley) using  ZAP-cDNA synthesis kit
                  (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match             51.3%;  Score 531.4;  DB 2;  Length 545;
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Qy        451 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 510
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Qy        511 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 570
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Qy        631 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 690
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Qy        810 AGTGG 814
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Db        541 AGTGG 545


RESULT 15
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LOCUS       BI551784                 732 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603197479F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277115 5',
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ACCESSION   BI551784
VERSION     BI551784.1  GI:15439096
KEYWORDS    EST.
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  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 732)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11699  row: m  column: 20
            High quality sequence stop: 732.
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                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for  average
                     insert size 2.5 kb and normalized to ROT 5. This is a
                     primary library enriched for  full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health).  Note: this
                     is a NIH_MGC Library."
ORIGIN

  Query Match             50.3%;  Score 521;  DB 4;  Length 732;
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  Matches  543;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

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Qy         61 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
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Qy        181 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 240
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Job time : 3837.97 secs

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                          GenCore version 5.1.6
               Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:         June 16, 2005, 11:41:38 ; Search time 5167 Seconds
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                                          3225.971 Million cell updates/sec

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Perfect score:  1806
Sequence:       1 MKTIQPKMHNSISWAIFTGL..........RRAGCVWLLPLLVLHLLLKF 344

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                Ygapop 10.0 , Ygapext  0.5
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                Delop   6.0 , Delext   7.0

Searched:       4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:      9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Command line parameters:
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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   16     1644     91.0    1104  6  AX665346                  AX665346 Sequence
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   24     1428     79.1    1058  5  AF292935                  AF292935 Gallus ga
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   39     1268     70.2    3110  6  AX665340                  AX665340 Sequence
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   85   768.5   42.6    5605  9  BC036771                BC036771 Homo sapi
   86     761   42.1    1017  6  AX644995                AX644995 Sequence
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   88     757   41.9    1136  6  AX644997                AX644997 Sequence
   89   755.5   41.8    2070  5  BC080221                BC080221 Danio rer
   90   755.5   41.8    2455  5  AF241637                AF241637 Danio rer
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c  93     704   39.0 203572  9  AC016769                AC016769 Homo sapi
c  94     670   37.1 197553  2  AC146103                AC146103 Pan trogl
   95   656.5   36.4    4323  10  AK122576                AK122576 Mus muscu
   96     652   36.1    5666  6  AX740565                AX740565 Sequence
   97     632   35.0     537  6  AX593044                AX593044 Sequence
   98     599   33.2     786  5  GGA132998               AJ132998 Gallus Ga
   99     578   32.0     452  6  AX079423                AX079423 Sequence
  100     545   30.2     333  6  AX907426                AX907426 Sequence
  101     545   30.2     333  6  BD042959                BD042959 Sequence
  102   509.5   28.2     531  6  CQ719449                CQ719449 Sequence
  103   490.5   27.2     585  6  AX079674                AX079674 Sequence
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  105     430   23.8     504  6  CQ715694                CQ715694 Sequence
  106   429.5   23.8   20731  9  AP004721                AP004721 Homo sapi
  107   429.5   23.8   43087  9  AP005155                AP005155 Homo sapi
  108   424.5   23.5 168745  2  AC119552                AC119552 Rattus no
  109   424.5   23.5 248329  2  AC109989                AC109989 Rattus no
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c 111   400.5   22.2     408  6  AX684132                AX684132 Sequence
  112   391.5   21.7     540  6  AX665354                AX665354 Sequence
  113   391.5   21.7 116069  2  AP000784                AP000784 Homo sapi
c 114   391.5   21.7 123320  9  AP000863                AP000863 Homo sapi
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  116   391.5   21.7 177102  2  AP002808                AP002808 Homo sapi
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  118     382   21.2 184012  10  AC116523                AC116523 Mus muscu
c 119     382   21.2 242565  2  AC094728                AC094728 Rattus no
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  121     378   20.9     371  6  CQ731074                CQ731074 Sequence
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  129   338.5   18.7    1242  6  CQ607488                CQ607488 Sequence
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  131     336   18.6     292  6  CQ716587                CQ716587 Sequence
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  134   308.5   17.1    3927  3  DMU78177                U78177 Drosophila
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  137   303.5   16.8     950  3  AY052162                AY052162 Drosophil
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  148   297.5   16.5    2135  3  DROAMA                  M23561 D.melanogas
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  151   297.5   16.5  84246  3  AC002512                AC002512 Drosophil
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  156   290.5   16.1    8546  6  AX828406                AX828406 Sequence
  157   290.5   16.1    8546  9  HSA306906               AJ306906 Homo sapi
  158   290.5   16.1   18207  6  AX828384                AX828384 Sequence
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  162   284.5   15.8    1710  6  CQ588165                CQ588165 Sequence
  163   283.5   15.7    2583  10  MMNCAMR                 Y00051 Mouse mRNA
  164   282.5   15.6    2262  10  MMNCAMRI                X15049 Mouse commo
  165   282.5   15.6    2544  10  BC011310                BC011310 Mus muscu
  166   279.5   15.5    2178  5  AB008162                AB008162 Xenopus l
  167     279   15.4 237376  2  AC124949                AC124949 Rattus no
c 168     279   15.4 277228  2  AC106911                AC106911 Rattus no
  169   278.5   15.4    1580  5  CR354352                CR354352 Gallus ga
  170   278.5   15.4   12699  5  D83390                  D83390 Gallus gall
  171   277.5   15.4    3170  10  RNNCAM14                X06564 Rat mRNA fo
  172   277.5   15.4    3720  5  XELNCAM                 M25696 X.laevis ne
  173   277.5   15.4    4454  5  BC081181                BC081181 Xenopus l
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  175     276   15.3    2799  9  HSNCAME                 X16841 Human mRNA
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  178     276   15.3    3266  6  CQ728451                CQ728451 Sequence
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  181     276   15.3    8513  6  AX207284                AX207284 Sequence
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  183     275   15.2    2633  6  AR380405                AR380405 Sequence
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  185     274   15.2    5807  6  AR447664                AR447664 Sequence
  186   273.5   15.1    2118  6  AR506699                AR506699 Sequence
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  190     273   15.1 191071  9  AP004248                AP004248 Homo sapi
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  192   272.5   15.1    3971  5  CHKCONNE                D16541 Gallus gall
  193     272   15.1 131490  10  AC122207                AC122207 Mus muscu
  194     272   15.1 177251  10  AC124565                AC124565 Mus muscu
  195   271.5   15.0    4321  6  AX921112                AX921112 Sequence
c 196   271.5   15.0 169582  2  AC102190                AC102190 Mus muscu
  197     271   15.0    4050  9  BC047244                BC047244 Homo sapi
  198   270.5   15.0    3814  5  XELNCAMA                M76710 Xenopus lae
  199     270   15.0    2190  6  CQ604731                CQ604731 Sequence
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c 201     270   15.0 186110  2  AC102204                AC102204 Mus muscu
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c 203     269   14.9 142000  9  AC078813                AC078813 Homo sapi
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  223     262   14.5    3738  5  AY029401                AY029401 Danio rer
  224     262    14.5 134184  2  AC150028                    AC150028 Canis fam
  225   261.5    14.5   1314  9  AF538973                    AF538973 Homo sapi
  226   261.5    14.5   4619  5  GGF11                       X14877 Gallus gall
  227   261.5    14.5   4991  5  GGCONTAC                    Y00813 Chicken mRN
  228   261.5    14.5  18848  4  OCY14852                    Y14852 Oryctolagus
  229     261    14.5    863  5  BX935847                    BX935847 Gallus ga
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  233   260.5    14.4   1956  3  AF134113                    AF134113 Drosophil
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  235   260.5    14.4   2113  6  CQ585189                    CQ585189 Sequence
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  239     259    14.3  23887  9  HSTITINN2                   X90569 H.sapiens m
  240     259    14.3  93801  6  BD186121                    BD186121 Preventio
  241     259    14.3  93805  6  CQ730837                    CQ730837 Sequence
  242     259    14.3 103053  6  CQ848088                    CQ848088 Sequence
  243   258.5    14.3   4272  6  CQ715893                    CQ715893 Sequence
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c 246     258    14.3 277603  2  AC079543                    AC079543 Mus muscu
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  248     256    14.2   2110  3  DROLACH                     L13255 Fruitfly la
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  251   255.5    14.1   2726  5  AY029402                    AY029402 Danio rer
c 252   255.5    14.1 202505  2  AP000912                    AP000912 Homo sapi
  253   254.5    14.1  15597  3  AF074901                    AF074901 Caenorhab
  254   253.5    14.0   2116  6  AX058616                    AX058616 Sequence
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  256     252    14.0 187746  2  AC087123                    AC087123 Mus muscu
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  273   249.5    13.8   4306  9  AK124736                    AK124736 Homo sapi
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  277   249.5    13.8   4548  9  HSTAG1A                     X67734 H.sapiens m
  278   249.5    13.8   6137  6  CQ870414                    CQ870414 Sequence
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  280   248.5    13.8    295  6  CQ732164                    CQ732164 Sequence
  281   248.5    13.8   1880  6  AX714170                    AX714170 Sequence
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  284     248    13.7   2229  6  CQ729908                    CQ729908 Sequence
c 285     248    13.7  74368  9  AL391239                    AL391239 Human DNA
c 286     248    13.7 131457  9  AL356600                    AL356600 Human DNA
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c 288     248    13.7 214942 10   AC125214                    AC125214 Mus muscu
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  312     245    13.6 212752  9  AC063977                    AC063977 Homo sapi
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c 314   244.5    13.5 163120  5  BX296535                    BX296535 Zebrafish
c 315   244.5    13.5 180842  2  CR536619                    CR536619 Danio rer
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  320   243.5    13.5   3648  9  AY369208                    AY369208 Homo sapi
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  324   241.5    13.4   3412  4  BOVF3F11C                   D32135 Bovine mRNA
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c 332     241    13.3 242260  2  AC094567                    AC094567 Rattus no
c 333     241    13.3 255120  2  AC127219                    AC127219 Rattus no
  334     240    13.3  12667 10   MUSPERPA                    M77174 Mouse perle
  335     239    13.2   1174  5  BC078550                    BC078550 Xenopus l
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  364   233.5    12.9   3904  6  CQ875308                    CQ875308 Sequence
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c 366   233.5    12.9   8410  6  CQ603803                    CQ603803 Sequence
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c 368   233.5    12.9 169534  3  AC008350                    AC008350 Drosophil
c 369   233.5    12.9 302225  3  AE003458                    AE003458 Drosophil
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  372   232.5   12.9   1073  5   DRU63292            U63292 Danio rerio
  373   232.5   12.9   2611  10  AF115400             AF115400 Mus muscu
c 374   232.5   12.9  36859  3   U80022              U80022 Caenorhabdi
  375   232.5   12.9 126899  3   AY130758            AY130758 Caenorhab
  376     232   12.8   7876  6   AX592082            AX592082 Sequence
  377     232   12.8   8270  6   AX592092            AX592092 Sequence
  378     232   12.8 152686  2   AC018913            AC018913 Homo sapi
  379   231.5   12.8   3218  5   D86505              D86505 Xenopus lae
  380   231.5   12.8   3821  10  MUSLRAM              L02844 Mus musculu
  381   231.5   12.8 173270  9   AC024886            AC024886 Homo sapi
  382     231   12.8   3087  10  AB032602             AB032602 Mus muscu
  383     231   12.8   3346  6   CQ728965            CQ728965 Sequence
  384     231   12.8   3442  6   BD190857            BD190857 Secreted
  385     231   12.8   3530  9   AB003592            AB003592 Homo sapi
  386     231   12.8   4189  10  AF317839             AF317839 Mus muscu
  387   230.5   12.8   1766  6   CQ731700            CQ731700 Sequence
  388   230.5   12.8   2855  10  RNU34985             U34985 Rattus norv
  389   230.5   12.8   2869  6   A72401              A72401 Sequence 2
  390   230.5   12.8   2869  6   AR043363            AR043363 Sequence
  391   230.5   12.8   2869  6   I60497              I60497 Sequence 2
  392   230.5   12.8   2869  6   AR217165            AR217165 Sequence
  393   230.5   12.8   4988  5   BC066766            BC066766 Danio rer
  394   230.5   12.8   5868  10  BC066106             BC066106 Mus muscu
  395   230.5   12.8   8455  6   CQ870409            CQ870409 Sequence
  396   230.5   12.8  10976  6   CQ869763            CQ869763 Sequence
  397     230   12.7   2610  6   AR043379            AR043379 Sequence
  398     230   12.7   2610  6   CQ847968            CQ847968 Sequence
  399     230   12.7   2610  6   I60505              I60505 Sequence 17
  400     230   12.7   2610  6   AR217181            AR217181 Sequence
  401     230   12.7   2659  10  AK129481             AK129481 Mus muscu
  402     230   12.7   2666  9   AF006464            AF006464 Homo sapi
  403     230   12.7   2692  9   AY358128            AY358128 Homo sapi
  404     230   12.7  13793  9   HSBMHSP             X62515 H.sapiens m
  405   229.5   12.7   2004  6   AX834890            AX834890 Sequence
  406   229.5   12.7   2004  9   AK097578            AK097578 Homo sapi
  407     229   12.7   5396  5   AF388036            AF388036 Xenopus l
  408   228.5   12.7   3707  10  BC065142             BC065142 Mus muscu
  409   228.5   12.7   3893  10  AY505341             AY505341 Mus muscu
  410   228.5   12.7   3980  5   AF064799            AF064799 Danio rer
  411     228   12.6   3613  10  BC076594             BC076594 Mus muscu
  412   227.5   12.6   1954  10  AB114443             AB114443 Rattus no
  413   227.5   12.6   3341  10  D87212               D87212 Rattus norv
  414   227.5   12.6   3788  5   CHKKLGG             M63437 Chicken KLG
c 415   227.5   12.6 211829  10  AL645854             AL645854 Mouse DNA
  416     227   12.6   4009  6   AX405987            AX405987 Sequence
  417     227   12.6   4036  9   AB037776            AB037776 Homo sapi
  418     227   12.6   4230  10  BC040281             BC040281 Mus muscu
  419     227   12.6   4542  6   CQ718773            CQ718773 Sequence
  420     227   12.6  13149  6   CQ728817            CQ728817 Sequence
  421     227   12.6 186110  2   AC102204            AC102204 Mus muscu
  422   226.5   12.5   1801  10  BC078966             BC078966 Rattus no
  423   226.5   12.5   3870  10  BC036291             BC036291 Mus muscu
  424     226   12.5   5171  5   BC060500            BC060500 Xenopus l
  425     226   12.5  46638  3   CEU33058            U33058 Caenorhabdi
  426     226   12.5  46996  3   U88310              U88310 Caenorhabdi
  427     226   12.5  65649  3   AF003131            AF003131 Caenorhab
  428     226   12.5 294136  2   AC006901            AC006901 Caenorhab
  429     226   12.5 299719  2   AC006858            AC006858 Caenorhab
  430   225.5   12.5   3328  10  MMU37708             U37708 Mus musculu
  431   225.5   12.5   3352  10  MMU37709             U37709 Mus musculu
  432     225   12.5   2607  6   AX179390            AX179390 Sequence
  433     225   12.5   2607  6   AX259864            AX259864 Sequence
  434     225   12.5   5586  6   CQ729937            CQ729937 Sequence
  435     225   12.5  14327  9   HUMHSPG2B           M85289 Human hepar
c 436     225   12.5  39158  3   CBRG19K24           AC087734 Caenorhab
  437   224.5   12.4   2404  6   CQ728038            CQ728038 Sequence
  438   224.5   12.4   2611  10  AF115401             AF115401 Mus muscu
  439   224.5   12.4   3960  6   CQ849821            CQ849821 Sequence
  440   224.5   12.4   3960  9   AK126878            AK126878 Homo sapi
  441   224.5   12.4   7642  6   CQ776627            CQ776627 Sequence
  442   224.5   12.4   7642  6   AX818174            AX818174 Sequence

  443   224.5   12.4   7642  9   AF002246            AF002246 Homo sapi
  444   224.5   12.4   7647  6   AR454602            AR454602 Sequence
  445     224   12.4   2436  9   HSM805023           AL833710 Homo sapi
  446     224   12.4   2500  6   CQ783752            CQ783752 Sequence
  447     224   12.4   2500  6   BD127814            BD127814 Primer fo
  448     224   12.4   2500  9   AK074921            AK074921 Homo sapi
  449     224   12.4   3662  6   BD172466            BD172466 Secreted
  450     224   12.4   3662  6   BD172785            BD172785 Secreted
  451     224   12.4   3662  6   BD173104            BD173104 Secreted
  452     224   12.4   3662  6   BD173423            BD173423 Secreted
  453     224   12.4   3662  6   BD175457            BD175457 Secretory
  454     224   12.4   3662  6   AR410836            AR410836 Sequence
  455     224   12.4   3662  6   AR439200            AR439200 Sequence
  456     224   12.4   3662  6   AR473220            AR473220 Sequence
  457     224   12.4   3662  6   AR527206            AR527206 Sequence
  458     224   12.4   3662  6   AR566239            AR566239 Sequence
  459     224   12.4   3662  6   AX098383            AX098383 Sequence
  460     224   12.4   3662  6   AX697698            AX697698 Sequence
  461     224   12.4   3662  6   BD075606            BD075606 Secretory
  462     224   12.4   3662  9   AY358295            AY358295 Homo sapi
  463     224   12.4   3810  10  AF531873             AF531873 Mus muscu
  464     224   12.4   3864  9   AY505340            AY505340 Homo sapi
  465     224   12.4   4053  6   BD172468            BD172468 Secreted
  466     224   12.4   4053  6   BD172787            BD172787 Secreted
  467     224   12.4   4053  6   BD173106            BD173106 Secreted
  468     224   12.4   4053  6   BD173425            BD173425 Secreted
  469     224   12.4   4053  6   BD175459            BD175459 Secretory
  470     224   12.4   4053  6   AR410838            AR410838 Sequence
  471     224   12.4   4053  6   AR439202            AR439202 Sequence
  472     224   12.4   4053  6   AR473222            AR473222 Sequence
  473     224   12.4   4053  6   AR527208            AR527208 Sequence
  474     224   12.4   4053  6   AR528627            AR528627 Sequence
  475     224   12.4   4053  6   AR566241            AR566241 Sequence
  476     224   12.4   4053  6   AX056647            AX056647 Sequence
  477     224   12.4   4053  6   AX098387            AX098387 Sequence
  478     224   12.4   4053  6   AX464218            AX464218 Sequence
  479     224   12.4   4053  6   AX697702            AX697702 Sequence
  480     224   12.4   4053  6   BD075608            BD075608 Secretory
  481     224   12.4   4053  9   AY358288            AY358288 Homo sapi
  482     224   12.4   4256  10  BC076578             BC076578 Mus muscu
  483     223   12.3   1254  10  AB183401             AB183401 Mus muscu
  484     223   12.3   1254  10  AY351388             AY351388 Mus muscu
  485     223   12.3   1674  9   BC047021            BC047021 Homo sapi
  486     223   12.3 184716  2   AC018368            AC018368 Homo sapi
c 487     223   12.3 213331  2   AC125960            AC125960 Rattus no
  488   222.5   12.3   3795  10  MUSCD22A             L16928 Mus musculu
  489   222.5   12.3  95745  9   AL359510            AL359510 Human DNA
  490     222   12.3   4783  6   E34509              E34509 Novel rpoA.
  491     222   12.3   4783  6   E34511              E34511 Novel ratA.
  492     222   12.3   4783  6   E34513              E34513 Novel utili
  493     222   12.3   4783  6   E34515              E34515 Human LIG-1
c 494     222   12.3   7171  6   CQ604730            CQ604730 Sequence
  495     222   12.3 100002  2   AC020372            AC020372 Drosophil
c 496     222   12.3 149801  2   CR382301            CR382301 Danio rer
  497     222   12.3 156022  2   BX324195            BX324195 Danio rer
  498     222   12.3 157314  2   CR352289            CR352289 Danio rer
  499     222   12.3 168601  3   AC007471            AC007471 Drosophil
c 500     222   12.3 180916  2   CR381704            CR381704 Danio rer
  501     222   12.3 201070  5   BX004830            BX004830 Zebrafish
  502     222   12.3 271696  3   AE003835            AE003835 Drosophil
  503   221.5   12.3   1112  9   AB094146            AB094146 Homo sapi
  504   221.5   12.3   1112  10  AB092414             AB092414 Mus muscu
  505   221.5   12.3   5314  5   BC074401            BC074401 Xenopus l
  506     221   12.2   1308  3   AF456362            AF456362 Caenorhab
  507     221   12.2   4525  9   HSM805354           AL834139 Homo sapi
  508     221   12.2   5374  9   AF289030            AF289030 Homo sapi
  509     221   12.2   5387  6   CQ731799            CQ731799 Sequence
  510     221   12.2   6110  9   AF023449            AF023449 Homo sapi
  511     221   12.2   6413  9   AF023450            AF023450 Homo sapi
  512     221   12.2   6435  5   AF461119            AF461119 Xenopus l
  513     221   12.2   6649  9   AF217525            AF217525 Homo sapi
  514   220.5   12.2   1011  10  AB183402             AB183402 Mus muscu
  515   220.5   12.2   1287  10  AB183400             AB183400 Mus muscu
  516   220.5   12.2   1329   6  BD261770        BD261770 12 human
  517   220.5   12.2   1329   9  CR457157        CR457157 Homo sapi
  518   220.5   12.2   1338  10   AB183399        AB183399 Mus muscu
  519   220.5   12.2   1413   6  BD140567        BD140567 Polypepti
  520   220.5   12.2   1413   6  AR429086        AR429086 Sequence
  521   220.5   12.2   1413   6  AR534977        AR534977 Sequence
  522   220.5   12.2   1413   6  AX375966        AX375966 Sequence
  523   220.5   12.2   1413   9  AY358334        AY358334 Homo sapi
  524   220.5   12.2   1448   9  BC035930        BC035930 Homo sapi
  525   220.5   12.2   1450  10   AB064265        AB064265 Mus muscu
  526   220.5   12.2   1508   6  BD261716        BD261716 12 human
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  528   220.5   12.2   1548   6  AX136299        AX136299 Sequence
  529   220.5   12.2   1548   6  BD123602        BD123602 Secretory
  530   220.5   12.2   1548   9  AK075502        AK075502 Homo sapi
  531   220.5   12.2   1598   6  BD247472        BD247472 Molecules
  532   220.5   12.2   1598   6  AR278813        AR278813 Sequence
  533   220.5   12.2   1817  10   AF539424        AF539424 Mus muscu
  534   220.5   12.2   1862   6  AX399846        AX399846 Sequence
  535   220.5   12.2   1935   6  BD247473        BD247473 Molecules
  536   220.5   12.2   1935   6  AR278814        AR278814 Sequence
  537   220.5   12.2   1958  10   BC057125        BC057125 Mus muscu
  538   220.5   12.2   2024  10   AB052293        AB052293 Mus muscu
  539   220.5   12.2   2940   6  CQ870000        CQ870000 Sequence
  540   220.5   12.2   4444  10   AF434663        AF434663 Mus muscu
  541     220   12.2   2845   6  CQ716675        CQ716675 Sequence
  542     220   12.2   4717   6  AX463544        AX463544 Sequence
  543     220   12.2   4759   6  AX463530        AX463530 Sequence
  544     220   12.2   5287   9  AB050468        AB050468 Homo sapi
  545     220   12.2   5719   6  CQ869705        CQ869705 Sequence
  546   219.5   12.2    991   5  AF364047        AF364047 Gallus ga
  547   219.5   12.2   1247   5  BC078527        BC078527 Xenopus l
  548   219.5   12.2   1258   9  AF005070        AF005070 Homo sapi
  549   219.5   12.2   2259   6  BD204924        BD204924 Novel mol
  550   219.5   12.2   3512   9  AF132811        AF132811 Homo sapi
  551   219.5   12.2   3534   9  AY027658        AY027658 Homo sapi
  552   219.5   12.2   4002   9  BC075829        BC075829 Homo sapi
  553   219.5   12.2   4277   6  AX376372        AX376372 Sequence
  554   219.5   12.2   4277   6  AX454572        AX454572 Sequence
  555   219.5   12.2   4277   6  AX491050        AX491050 Sequence
  556   219.5   12.2   4277   6  AX696989        AX696989 Sequence
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  560     219   12.1    756   6  CQ729341        CQ729341 Sequence
  561     219   12.1   2638   6  AX833755        AX833755 Sequence
  562     219   12.1   2638   9  AK095729        AK095729 Homo sapi
  563     219   12.1   3210   5  AB015205        AB015205 Xenopus l
  564     219   12.1   3690   9  AF549455        AF549455 Homo sapi
  565     219   12.1   4129   6  CQ849703        CQ849703 Sequence
  566     219   12.1   4129   9  AK126745        AK126745 Homo sapi
  567     219   12.1   4762   9  AF381545        AF381545 Homo sapi
  568     219   12.1   4805   9  AY730707        AY730707 Homo sapi
  569     219   12.1   4822   6  E12950          E12950 cDNA GA3-43
  570     219   12.1   4822  10   D78572          D78572 Mus musculu
  571     219   12.1   4832   6  CQ869702        CQ869702 Sequence
  572     219   12.1   5035   9  AY090737        AY090737 Homo sapi
  573     219   12.1  12255   5  AJ584653        AJ584653 Gallus ga
  574   218.5   12.1   1425   6  CQ725721        CQ725721 Sequence
  575   218.5   12.1   4015   9  BC030141        BC030141 Homo sapi
  576   218.5   12.1   4020   6  CQ870598        CQ870598 Sequence
  577   218.5   12.1   6922  10   MMU17793        Y17793 Mus musculu
c 578   218.5   12.1 152686   2  AC018913        AC018913 Homo sapi
  579     218   12.1   1689   9  AB056375        AB056375 Macaca fa
  580     218   12.1   1884   6  CQ734341        CQ734341 Sequence
  581     218   12.1   2350   6  CQ878954        CQ878954 Sequence
  582     218   12.1   3958   9  AF531872        AF531872 Homo sapi
  583     218   12.1   4191   6  CQ789354        CQ789354 Sequence
  584     218   12.1   4191   9  AF531868        AF531868 Homo sapi
  585     218   12.1   4191   9  HSU40271        U40271 Homo sapien
  586     218   12.1   4193   6  CQ715771        CQ715771 Sequence
  587     218   12.1   4238   9  BC071557        BC071557 Homo sapi
  588     218   12.1   6267  10   AF315558        AF315558 Mus muscu

  589     218   12.1   6656  10   AF334385        AF334385 Rattus no
  590     218   12.1   6829  10   AY005483        AY005483 Mus muscu
  591     218   12.1 146352   2  CR548641        CR548641 Danio rer
  592     218   12.1 186279   5  BX950870        BX950870 Zebrafish
c 593     218   12.1 191779   2  CR376789        CR376789 Danio rer
  594     217   12.0   3429   4  SSC459296       AJ459296 Sus scrof
  595     217   12.0   4410   3  AY118274        AY118274 Drosophil
  596     217   12.0  41345   3  CEF15G9         Z47068 Caenorhabdi
  597   216.5   12.0   3057   6  CQ842487        CQ842487 Sequence
  598   216.5   12.0   3057   9  AK125460        AK125460 Homo sapi
  599   216.5   12.0   4054   3  MSU50719        U50719 Manduca sex
  600   216.5   12.0   4430  10   BC062892        BC062892 Mus muscu
c 601     216   12.0 260998   2  AC099089        AC099089 Rattus no
  602   215.5   11.9   2957   6  CQ591957        CQ591957 Sequence
  603   215.5   11.9   3264   3  AY119465        AY119465 Drosophil
  604   215.5   11.9   3397   6  AX780431        AX780431 Sequence
  605   215.5   11.9   3397   9  AF312678        AF312678 Homo sapi
  606   215.5   11.9   3498  10   RNU81035        U81035 Rattus norv
  607   215.5   11.9   3853   3  DRONRGAA        M28231 Drosophila
  608   215.5   11.9   4041   6  CQ573942        CQ573942 Sequence
  609   215.5   11.9   4044   9  BC002377        BC002377 Homo sapi
  610   215.5   11.9   4044   9  BC014626        BC014626 Homo sapi
  611   215.5   11.9   4433   3  AY058284        AY058284 Drosophil
c 612   215.5   11.9   5026   6  CQ591956        CQ591956 Sequence
  613   215.5   11.9   8574   3  DMNRG2          AF050085 Drosophil
  614   215.5   11.9   8883  10   AY273816        AY273816 Rattus no
  615   215.5   11.9  20510   6  CQ573941        CQ573941 Sequence
  616   215.5   11.9  62442   2  AC018325        AC018325 Drosophil
c 617   215.5   11.9  71320   2  AC020124        AC020124 Drosophil
  618   215.5   11.9 166512   3  AC099010        AC099010 Drosophil
c 619   215.5   11.9 174287   3  AC007977        AC007977 Drosophil
  620   215.5   11.9 174367   3  AC023696        AC023696 Drosophil
  621   215.5   11.9 185405   3  AC023743        AC023743 Drosophil
c 622   215.5   11.9 270766   3  AE003615        AE003615 Drosophil
  623   215.5   11.9 299686   3  AE003444        AE003444 Drosophil
  624     215   11.9   1332   3  AF456363        AF456363 Caenorhab
  625     215   11.9   3213   6  CQ847970        CQ847970 Sequence
  626     215   11.9   4236   9  HSU33635        U33635 Human colon
  627     215   11.9   5067   5  AF304131        AF304131 Danio rer
  628   214.5   11.9   4956  10   AF041082        AF041082 Rattus no
c 629     214   11.8  77635   2  DMBR40O10       AL122024 Drosophil
  630   213.5   11.8   1121   6  CQ727036        CQ727036 Sequence
  631   213.5   11.8   1242   9  AY046418        AY046418 Homo sapi
  632   213.5   11.8   1614   6  BD177640        BD177640 MBGP1 pol
  633   213.5   11.8   1614   6  E37854          E37854 MBGPI polyp
  634   213.5   11.8   1614   6  AX003003        AX003003 Sequence
  635   213.5   11.8   1680   9  BC033819        BC033819 Homo sapi
  636   213.5   11.8   1685   6  BD172296        BD172296 Secreted
  637   213.5   11.8   1685   6  BD172615        BD172615 Secreted
  638   213.5   11.8   1685   6  BD172934        BD172934 Secreted
  639   213.5   11.8   1685   6  BD173253        BD173253 Secreted
  640   213.5   11.8   1685   6  BD175287        BD175287 Secretory
  641   213.5   11.8   1685   6  AR410665        AR410665 Sequence
  642   213.5   11.8   1685   6  AR439029        AR439029 Sequence
  643   213.5   11.8   1685   6  AR473049        AR473049 Sequence
  644   213.5   11.8   1685   6  AR527035        AR527035 Sequence
  645   213.5   11.8   1685   6  AR528625        AR528625 Sequence
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  647   213.5   11.8   1685   6  AX454458        AX454458 Sequence
  648   213.5   11.8   1685   6  AX464214        AX464214 Sequence
  649   213.5   11.8   1685   6  AX490936        AX490936 Sequence
  650   213.5   11.8   1685   6  AX697492        AX697492 Sequence
  651   213.5   11.8   1685   6  BD075436        BD075436 Secretory
  652   213.5   11.8   1685   9  AY358332        AY358332 Homo sapi
  653   213.5   11.8   1718   6  BD247477        BD247477 Molecules
  654   213.5   11.8   1718   6  AR278800        AR278800 Sequence
  655   213.5   11.8   2496   6  BD191411        BD191411 Secreted
  656   213.5   11.8   3557   9  AF363367        AF363367 Homo sapi
  657   213.5   11.8   4155   6  AX704746        AX704746 Sequence
  658   213.5   11.8   4594   9  AB040929        AB040929 Homo sapi
  659   213.5   11.8   5384   5  AF337036        AF337036 Danio rer
  660     213   11.8    177   6  AR030585        AR030585 Sequence
  661     213   11.8    851   5  BX932255        BX932255 Gallus ga
  662    213   11.8   1605  6  CQ599856          CQ599856 Sequence
  663    213   11.8   1892  5  AB117614          AB117614 Xenopus l
  664    213   11.8   2043  6  CQ717926          CQ717926 Sequence
  665    213   11.8   4381 10   AK173340          AK173340 Mus muscu
  666    213   11.8   4479  5  AF538326          AF538326 Danio rer
  667  212.5   11.8   2650 10   AF102134          AF102134 Mus muscu
  668  212.5   11.8   2732 10   MMBIG2A           X99043 M.musculus
  669  212.5   11.8   4071  9  AF531869          AF531869 Homo sapi
  670  212.5   11.8   4631  9  HSU72391          U72391 Human neoge
  671  212.5   11.8   5021  6  CQ729613          CQ729613 Sequence
  672    212   11.7    177  6  AR030586          AR030586 Sequence
  673    212   11.7   3752 10   AY061639          AY061639 Rattus no
  674    212   11.7   4609 10   RNU35371          U35371 Rattus norv
  675  211.5   11.7   2818  3  DROPAS2A          M77165 D.melanogas
  676  211.5   11.7   2901  3  BT014661          BT014661 Drosophil
  677  211.5   11.7   3070  3  DROPAS2B          M77166 D.melanogas
  678  211.5   11.7   3132 10   MMNSK22           X86445 M.musculus
  679  211.5   11.7   3257 10   MMNSK21           X86444 M.musculus
  680  211.5   11.7   3414  6  CQ579258          CQ579258 Sequence
  681  211.5   11.7   3798 10   AF388037          AF388037 Mus muscu
  682  211.5   11.7   4376 10   BC078631          BC078631 Mus muscu
c 683  211.5   11.7   4460  2  AC020249          AC020249 Drosophil
  684  211.5   11.7   5297  6  AX587800          AX587800 Sequence
  685  211.5   11.7   5297  6  AX771417          AX771417 Sequence
  686  211.5   11.7   5297  9  HSU61262          U61262 Human neoge
  687  211.5   11.7   5506  6  AR447897          AR447897 Sequence
  688  211.5   11.7  66168  3  DMSEG0007         AL033125 Drosophil
  689  211.5   11.7 165928  3  AC023725          AC023725 Drosophil
  690  211.5   11.7 172784  3  AC105352          AC105352 Drosophil
c 691  211.5   11.7 295177  3  AE003430          AE003430 Drosophil
  692    211   11.7   1273  6  AR278799          AR278799 Sequence
  693    211   11.7   2377 10   AF195662          AF195662 Mus muscu
  694    211   11.7   3366 10   AY059393          AY059393 Mus muscu
  695    211   11.7   5563  9  AF069603          AF069603 Homo sapi
  696    211   11.7   5719  9  AF069601          AF069601 Homo sapi
  697    211   11.7  20435  9  HSAJ2535          AJ002535 Homo sapi
  698  210.5   11.7   1837  6  CQ869997          CQ869997 Sequence
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  703    210   11.6   4078  6  AR270557          AR270557 Sequence
  704    210   11.6   5193  4  AF509585          AF509585 Sus scrof
  705    210   11.6   5193  6  AX698036          AX698036 Sequence
  706    210   11.6   5193  6  AX698038          AX698038 Sequence
  707    210   11.6   5745  9  AY339601          AY339601 Homo sapi
  708    210   11.6   5770  9  AF069602          AF069602 Homo sapi
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  714    210   11.6   5926  6  AX337264          AX337264 Sequence
  715    210   11.6   5926  6  AX375038          AX375038 Sequence
  716    210   11.6   5926  6  AX410725          AX410725 Sequence
  717    210   11.6   5926  9  HSU48959          U48959 Homo sapien
  718    210   11.6   5992 10   BC058610          BC058610 Mus muscu
  719  209.5   11.6   7644  6  CQ727360          CQ727360 Sequence
  720  209.5   11.6  17193  6  CQ583538          CQ583538 Sequence
  721  209.5   11.6  58651  2  AC017558          AC017558 Drosophil
  722  209.5   11.6  69992  3  AC005421          AC005421 Drosophil
c 723  209.5   11.6 189315  3  AC008319          AC008319 Drosophil
  724  209.5   11.6 306696  3  AE003586          AE003586 Drosophil
  725    209   11.6   1248  6  CQ725953          CQ725953 Sequence
  726    209   11.6   1450  6  AX287596          AX287596 Sequence
  727    209   11.6   1489  9  AK172829          AK172829 Homo sapi
  728    209   11.6   1565  9  AF279689          AF279689 Homo sapi
  729    209   11.6   3080  6  AX287610          AX287610 Sequence
  730    209   11.6   3080  9  HSA277437         AJ277437 Homo sapi
  731    209   11.6   3112  6  AX287608          AX287608 Sequence
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  733    209   11.6   3305  9  BC036769          BC036769 Homo sapi
  734    209   11.6   3402  6  AR252460          AR252460 Sequence

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  736    209   11.6   3402  6  AX191426          AX191426 Sequence
  737    209   11.6   3402  6  AX403231          AX403231 Sequence
  738    209   11.6   3402  9  AY358303          AY358303 Homo sapi
  739  208.5   11.5   2811 10   AF487347          AF487347 Mus muscu
  740  208.5   11.5   3448 10   MUSNGP            L01991 Mus musculu
  741  208.5   11.5   3678  3  BT014656          BT014656 Drosophil
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  743  208.5   11.5   4956  9  AF040990          AF040990 Homo sapi
  744  208.5   11.5   5667  6  CQ606753          CQ606753 Sequence
  745    208   11.5   6592  6  CQ598305          CQ598305 Sequence
  746    208   11.5 152024  2  CR407703          CR407703 Danio rer
  747  207.5   11.5   2220  6  AX748214          AX748214 Sequence
  748  207.5   11.5   2220  9  AK093583          AK093583 Homo sapi
  749  207.5   11.5 188751 10   AC122038          AC122038 Mus muscu
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  752    207   11.5   2846  6  AX834922          AX834922 Sequence
  753    207   11.5   2846  9  AK097633          AK097633 Homo sapi
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  756    207   11.5 177736  3  AC005714          AC005714 Drosophil
  757    207   11.5 191467  3  AC008348          AC008348 Drosophil
  758    207   11.5 307323  3  AE003457          AE003457 Drosophil
  759  206.5   11.4    980  9  BC013797          BC013797 Homo sapi
  760    206   11.4   3762  3  AF456361          AF456361 Caenorhab
  761  205.5   11.4    708  5  CR385737          CR385737 Gallus ga
  762  205.5   11.4   1542  6  BD193028          BD193028 207 human
  763  205.5   11.4   1542  6  CQ822024          CQ822024 Sequence
  764  205.5   11.4   2067 10   AY210400          AY210400 Mus muscu
  765  205.5   11.4   2539  6  CQ782770          CQ782770 Sequence
  766  205.5   11.4   2539  6  BD127305          BD127305 Primer fo
  767  205.5   11.4   2539  9  AK074825          AK074825 Homo sapi
  768  205.5   11.4   4128 10   RNU11031          U11031 Rattus norv
  769  205.5   11.4   4465 10   MMU543322         AJ543322 Mus muscu
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  771  205.5   11.4  53424  3  AB055861          AB055861 Procambar
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  774    205   11.4   1820  6  AR278798          AR278798 Sequence
  775    205   11.4   2540  9  AF062733          AF062733 Homo sapi
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  779  204.5   11.3   6860  5  AF304130          AF304130 Danio rer
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  781    204   11.3   1038  5  BC083011          BC083011 Xenopus l
  782    204   11.3   4517 10   MMDCCTSG          X85788 M.musculus
  783    204   11.3   4784  5  GDU07644          U07644 Gallus gall
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c 785    204   11.3   5892  6  CQ588164          CQ588164 Sequence
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c 787    204   11.3 149752  9  AC004616          AC004616 Homo sapi
  788    204   11.3 174920  3  AC010701          AC010701 Drosophil
c 789    204   11.3 294272  3  AE003595          AE003595 Drosophil
  790  203.5   11.3   4435  5  AF388035          AF388035 Xenopus l
  791  203.5   11.3   5824  6  AR338581          AR338581 Sequence
  792  203.5   11.3   6811  9  AF334384          AF334384 Homo sapi
  793  203.5   11.3   6834  9  AB032958          AB032958 Homo sapi
  794  203.5   11.3   6899  9  AF491813          AF491813 Homo sapi
  795    203   11.2   2749  5  DRE574916         AJ574916 Danio rer
  796    203   11.2   2774  5  BC053245          BC053245 Danio rer
  797    203   11.2   4248  6  AX054979          AX054979 Sequence
  798    203   11.2   4775  3  CEU70618          U70618 Caenorhabdi
  799    203   11.2   6021 10   AY237726          AY237726 Mus muscu
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  801  202.5   11.2   2697  6  CQ728585          CQ728585 Sequence
  802  202.5   11.2   3801  9  AF531870          AF531870 Homo sapi
  803  202.5   11.2   4340  3  AY118645          AY118645 Drosophil
  804  202.5   11.2   8487  6  CQ717135          CQ717135 Sequence
  805  202.5   11.2   9645  6  CQ875263          CQ875263 Sequence
  806  202.5   11.2   9645  9  AF245505          AF245505 Homo sapi
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   808     202  11.2    2472  6  CQ592467          CQ592467 Sequence
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   812     202  11.2    5604  5  AF394058          AF394058 Danio rer
   813     202  11.2    5680  5  AY082380          AY082380 Danio rer
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   817   201.5  11.2    1514  6  AX645011          AX645011 Sequence
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   824     201  11.1    3400  5  FSCTRKA           L11311 Torpedo cal
   825     201  11.1    3405  5  GGA535114         AJ535114 Gallus ga
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   827     201  11.1    5130  9  AF230073          AF230073 Homo sapi
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   829   200.5  11.1    1103  6  CQ728252          CQ728252 Sequence
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   833   200.5  11.1  294540  9  HSA277892         AJ277892 Homo sapi
   834     200  11.1    1967  6  AR156834          AR156834 Sequence
   835     200  11.1    1967  6  BD269852          BD269852 The poly
   836     200  11.1    2193  10  MUSPGCBMA         J04055 Mouse basem
   837     200  11.1    2274  10  MMU293947         AJ293947 Mus muscu
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   839     200  11.1    2339  10  BC058745          BC058745 Mus muscu
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   842   199.5  11.0    3727  6  CQ726408          CQ726408 Sequence
   843   199.5  11.0    4924  10  RNU68725          U68725 Rattus norv
   844   199.5  11.0    5443  10  BC054540          BC054540 Mus muscu
   845   199.5  11.0    7855  9  AK122586          AK122586 Homo sapi
   846     199  11.0    2943  10  AY167411          AY167411 Rattus no
   847     199  11.0    3726  9  AF190637          AF190637 Homo sapi
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   854   198.5  11.0    6729  9  AF304304          AF304304 Homo sapi
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c  856   198.5  11.0  155666  3  AC007854          AC007854 Drosophil
c  857   198.5  11.0  168471  3  AC006170          AC006170 Drosophil
c  858   198.5  11.0  231562  3  AE003767          AE003767 Drosophil
   859     198  11.0    3233  6  CQ721186          CQ721186 Sequence
   860     198  11.0    3260  9  HSRNACD22         X59350 H.sapiens m
   861     198  11.0    4844  6  CQ728171          CQ728171 Sequence
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c  863     198  11.0  202887  10  AL928789          AL928789 Mouse DNA
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   866   197.5  10.9    1861  10  AF061260          AF061260 Mus muscu
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   873   197.5  10.9    4715  3  AY121698          AY121698 Drosophil
   874   197.5  10.9    4726  3  AF210316          AF210316 Drosophil
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   885   196.5  10.9    3651  10  RNU81036          U81036 Rattus norv
   886   196.5  10.9    4041  5  GGNEUFASC         X65224 G.gallus mR
   887   196.5  10.9    5822  10  RATANKBIND        L11002 Rat ankyrin
   888   196.5  10.9    6218  9  AB002341          AB002341 Homo sapi
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   896     196  10.9    2351  10  RNO536020         AJ536020 Rattus no
   897     196  10.9    7631  5  GGFMYLCK          X52876 G.gallus mR
   898     196  10.9   96468  2  AC006902          AC006902 Caenorhab
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   908     195  10.8    6318  3  DMU71002          U71002 Drosophila
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   916   194.5  10.8    3211  3  BT001692          BT001692 Drosophil
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   923   193.5  10.7     826  6  CQ780202          CQ780202 Sequence
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   935     193  10.7    4846  5  XLU10986          U10986 Xenopus lae
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  977   191.5   10.6   61468  2  AC149898        AC149898 Xenopus t
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  980   190.5   10.5    1788  6  AX287613        AX287613 Sequence
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  997     190   10.5   90803  5  AL732421        AL732421 Zebrafish
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 1012     189   10.5    2250  3  AY724774        AY724774 Caenorhab
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 1133     184   10.2    2348 10   RNMAGLR                    X05301 Rat mRNA fo
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 1138     184   10.2    4640  3  DMDTRK                     X63453 D.melanogas
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 1140     184   10.2    4645  6  CQ847776                   CQ847776 Sequence
 1141     184   10.2    4775  3  BT015249                   BT015249 Drosophil
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 1158   182.5   10.1    3252  3  AF188751                   AF188751 Caenorhab
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 1233     179    9.9     900  6  A91702                     A91702 Sequence 6
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 1253     178    9.9   1580  10  AF205078               AF205078 Mus muscu
 1254     178    9.9   2107  10  AY271309               AY271309 Rattus no
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                              ALIGNMENTS

RESULT 1
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DEFINITION  Sequence 1 from patent US 6664383.
ACCESSION   AR439648
VERSION     AR439648.1  GI:42665572
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1032)
  AUTHORS   Fukushima,D., Shibayama,S. and Tada,H.
  TITLE     Polypeptides, cDNA encoding the same and utilization thereof
  JOURNAL   Patent: US 6664383-A 1 16-DEC-2003;
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
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Score:                  1806.00        Matches:       344
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     6              Gaps:          0

US-10-017-084A-523 (1-344) x AR439648 (1-1032)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Qy          21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Qy          61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db         181 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 240

Qy          81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 300

Qy         101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db         301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360

Qy         121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db         361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420

Qy         141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480

Qy         161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db         481 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 540

Qy         181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600

Qy         201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660

Qy         221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720

Qy         241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780

Qy         261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840

Qy         281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900

Qy         301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960

Qy         321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020

Qy         341 LeuLeuLysPhe 344
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Db        1021 CTTCTCAAATTT 1032

RESULT 2
CQ768055
LOCUS       CQ768055                1679 bp    DNA     linear   PAT 04-MAR-2004
DEFINITION  Sequence 522 from Patent EP1386931.
ACCESSION   CQ768055
VERSION     CQ768055.1  GI:45108887
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wood,W.I., Goddard,A., Gurney,A., Yuan,J., Baker,K.P. and Chen,J.
  TITLE     Human neurotrimin homologue
  JOURNAL   Patent: EP 1386931-A 522 04-FEB-2004;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.19e-157      Length:         1679
Score:                  1806.00        Matches:        344
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     6              Gaps:           0

US-10-017-084A-523 (1-344) x CQ768055 (1-1679)

Qy           1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy          21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy          41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db         254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy          61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy          81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy         101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy         121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy         141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db         554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy         161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db         614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy         181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy         201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793
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Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 3
AR528639
LOCUS       AR528639                1679 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 375 from patent US 6725730.
ACCESSION   AR528639
VERSION     AR528639.1  GI:53916717
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Bollinger,C.L. Jr.
  TITLE     Crane test weight assembly and method
  JOURNAL   Patent: US 6725730-A 375 27-APR-2004;
FEATURES             Location/Qualifiers
     source          1..1679
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.19e-157     Length:        1679
Score:                  1806.00       Matches:       344
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     6             Gaps:          0

US-10-017-084A-523 (1-344) x AR528639 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 4
AX358872
LOCUS       AX358872                1679 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 125 from Patent WO0193983.
ACCESSION   AX358872
VERSION     AX358872.1  GI:18675337
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
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  JOURNAL   Patent: WO 0193983-A 125 13-DEC-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
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ORIGIN

Alignment Scores:
Pred. No.:              1.19e-157       Length:         1679
Score:                  1806.00         Matches:        344
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-017-084A-523 (1-344) x AX358872 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 5
AX362365
LOCUS       AX362365                 1679 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 125 from Patent WO0208288.
ACCESSION   AX362365
VERSION     AX362365.1  GI:18694640
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0208288-A 125 31-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.19e-157       Length:         1679
Score:                  1806.00         Matches:        344
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-017-084A-523 (1-344) x AX362365 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy         101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db         434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy         121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db         494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy         141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db         554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy         161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db         614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy         181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy         201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db         734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy         221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db         794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy         241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Db         854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy         261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy         281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db         974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy         301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Db        1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093

Qy         321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db        1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy         341 LeuLeuLysPhe 344
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Db        1154 CTTCTCAAATTT 1165

RESULT 6
AX403748
LOCUS       AX403748                1679 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 103 from Patent WO0077037.
ACCESSION   AX403748
VERSION     AX403748.1  GI:21437184
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A., Baker,K., Botstein,D., Desnoyers,L., Eaton,D.L.,
            Ferrara,N., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
            Goddard,A., Godowski,P., Gurney,A., Kljavin,I.J., Mather,J.,
            Napier,M., Pan,J., Paoni,N., Roy,M., Tumas,D., Watanabe,C.,
            Williams,P.M., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   `Patent: WO 0077037-A 103 21-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1679
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.19e-157     Length:         1679
Score:                  1806.00       Matches:        344
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     6             Gaps:           0

US-10-017-084A-523 (1-344) x AX403748 (1-1679)

Qy           1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db         134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy          21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy          41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy          61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy          81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

Qy         101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db         434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy         121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db         494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

Qy         141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db         614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy         181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db         674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy         201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db         734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy         221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db         794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy         241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Qy         261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 7
AX454470
LOCUS       AX454470                1679 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 55 from Patent WO0208284.
ACCESSION   AX454470
VERSION     AX454470.1  GI:21713859
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0208284-A 55 31-JAN-2002;
            Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
            (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
            Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
            Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
            ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
            Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
            I. (US)
FEATURES             Location/Qualifiers
     source          1..1679
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.19e-157      Length:         1679
Score:                    1806.00        Matches:        344
Percent Similarity:       100.00%        Conservative:   0
Best Local Similarity:    100.00%        Mismatches:     0
Query Match:              100.00%        Indels:         0
DB:                       6              Gaps:           0

US-10-017-084A-523 (1-344) x AX454470 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

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Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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Db        494 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 553

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Db        554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613

Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733

Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 913

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 973

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 8
AX464242
LOCUS       AX464242                1679 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 375 from Patent WO0140466.
ACCESSION   AX464242
VERSION     AX464242.1  GI:21899137
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
            Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Wood,W.L. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            same
  JOURNAL   Patent: WO 0140466-A 375 07-JUN-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.19e-157       Length:         1679
Score:                  1806.00         Matches:        344
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-017-084A-523 (1-344) x AX464242 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        134 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 193

Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313

Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Db        374 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 433

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Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

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Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Qy        341 LeuLeuLysPhe 344
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RESULT 9
AX490948
LOCUS       AX490948                1679 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 55 from Patent WO0200690.
ACCESSION   AX490948
VERSION     AX490948.1  GI:22323811
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0200690-A 55 03-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="Homo sapiens"
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ORIGIN

Alignment Scores:
Pred. No.:              1.19e-157       Length:         1679
Score:                  1806.00         Matches:        344
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-017-084A-523 (1-344) x AX490948 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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Db        794 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 853

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Db        974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1033

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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RESULT 10
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LOCUS       AY358331                1679 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA43316 HNT (UNQ297) mRNA, complete cds.
ACCESSION   AY358331
VERSION     AY358331.1  GI:37181786
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
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            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1679)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

Alignment Scores:
Pred. No.:              1.19e-157      Length:          1679
Score:                  1806.00        Matches:         344
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     9              Gaps:            0

US-10-017-084A-523 (1-344) x AY358331 (1-1679)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 373

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Db        614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 673

Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Db        734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 793

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
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Db       1094 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1153

Qy        341 LeuLeuLysPhe 344
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Db       1154 CTTCTCAAATTT 1165

RESULT 11
AR439649
LOCUS       AR439649                1693 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 2 from patent US 6664383.
ACCESSION   AR439649
VERSION     AR439649.1  GI:42665573
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1693)
  AUTHORS   Fukushima,D., Shibayama,S. and Tada,H.
  TITLE     Polypeptides, cDNA encoding the same and utilization thereof
  JOURNAL   Patent: US 6664383-A 2 16-DEC-2003;
FEATURES             Location/Qualifiers
     source          1..1693
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                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.21e-157      Length:        1693
Score:                  1806.00        Matches:       344
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     6              Gaps:          0

US-10-017-084A-523 (1-344) x AR439649 (1-1693)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Db        730 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 789

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 849

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 909

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 969

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1029

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1089

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1090 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1149

Qy         341 LeuLeuLysPhe 344
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Db        1150 CTTCTCAAATTT 1161

RESULT 12
AX665342
LOCUS       AX665342                1839 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 100 from Patent WO03002765.
ACCESSION   AX665342
VERSION     AX665342.1  GI:29290464
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sellar,G.C. and Gabra,H.
  TITLE     Cancer
  JOURNAL   Patent: WO 03002765-A 100 09-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .1839
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.44e-144      Length:         1839
Score:                  1665.50        Matches:        322
Percent Similarity:     97.31%         Conservative:   3
Best Local Similarity:  96.41%         Mismatches:     8
Query Match:            92.22%         Indels:         2
DB:                     6              Gaps:           1

US-10-017-084A-523 (1-344) x AX665342 (1-1839)

Qy          11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
               |||   ||||||:::      :::|||      :::|||            |||||||||
Db         299 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 354

Qy          31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         355 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 414

Qy          51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         415 GAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAAC 474

Qy          71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         475 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 534

Qy          91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         535 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 594

Qy         111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         595 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 654

Qy         131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         655 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 714

Qy         151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         715 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 774

Qy         171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
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Db         775 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 834

Qy         191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
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Db         835 ATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 894

Qy         211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         895 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 954

Qy         231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
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Db         955 ACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCA 1014

Qy         251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1015 GCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAA 1074

Qy         271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1075 GTGGAAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTAT 1134

Qy         291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
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Db        1135 GGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTA 1194

Qy         311 PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVal 330
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1195 TTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTC 1254

Qy         331 TrpLeuLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
               ||||||||||||||||||||||||||||||||||||||||||
Db        1255 TGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 1296

RESULT 13
AF126426
LOCUS       AF126426                1839 bp    mRNA    linear   PRI 10-JUN-2002
DEFINITION  Homo sapiens neurotrimin (HNT) mRNA, complete cds.
ACCESSION   AF126426
VERSION     AF126426.1  GI:7158997
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1839)
  AUTHORS   Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
  TITLE     Cloning and identification of human neurotrimin full length cDNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1839)
  AUTHORS   Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical
            Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
FEATURES             Location/Qualifiers
     source          1. .1839
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                     /db_xref="taxon:9606"
     gene            1. .1839
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     CDS             265. .1299
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                     /product="neurotrimin"
                     /protein_id="AAF37591.1"
                     /db_xref="GI:7158998"
                     /translation="MGVCGYLFLPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDN
                     VTVRQGESATLRCTIDNRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEI
                     QNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIAT
                     GRPEPTVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDVAAPVVRRVKVT
                     VNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPF
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                  LSKLIFFNVSEHDYGNYTCVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLP
                  LLVLHLLLKF"
ORIGIN

Alignment Scores:
Pred. No.:                1.44e-144     Length:          1839
Score:                    1665.50       Matches:         322
Percent Similarity:       97.31%        Conservative:    3
Best Local Similarity:    96.41%        Mismatches:      8
Query Match:              92.22%        Indels:          2
DB:                       9             Gaps:            1

US-10-017-084A-523  (1-344) x AF126426 (1-1839)

Qy         11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
              |||   ||||||:::      :::|||      :::|||          . |||||||||
Db        299 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 354

Qy         31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 414

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 GAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAAC 474

Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 534

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 594

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 654

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
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Db        655 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 714

Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
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Db        715 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 774

Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 834

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
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Db        835 ATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 894

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
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Db        895 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 954

Qy        231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 ACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCA 1014

Qy        251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1015 GCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAGGGGGTGAAA 1074

Qy        271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1075 GTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTAT 1134

Qy        291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
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Db       1135 GGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTA 1194

Qy        311 PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVal 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1195 TTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTC 1254

Qy        331 TrpLeuLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
              ||||||||||||||||||||||||||||||||||||||||||
Db       1255 TGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 1296

RESULT 14
AX665344
LOCUS       AX665344                1068 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 102 from Patent WO03002765.
ACCESSION   AX665344
VERSION     AX665344.1  GI:29290465
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sellar,G.C. and Gabra,H.
  TITLE     Cancer
  JOURNAL   Patent: WO 03002765-A 102 09-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
     source          1..1068
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.99e-143     Length:          1068
Score:                    1650.00       Matches:         322
Percent Similarity:       94.20%        Conservative:    3
Best Local Similarity:    93.33%        Mismatches:      8
Query Match:              91.36%        Indels:          13
DB:                       6             Gaps:            2

US-10-017-084A-523  (1-344) x AX665344 (1-1068)

Qy         11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
              |||   ||||||:::      :::|||      :::|||            |||||||||
Db         35 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 90

Qy         31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 150

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAAC 210

Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
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Db        211 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 270

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
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Db        271 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 330

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
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Db        331 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 390

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
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Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
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Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
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Db        511 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 570

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
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Db        571 ATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 630

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
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Db        631 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 690

Qy        231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 ACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCA 750

Qy        251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
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Db        751 GCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAA 810

Qy        271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 GTGGAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTAT 870

Qy        291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 GGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTA 930

Qy        311 Phe---------------------------------GlyProGlyAlaValSerGluVal 319
              |||                                 ||||||||||||||||||||||||
Db        931 TTTGAAGTGAAAACTACAGCCCTGACCCCTTGGAAAGGTCCAGGCGCCGTCAGCGAGGTG 990

Qy        320 SerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHis 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 AGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCAC 1050

Qy        340 LeuLeuLeuLysPhe 344
              |||||||||||||||
Db       1051 CTGCTTCTCAAATTT 1065

RESULT 15
BC023307
LOCUS       BC023307                1615 bp    mRNA    linear   ROD 06-OCT-2003
DEFINITION  Mus musculus neurotrimin, mRNA (cDNA clone MGC:30504
            IMAGE:4480983), complete cds.
ACCESSION   BC023307
VERSION     BC023307.1  GI:23958300
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1615)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   MEDLINE  22388257
    PUBMED  12477932
REFERENCE   2  (bases 1 to 1615)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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US-10-017-084A-523 (1-344) x BC023307 (1-1615)

Qy          12 IleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe---------GlnGly 28
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Db          68 CTGCCCTGGAAGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTATTCCTTGTACCCACAGGA 127

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                    Copyright (c) 1993 - 2005  Compugen Ltd.
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Searched:        4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters:      8780412
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ID   AAZ47892 standard; cDNA; 1032 BP.
DE   Human protein encoding cDNA SEQ ID NO:2.
PN   WO9958668-A1.
PD   18-NOV-1999.
PA   (ONOY ) ONO PHARM CO LTD.
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PN   WO9946281-A2.
PD   16-SEP-1999.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
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PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
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ID   AAC87037 standard; cDNA; 1679 BP.
DE   Nucleotide sequence of human polypeptide PRO337.
PN   WO200077037-A2.
PD   21-DEC-2000.
PA   (GETH ) GENENTECH INC.
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Best Local Similarity:  100.00%        Mismatches:    0
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ID   AAS21431 standard; cDNA; 1679 BP.
DE   Human cDNA sequence encoding for PRO337 polypeptide.
PN   WO200140466-A2.
PD   07-JUN-2001.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
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ID   ABK33598 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO protein, Seq ID No 125.
PN   WO200208288-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
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ID   ABL88099 standard; cDNA; 1679 BP.
DE   Human PRO337 cDNA sequence SEQ ID NO:55.
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PD   03-JAN-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
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DE   Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.
PN   WO200208284-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
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PN   US2002192706-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
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DE   cDNA encoding human PRO polypeptide #188.
PN   US2003036180-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:   100.00%        Mismatches:    0
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PN   US2003032063-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
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DE   Human secreted and transmembrane PRO polypeptide #37 cDNA.
PN   US2002177553-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
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ID   ABX89328 standard; cDNA; 1679 BP.
DE   DNA encoding novel secreted and transmembrane protein PRO337.
PN   US2003017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:   100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 14
ID   ABX92696 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO337 polypeptide.
PN   US2002169284-A1.
PD   14-NOV-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:   100.00%        Mismatches:    0
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ID   ACD41982 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #188.
PN   US2003036179-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
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Query Match:             100.00%        Indels:        0
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PN   US2002177165-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:   100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
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PN   US2003032062-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:   100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
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RESULT 18
ID   ACA66437 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO337.
PN   US2003004102-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
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PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
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ID   ACA04211 standard; cDNA; 1679 BP.
DE   Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
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DE   Human cDNA encoding secreted/transmembrane protein PRO337.
PN   US2003032057-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:   100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
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DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
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Query Match:             100.00%        Indels:        0
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PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
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Query Match:             100.00%        Indels:        0
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ID   ABT44288 standard; cDNA; 1679 BP.
DE   Human PRO337 cDNA.
PN   US2003050448-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:   100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
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PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
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RESULT 26
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PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
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ID   ADB19383 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
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RESULT 28
ID   ADB27924 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
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ID   ADA86403 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 30
ID   ADB15967 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 31
ID   ADA47753 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 32
ID   ADA67548 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 33
ID   ADB30555 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003068794-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 34
ID   ADA85851 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082693-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 35
ID   ADA97063 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082705-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 36
ID   ADA79367 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082763-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 37
ID   ADA87506 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087345-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 38
ID   ADB16708 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087349-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 39
ID   ADA91800 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082694-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 40
ID   ADB14863 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087351-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 41
ID   ADA25061 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003050241-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 42
ID   ADA47275 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
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PN   US2003044844-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 43
ID   ADB18824 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073211-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 44
ID   ADA94039 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077722-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 45
ID   ADB19935 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082691-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 46
ID   ADB13247 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082710-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 47
ID   ACD98611 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003044945-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 48
ID   ACD30038 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003050240-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 49
ID   ADA12722 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO337.
PN   US2003055216-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 50
ID   ADA74501 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003068798-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 51
ID   ADB24734 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077713-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 52
ID   ADA82258 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082701-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 53
ID   ADA75221 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003073216-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 54
ID   ADA85299 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082695-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 55
ID   ADA84747 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 56
ID   ADB30003 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 57
ID   ADA80531 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 58
ID   ADA75773 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082703-A1.
PD   01-MAY-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 59
ID   ADA46998 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003073210-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 60
ID   ADB25294 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 61
ID   ADA93470 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077721-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 62
ID   ADB26820 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 63
ID   ADB31107 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 64
ID   ABT44571 standard; cDNA; 1679 BP.
DE   Human PRO337 cDNA.
PN   US2003027988-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 65
ID   ADA61035 standard; cDNA; 1679 BP.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 66
ID   ADB24182 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 67
ID   ADA96511 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082690-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 68
ID   ADA81083 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082702-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 69
ID   ADA95959 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 70
ID   ADB26268 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 71
ID   ADB21753 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 72
ID   ACD82238 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO 337 cDNA.
PN   US2003044934-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 73
ID   ACD29453 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane polypeptide cDNA #133.
PN   US2003049633-A1.
PD   13-MAR-2003.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 74
ID   ADA77532 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003068797-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
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Query Match:             100.00%         Indels:         0
RESULT 75
ID   ADB18272 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003077710-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 76
ID   ADA86955 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082709-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 77
ID   ADA88058 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082700-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 78
ID   ADA46446 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003054516-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 79
ID   ADB28476 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082699-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 80
ID   ADB29028 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003082706-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 81
ID   ADA76980 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003059909-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 82
ID   ADA88610 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073213-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
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RESULT 83
ID   ADA97615 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082686-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 84
ID   ADB27372 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003022239-A1.
PD   30-JAN-2003.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 85
ID   ADB22305 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087344-A1.
PD   08-MAY-2003.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 86
ID   ACD30273 standard; cDNA; 1679 BP.
DE   Human cDNA encoding Pro337.
PN   US2003044902-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 87
ID   ABT43944 standard; cDNA; 1679 BP.
DE   Human membrane bound receptor/protein PRO337 cDNA sequence.
PN   US2003065147-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 88
ID   ADA66996 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003068793-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 89
ID   ADB22857 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077711-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 90
ID   ADB23630 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077712-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             100.00%         Indels:         0
RESULT 91
ID   ADA92352 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
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PN   US2003082712-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 92
ID   ADB15415 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087352-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 93
ID   ADB83615 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 94
ID   ADB80721 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088068-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 95
ID   ADB73262 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096968-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 96
ID   ADB38667 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082766-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 97
ID   ADB78344 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092889-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 98
ID   ADB38115 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087347-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 99
ID   ADB66587 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082689-A1.
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PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 100
ID   ADB84992 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003073817-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 101
ID   ADB89667 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082698-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 102
ID   ADB90399 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082762-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 103
ID   ADB39500 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082764-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 104
ID   ADB78098 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092886-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 105
ID   ADB74028 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide sequence #133.
PN   US2003045462-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 106
ID   ADB87164 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003088067-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 107
ID   ADB84746 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003092890-A1.
PD   15-MAY-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 108
ID   ADB47123 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082687-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 109
ID   ADB83861 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003069397-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 110
ID   ADB86730 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003082697-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 111
ID   ADB73016 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092887-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 112
ID   ADB76744 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide sequence #133.
PN   US2003083248-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 113
ID   ADB77335 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082696-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 114
ID   ADB34492 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077717-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 115
ID   ADB35596 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 116
ID   ADB33940 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077716-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 117
ID   ADB35044 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 118
ID   ADB36148 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide SEQ ID NO 375.
PN   US2003077720-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 119
ID   ADB46543 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003082692-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 120
ID   ADC44170 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003054986-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 121
ID   ADC61930 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003049684-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 122
ID   ADC63894 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003054405-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 123
ID   ADC66994 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003060406-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
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Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 124
ID   ADC69118 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003064407-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 125
ID   ADC63178 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003068648-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 126
ID   ADC68243 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003069178-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 127
ID   ADC41563 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003072745-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 128
ID   ADC67618 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003073131-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 129
ID   ADC62554 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003073624-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 130
ID   ADC36854 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003088065-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 131
ID   ADC42187 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003104998-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
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Query Match:            100.00%        Indels:        0
RESULT 132
ID   ADC21844 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 133
ID   ADC50416 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092106-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 134
ID   ADC71963 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 135
ID   ADC59942 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 136
ID   ADC49875 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088064-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 137
ID   ADC49074 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088070-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 138
ID   ADC49591 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088071-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 139
ID   ADC47452 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088072-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
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RESULT 140
ID   ADC52949 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087365-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 141
ID   ADC57303 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087366-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 142
ID   ADC60494 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 143
ID   ADC50969 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 144
ID   ADC65496 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 145
ID   ADC54594 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 146
ID   ADC53555 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087364-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 147
ID   ADC59078 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087359-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 148
ID   ADC55956 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087360-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 149
ID   ADC58526 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID375.
PN   US2003087346-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 150
ID   ADC47197 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105288-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 151
ID   ADD03200 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092104-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 152
ID   ADC90192 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087348-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 153
ID   ADC69611 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194770-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 154
ID   ADC48500 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194773-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 155
ID   ADD10029 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 156
ID   ADC78072 standard; cDNA; 1679 BP.
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DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096972-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 157
ID   ADD04604 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 158
ID   ADD06307 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003073816-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 159
ID   ADC80560 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 160
ID   ADD11067 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 161
ID   ADD10344 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003105011-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 162
ID   ADC47948 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 163
ID   ADC77826 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003088066-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 164
ID   ADC80008 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
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PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 165
ID   ADD11304 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 166
ID   ADD09477 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 167
ID   ADD50789 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105291-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 168
ID   ADD41190 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 169
ID   ADD52329 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 170
ID   ADD51035 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 171
ID   ADD53069 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 172
ID   ADD53621 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003203437-A1.
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PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 173
ID   ADD37097 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 174
ID   ADD51777 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 175
ID   ADD02576 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203431-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 176
ID   ADD50516 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096971-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 177
ID   ADD02010 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203430-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 178
ID   ADD54192 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003203432-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 179
ID   ADD50270 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096970-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 180
ID   ADD51281 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003105289-A1.
PD   05-JUN-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 181
ID   ADE49556 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003096744-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 182
ID   ADD92509 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199030-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 183
ID   ADD91405 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199055-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 184
ID   ADE04019 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199057-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 185
ID   ADE32316 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194765-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 186
ID   ADE22248 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199056-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 187
ID   ADD79472 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003203428-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 188
ID   ADE35610 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203434-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 189
ID   ADE16724 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203435-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 190
ID   ADD73339 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203436-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 191
ID   ADE42008 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194772-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 192
ID   ADE17825 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199023-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 193
ID   ADD91957 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199053-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 194
ID   ADE33420 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194767-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 195
ID   ADE33972 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194791-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 196
ID   ADD80024 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207417-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
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Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 197
ID   ADD93061 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194768-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 198
ID   ADD72697 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003194781-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 199
ID   ADE19481 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199025-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 200
ID   ADE18929 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199026-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 201
ID   ADE43125 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 202
ID   ADD95914 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199059-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 203
ID   ADE22800 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
RESULT 204
ID   ADD78918 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
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Query Match:            100.00%        Indels:        0
RESULT 205
ID   ADE32868 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 206
ID   ADE42560 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 207
ID   ADE17348 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203433-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 208
ID   ADD80576 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 209
ID   ADD89604 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 210
ID   ADE40888 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 211
ID   ADE04687 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 212
ID   ADE92816 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194777-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
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RESULT 213
ID   ADF47362 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195333-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 214
ID   ADG21525 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 215
ID   ADG23166 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 216
ID   ADF97501 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 217
ID   ADG80565 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 218
ID   ADG53119 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003216561-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 219
ID   ADG60439 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003206915-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 220
ID   ADG80013 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 221
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ID   ADG63784 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
PN   US2003170721-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 222
ID   ADH55305 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207381-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 223
ID   ADH55857 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207379-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 224
ID   ADI61199 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003077700-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 225
ID   ADI64076 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207385-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 226
ID   ADI65025 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207386-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 227
ID   ADI63524 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207387-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 228
ID   ADH81938 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207388-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 229
ID   ADH81386 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207377-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 230
ID   ACD24040 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003032156-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 231
ID   ACA66903 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #63.
PN   US2003036635-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 232
ID   ACD42387 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003040014-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 233
ID   ACD42857 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003050239-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 234
ID   ACD68655 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003045687-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 235
ID   ACA67181 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003004311-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 236
ID   ADM82555 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087355-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 237
ID   ADN15954 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
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PN   US2003087353-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 238
ID   ADN16583 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087385-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 239
ID   ADN15402 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087356-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 240
ID   ADN14850 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003087357-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 241
ID   ADC48828 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092888-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 242
ID   ADC81112 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003092115-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 243
ID   ADE20999 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100735-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 244
ID   ADE05843 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100728-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 245
ID   ADD76560 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003100087-A1.
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PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 246
ID   ADD75072 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100712-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 247
ID   ADD75818 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100717-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 248
ID   ADD85050 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100722-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 249
ID   ADD86876 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100738-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 250
ID   ADE20753 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100734-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 251
ID   ADE39050 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096362-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 252
ID   ADD87924 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003092113-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 253
ID   ADD86328 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203440-A1.
PD   30-OCT-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 254
ID   ADE05597 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100727-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 255
ID   ADD73582 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100711-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 256
ID   ADE75776 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003211571-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 257
ID   ADE48856 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003104536-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 258
ID   ADD78422 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100737-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 259
ID   ADE41305 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #28.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 260
ID   ADE23352 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092108-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 261
ID   ADE21245 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100736-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 262
ID   ADD77360 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100732-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 263
ID   ADE20507 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100733-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 264
ID   ADD75572 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100064-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 265
ID   ADD74088 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100708-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 266
ID   ADD74334 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100709-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 267
ID   ADD76064 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100718-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 268
ID   ADD85556 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100721-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 269
ID   ADE23904 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092110-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
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Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 270
ID   ADE24547 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003092111-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 271
ID   ADD87372 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 272
ID   ADE05105 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100726-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 273
ID   ADD75318 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 274
ID   ADD76862 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 275
ID   ADD86630 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 276
ID   ADE89238 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 277
ID   ADE41198 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
PN   US2003104558-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
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Query Match:            100.00%        Indels:         0
RESULT 278
ID   ADD78098 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 279
ID   ADE18377 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003194794-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 280
ID   ADE88686 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 281
ID   ADE89957 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003130181-A1.
PD   10-JUL-2003.
PA   (ASHK/) ASHKENAZI A J.
PA   (BAKE/) BAKER K P.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GIRM/) GIRMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (KUOS/) KUO S S.
PA   (NAPI/) NAPIER M A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (SHEL/) SHELTON D L.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 282
ID   ADD77606 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
RESULT 283
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ID   ADD77852 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100730-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 284
ID   ADD85310 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100725-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 285
ID   ADD73842 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 286
ID   ADD74580 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 287
ID   ADD77108 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100716-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 288
ID   ADD85802 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003100720-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 289
ID   ADE05351 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100723-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 290
ID   ADD74826 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003100724-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 291
ID   ADF61597 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195345-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 292
ID   ADF40289 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003198994-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 293
ID   ADF46085 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195148-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 294
ID   ADE94706 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199027-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 295
ID   ADE91117 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 296
ID   ADE95258 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 297
ID   ADE93368 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 298
ID   ADF24481 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003204055-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 299
ID   ADF40913 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
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PN   US2003199021-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 300
ID   ADF23857 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003203402-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 301
ID   ADF33840 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003194780-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 302
ID   ADF34949 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003199029-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 303
ID   ADF27307 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199436-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 304
ID   ADF27943 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199437-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 305
ID   ADE92264 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 306
ID   ADE90565 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 307
ID   ADF41537 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199435-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 308
ID   ADF33216 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003211091-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 309
ID   ADF25582 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003211092-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 310
ID   ADF26683 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003199674-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 311
ID   ADF34472 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003194410-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 312
ID   ADF46709 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003195344-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 313
ID   ADE91712 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 314
ID   ADG05638 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096959-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 315
ID   ADG27192 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096962-A1.
PD   22-MAY-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 316
ID   ADG02291 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 317
ID   ADG22077 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 318
ID   ADG20147 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 319
ID   ADF98053 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 320
ID   ADG24270 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207426-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 321
ID   ADF98624 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 322
ID   ADG03455 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 323
ID   ADF99176 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 324
ID   ADG16761 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 325
ID   ADG05220 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 326
ID   ADG19487 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 327
ID   ADG11255 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 328
ID   ADG13324 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 329
ID   ADG08381 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 330
ID   ADG15551 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
Best Local Similarity:   100.00%         Mismatches:    0
Query Match:             100.00%         Indels:        0
RESULT 331
ID   ADG12034 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:  0
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Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 332
ID   ADF96949 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 333
ID   ADG06134 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 334
ID   ADG23718 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 335
ID   ADG04007 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 336
ID   ADG24908 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 337
ID   ADF94591 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 338
ID   ADG07205 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 339
ID   ADG07757 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207356-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 340
ID   ADG06687 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096966-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 341
ID   ADG55252 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 342
ID   ADG60916 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 343
ID   ADG62020 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 344
ID   ADG82221 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 345
ID   ADG57460 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 346
ID   ADG56908 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 347
ID   ADG55804 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
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RESULT 348
ID   ADG58564 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 349
ID   ADG70930 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 350
ID   ADH39031 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096965-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 351
ID   ADG58012 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 352
ID   ADG53596 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 353
ID   ADG71482 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 354
ID   ADG50695 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003207803-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 355
ID   ADG81669 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003207805-A1.
PD   06-NOV-2003.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 356
ID   ADH30631 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 357
ID   ADG63633 standard; cDNA; 1679 BP.
DE   Human secreted/transmembrane polypeptide PRO337 cDNA.
PN   US2003180796-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 358
ID   ADH11998 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 359
ID   ADG50071 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003215905-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 360
ID   ADG51943 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003215908-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 361
ID   ADG52420 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 362
ID   ADG54148 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 363
ID   ADG49447 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003216305-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 364
ID   ADG81117 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
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PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 365
ID   ADG56356 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 366
ID   ADH12622 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 367
ID   ADG48823 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2003216560-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 368
ID   ADG61468 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 369
ID   ADH28555 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 370
ID   ADG54700 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 371
ID   ADG59740 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 372
ID   ADG51319 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004005312-A1.
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PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 373
ID   ADH43488 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #28.
PN   US2003224984-A1.
PD   04-DEC-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 374
ID   ADG59263 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004005657-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 375
ID   ADG34121 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004006206-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 376
ID   ADG62719 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004006219-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 377
ID   ADI81164 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003207361-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 378
ID   ADI33591 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2003096960-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 379
ID   ADH69685 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2004019183-A1.
PD   29-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 380
ID   ADH25744 standard; cDNA; 1679 BP.
DE   Human PRO337 encoding cDNA SEQ ID NO:522.
PN   EP1386931-A1.
PD   04-FEB-2004.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 381
ID   ADG09907 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004009548-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 382
ID   ADI15378 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207382-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 383
ID   ADG09255 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004009547-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 384
ID   ADI14710 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207383-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 385
ID   ADI29846 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003096961-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 386
ID   ADI18305 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207349-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 387
ID   ADM27243 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004044179-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 388
ID   ADJ63586 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 389
ID   ADJ77481 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #188.
PN   US2004038336-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 390
ID   ADK82833 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #28.
PN   US2004043927-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 391
ID   ADK66601 standard; cDNA; 1679 BP.
DE   Human PRO polynucleotide #63.
PN   US2004044180-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 392
ID   ADJ65603 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004038335-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 393
ID   ADM27739 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004048333-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 394
ID   ADM17521 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004048332-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 395
ID   ADL07355 standard; cDNA; 1679 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO337.
PN   US2004063921-A1.
PD   01-APR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 396
ID   ADM42463 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004058424-A1.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
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Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 397
ID   ADM28325 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2004077064-A1.
PD   22-APR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 398
ID   ADI95807 standard; cDNA; 1679 BP.
DE   cDNA encoding human PRO polypeptide #188.
PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 399
ID   ADI96359 standard; cDNA; 1679 BP.
DE   Novel human secreted and transmembrane protein PRO337 cDNA.
PN   US2003207354-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 400
ID   AAZ47893 standard; cDNA; 1693 BP.
DE   Human protein encoding cDNA SEQ ID NO:3.
PN   WO9958668-A1.
PD   18-NOV-1999.
PA   (ONOY ) ONO PHARM CO LTD.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
RESULT 401
ID   AAA88790 standard; cDNA; 1603 BP.
DE   Human SECX cDNA Clone 11753149.0.6.
PN   WO200061754-A2.
PD   19-OCT-2000.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     99.71%         Conservative:  0
Best Local Similarity:  99.71%         Mismatches:    1
Query Match:            99.61%         Indels:        0
RESULT 402
ID   ADD18288 standard; DNA; 1603 BP.
DE   Human molecule (MOL) protein MOL10 DNA sequence.
PN   WO2003003984-A2.
PD   16-JAN-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     99.71%         Conservative:  0
Best Local Similarity:  99.71%         Mismatches:    1
Query Match:            99.61%         Indels:        0
RESULT 403
ID   AAA88791 standard; cDNA; 2012 BP.
DE   Human SECX cDNA Clone 11753149.0.37.
PN   WO200061754-A2.
PD   19-OCT-2000.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     99.71%         Conservative:  0
Best Local Similarity:  99.71%         Mismatches:    1
Query Match:            99.61%         Indels:        0
RESULT 404
ID   ADD18290 standard; DNA; 2012 BP.
DE   Human molecule (MOL) protein MOL11 DNA sequence.
PN   WO2003003984-A2.
PD   16-JAN-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     99.71%         Conservative:  0
Best Local Similarity:  99.71%         Mismatches:    1
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Query Match:            99.61%         Indels:        0
RESULT 405
ID   ABK49272 standard; cDNA; 1873 BP.
DE   Human Kruppel associated DNA binding protein 42 cDNA.
PN   WO200183541-A1.
PD   08-NOV-2001.
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Percent Similarity:     89.32%         Conservative:  0
Best Local Similarity:  89.32%         Mismatches:    1
Query Match:            97.23%         Indels:        41
RESULT 406
ID   AAI59655 standard; cDNA; 1690 BP.
DE   Human polynucleotide SEQ ID NO 3644.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     99.13%         Conservative:  0
Best Local Similarity:  99.13%         Mismatches:    1
Query Match:            97.01%         Indels:        3
RESULT 407
ID   ADI21360 standard; cDNA; 1690 BP.
DE   Novel human expressed sequence tag, EST #59.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     99.13%         Conservative:  0
Best Local Similarity:  99.13%         Mismatches:    1
Query Match:            97.01%         Indels:        3
RESULT 408
ID   ABT17393 standard; DNA; 1061 BP.
DE   Human IG gene related nucleic acid SEQ ID No 19.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     97.31%         Conservative:  3
Best Local Similarity:  96.41%         Mismatches:    8
Query Match:            92.22%         Indels:        2
RESULT 409
ID   AAI57869 standard; cDNA; 1678 BP.
DE   Human polynucleotide SEQ ID NO 72.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     97.31%         Conservative:  3
Best Local Similarity:  96.41%         Mismatches:    8
Query Match:            92.22%         Indels:        2
RESULT 410
ID   ABT17390 standard; DNA; 1839 BP.
DE   Human IG gene related nucleic acid SEQ ID No 16.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     97.31%         Conservative:  3
Best Local Similarity:  96.41%         Mismatches:    8
Query Match:            92.22%         Indels:        2
RESULT 411
ID   ABX76448 standard; DNA; 1839 BP.
DE   Lung cancer-associated polynucleotide #312.
PN   WO200286443-A2.
PD   31-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity:     97.31%         Conservative:  3
Best Local Similarity:  96.41%         Mismatches:    8
Query Match:            92.22%         Indels:        2
RESULT 412
ID   ADG63208 standard; DNA; 1839 BP.
DE   Human neurotrimin DNA.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity:     97.31%         Conservative:  3
Best Local Similarity:  96.41%         Mismatches:    8
Query Match:            92.22%         Indels:        2
```

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RESULT 413
ID   ADN39137 standard; cDNA; 1839 BP.
DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:455.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity:     97.31%          Conservative:  3
Best Local Similarity:  96.41%          Mismatches:    8
Query Match:            92.22%          Indels:        2
RESULT 414
ID   ADI21817 standard; cDNA; 2884 BP.
DE   Novel human protein cDNA #76.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     97.31%          Conservative:  3
Best Local Similarity:  96.41%          Mismatches:    8
Query Match:            92.22%          Indels:        2
RESULT 415
ID   ADQ22984 standard; DNA; 3987 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5804.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity:     97.31%          Conservative:  3
Best Local Similarity:  96.41%          Mismatches:    8
Query Match:            92.22%          Indels:        2
RESULT 416
ID   ADQ24601 standard; DNA; 3987 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7421.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity:     97.31%          Conservative:  3
Best Local Similarity:  96.41%          Mismatches:    8
Query Match:            92.22%          Indels:        2
RESULT 417
ID   ADG63210 standard; DNA; 1068 BP.
DE   Human neurotrimin DNA +33bp isoform.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity:     94.20%          Conservative:  3
Best Local Similarity:  93.33%          Mismatches:    8
Query Match:            91.36%          Indels:        13
RESULT 418
ID   ABT17391 standard; DNA; 1094 BP.
DE   Human IG gene related nucleic acid SEQ ID No 17.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     94.20%          Conservative:  3
Best Local Similarity:  93.33%          Mismatches:    8
Query Match:            91.36%          Indels:        13
RESULT 419
ID   ADI35771 standard; DNA; 2129 BP.
DE   Human neurotrimin DNA.
PN   US2003100485-A1.
PD   29-MAY-2003.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:     94.20%          Conservative:  3
Best Local Similarity:  93.33%          Mismatches:    8
Query Match:            91.36%          Indels:        13
RESULT 420
ID   ADG63212 standard; DNA; 1104 BP.
DE   Human neurotrimin DNA +69bp isoform.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity:     91.04%          Conservative:  3
Best Local Similarity:  90.20%          Mismatches:    8
Query Match:            91.03%          Indels:        25
RESULT 421
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ID   ABT17392 standard; DNA; 1130 BP.
DE   Human IG gene related nucleic acid SEQ ID No 18.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     91.04%          Conservative:  3
Best Local Similarity:  90.20%          Mismatches:    8
Query Match:            91.03%          Indels:        25
RESULT 422
ID   AAZ47894 standard; cDNA; 939 BP.
DE   Human protein encoding cDNA SEQ ID NO:5.
PN   WO9958668-A1.
PD   18-NOV-1999.
PA   (ONOY ) ONO PHARM CO LTD.
Percent Similarity:     100.00%         Conservative:  0
Best Local Similarity:  100.00%         Mismatches:    0
Query Match:            90.92%          Indels:        0
RESULT 423
ID   ADG63214 standard; DNA; 1140 BP.
DE   Human neurotrimin DNA +108bp isoform.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity:     88.08%          Conservative:  3
Best Local Similarity:  87.26%          Mismatches:    8
Query Match:            90.70%          Indels:        37
RESULT 424
ID   ADE07017 standard; DNA; 3298 BP.
DE   Novel coding sequence (useful for identifying genetic disorders) #83.
PN   WO2003054152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     82.89%          Conservative:  39
Best Local Similarity:  71.39%          Mismatches:    57
Query Match:            71.79%          Indels:        1
RESULT 425
ID   AAQ51015 standard; cDNA; 3069 BP.
DE   Rat opioid receptor gene.
PN   WO9321309-A1.
PD   28-OCT-1993.
PA   (LEEN/) LEE N M.
PA   (LOHH/) LOH H H.
PA   (LIPP/) LIPPMAN D.
Percent Similarity:     82.01%          Conservative:  36
Best Local Similarity:  71.39%          Mismatches:    60
Query Match:            71.23%          Indels:        1
RESULT 426
ID   ABT17408 standard; DNA; 1071 BP.
DE   Human IG gene related nucleic acid SEQ ID No 34.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     83.28%          Conservative:  37
Best Local Similarity:  72.24%          Mismatches:    54
Query Match:            70.21%          Indels:        3
RESULT 427
ID   ABT17407 standard; DNA; 1080 BP.
DE   Human IG gene related nucleic acid SEQ ID No 33.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     83.28%          Conservative:  37
Best Local Similarity:  72.24%          Mismatches:    54
Query Match:            70.21%          Indels:        3
RESULT 428
ID   ABT17409 standard; DNA; 1478 BP.
DE   Human IG gene related nucleic acid SEQ ID No 35.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     83.28%          Conservative:  37
Best Local Similarity:  72.24%          Mismatches:    54
Query Match:            70.21%          Indels:        3
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RESULT 429
ID   ABT17406 standard; DNA; 3110 BP.
DE   Human IG gene related nucleic acid SEQ ID No 32.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     83.28%         Conservative:  37
Best Local Similarity:  72.24%         Mismatches:    54
Query Match:            70.21%         Indels:        3
RESULT 430
ID   ADG63206 standard; DNA; 3110 BP.
DE   Opioid-binding protein/cell adhesion molecule-like DNA.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity:     83.28%         Conservative:  37
Best Local Similarity:  72.24%         Mismatches:    54
Query Match:            70.21%         Indels:        3
RESULT 431
ID   AAQ51017 standard; cDNA; 2179 BP.
DE   Rat opioid receptor gene.
PN   WO9321309-A1.
PD   28-OCT-1993.
PA   (LEEN/) LEE N M.
PA   (LOHH/) LOH H H.
PA   (LIPP/) LIPPMAN D.
Percent Similarity:     81.31%         Conservative:  34
Best Local Similarity:  71.22%         Mismatches:    59
Query Match:            69.77%         Indels:        4
RESULT 432
ID   AAQ51016 standard; cDNA; 2337 BP.
DE   Rat opioid receptor gene.
PN   WO9321309-A1.
PD   28-OCT-1993.
PA   (LEEN/) LEE N M.
PA   (LOHH/) LOH H H.
PA   (LIPP/) LIPPMAN D.
Percent Similarity:     81.31%         Conservative:  34
Best Local Similarity:  71.22%         Mismatches:    59
Query Match:            69.71%         Indels:        4
RESULT 433
ID   AAA44536 standard; cDNA; 832 BP.
DE   Human secreted expressed sequence tag SEQ ID NO:1111.
PN   WO200021991-A1.
PD   20-APR-2000.
PA   (GEMY ) GENETICS INST INC.
Percent Similarity:     99.56%         Conservative:  1
Best Local Similarity:  99.11%         Mismatches:    1
Query Match:            64.95%         Indels:        0
RESULT 434
ID   ABT17404 standard; DNA; 1017 BP.
DE   Human IG gene related nucleic acid SEQ ID No 30.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     73.85%         Conservative:  60
Best Local Similarity:  55.38%         Mismatches:    80
Query Match:            51.63%         Indels:        5
RESULT 435
ID   AAL50356 standard; cDNA; 1411 BP.
DE   Human limbic system associated membrane protein 36-85 coding sequence.
PN   CN1345756-A.
PD   24-APR-2002.
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Percent Similarity:     72.62%         Conservative:  63
Best Local Similarity:  53.87%         Mismatches:    85
Query Match:            51.63%         Indels:        7
RESULT 436
ID   ABT17402 standard; DNA; 1017 BP.
DE   Human IG gene related nucleic acid SEQ ID No 28.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     73.85%         Conservative:  60
Best Local Similarity:  55.38%         Mismatches:    80
Query Match:            51.58%         Indels:        5
RESULT 437
ID   ABX63560 standard; cDNA; 1195 BP.
DE   Human cDNA #560 differentially expressed in activated vascular tissue.
PN   US2002137081-A1.
PD   26-SEP-2002.
PA   (BAND/) BANDMAN O.
Percent Similarity:     73.85%         Conservative:  60
Best Local Similarity:  55.38%         Mismatches:    80
Query Match:            51.58%         Indels:        5
RESULT 438
ID   ADL12674 standard; cDNA; 1195 BP.
DE   Human steroid-induced C3A liver cell cDNA #403.
PN   US6673549-B1.
PD   06-JAN-2004.
PA   (INCY-) INCYTE CORP.
Percent Similarity:     73.85%         Conservative:  60
Best Local Similarity:  55.38%         Mismatches:    80
Query Match:            51.58%         Indels:        5
RESULT 439
ID   AAT42081 standard; cDNA to mRNA; 1014 BP.
DE   Rat LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     73.54%         Conservative:  60
Best Local Similarity:  55.08%         Mismatches:    81
Query Match:            51.30%         Indels:        5
RESULT 440
ID   AAT42080 standard; cDNA to mRNA; 1238 BP.
DE   Rat LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     73.54%         Conservative:  60
Best Local Similarity:  55.08%         Mismatches:    81
Query Match:            51.30%         Indels:        5
RESULT 441
ID   ABT17403 standard; DNA; 1075 BP.
DE   Human IG gene related nucleic acid SEQ ID No 29.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     71.51%         Conservative:  60
Best Local Similarity:  53.71%         Mismatches:    79
Query Match:            51.19%         Indels:        17
RESULT 442
ID   AAT42079 standard; cDNA to mRNA; 977 BP.
DE   Human LAMP residues 8-332 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     74.06%         Conservative:  60
Best Local Similarity:  55.31%         Mismatches:    78
Query Match:            51.14%         Indels:        5
RESULT 443
ID   AAT42116 standard; cDNA to mRNA; 1307 BP.
DE   Rat LAMP clone 6c coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     68.97%         Conservative:  60
Best Local Similarity:  51.72%         Mismatches:    80
Query Match:            50.55%         Indels:        28
RESULT 444
ID   AAT42084 standard; cDNA to mRNA; 924 BP.
DE   Human LAMP residues 8-315 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     75.50%         Conservative:  58
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Best Local Similarity:  56.29%          Mismatches:     70
Query Match:            50.28%          Indels:         4
RESULT 445
ID   AAT42085 standard; cDNA to mRNA; 945 BP.
DE   Rat LAMP residues 1-315 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     75.50%          Conservative:   58
Best Local Similarity:  56.29%          Mismatches:     70
Query Match:            50.22%          Indels:         4
RESULT 446
ID   AAT42083 standard; cDNA to mRNA; 930 BP.
DE   Rat mature LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     74.12%          Conservative:   59
Best Local Similarity:  55.27%          Mismatches:     77
Query Match:            50.11%          Indels:         4
RESULT 447
ID   AAT42082 standard; cDNA to mRNA; 912 BP.
DE   Human mature LAMP coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     74.68%          Conservative:   59
Best Local Similarity:  55.52%          Mismatches:     74
Query Match:            49.94%          Indels:         4
RESULT 448
ID   ABZ76264 standard; cDNA; 1757 BP.
DE   Human GENSET cDNA clone name SLAMP.
PN   WO2003014151-A2.
PD   20-FEB-2003.
PA   (GEST ) GENSET SA.
Percent Similarity:     72.14%          Conservative:   61
Best Local Similarity:  53.25%          Mismatches:     76
Query Match:            49.45%          Indels:         14
RESULT 449
ID   AAT42086 standard; cDNA to mRNA; 861 BP.
DE   Human LAMP residues 29-315 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     76.21%          Conservative:   57
Best Local Similarity:  56.55%          Mismatches:     66
Query Match:            49.09%          Indels:         3
RESULT 450
ID   AAT42087 standard; cDNA to mRNA; 861 BP.
DE   Rat LAMP residues 29-315 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     76.21%          Conservative:   57
Best Local Similarity:  56.55%          Mismatches:     66
Query Match:            49.03%          Indels:         3
RESULT 451
ID   AAH34425 standard; cDNA; 1153 BP.
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:1507.
PN   WO200122920-A2.
PD   05-APR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity:     68.68%          Conservative:   60
Best Local Similarity:  51.44%          Mismatches:     81
Query Match:            49.00%          Indels:         29
RESULT 452
ID   ADM47274 standard; DNA; 617 BP.
DE   Oestrogen regulated protein like NOVX 25b gene.
PN   WO2003083039-A2.
PD   09-OCT-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     56.59%          Conservative:   4
Best Local Similarity:  55.39%          Mismatches:     8
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Query Match:            48.37%          Indels:         138
RESULT 453
ID   AAZ34325 standard; DNA; 503 BP.
DE   Human EST DNA42301.
PN   WO9946281-A2.
PD   16-SEP-1999.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            47.56%          Indels:         0
RESULT 454
ID   AAC78591 standard; cDNA; 503 BP.
DE   Human EST DNA42301 nucleotide sequence SEQ ID NO:524.
PN   WO200053756-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            47.56%          Indels:         0
RESULT 455
ID   ACA63893 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein DNA42301.
PN   US2002192706-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            47.56%          Indels:         0
RESULT 456
ID   ACA72057 standard; DNA; 503 BP.
DE   Human PRO polypeptide associated oligonucleotide SEQ ID NO 524.
PN   US2002177553-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            47.56%          Indels:         0
RESULT 457
ID   ABX92697 standard; cDNA; 503 BP.
DE   Human PRO337 EST polynucleotide sequence.
PN   US2002169284-A1.
PD   14-NOV-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            47.56%          Indels:         0
RESULT 458
ID   ACA66438 standard; cDNA; 503 BP.
DE   Human secreted/transmembrane protein EST DNA42301.
PN   US2003004102-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            47.56%          Indels:         0
RESULT 459
ID   ADA25063 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein EST DNA42301.
PN   US2003050241-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            47.56%          Indels:         0
RESULT 460
ID   ACD30039 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein EST DNA42301.
PN   US2003050240-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            47.56%          Indels:         0
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RESULT 461
ID   ADA12724 standard; cDNA; 503 BP.
DE   Human secreted/transmembrane polypeptide PRO337 EST.
PN   US2003055216-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 462
ID   ACD29454 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane polypeptide cDNA #134.
PN   US2003049633-A1.
PD   13-MAR-2003.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 463
ID   ADB74030 standard; cDNA; 503 BP.
DE   Human PRO polynucleotide sequence #134.
PN   US2003045462-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 464
ID   ADB76746 standard; cDNA; 503 BP.
DE   Human PRO polynucleotide sequence #134.
PN   US2003083248-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 465
ID   ADC44172 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003054986-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 466
ID   ADC61932 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003049684-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 467
ID   ADC63896 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003054405-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 468
ID   ADC66996 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003060406-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 469
ID   ADC69120 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003064407-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 470
ID   ADC63180 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003068648-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 471
ID   ADC68245 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003069178-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 472
ID   ADC41565 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003072745-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 473
ID   ADC67620 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003073131-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 474
ID   ADC62556 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003073624-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 475
ID   ADC42189 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003104998-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 476
ID   ADE49558 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003096744-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:             47.56%        Indels:        0
RESULT 477
ID   ADE35612 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
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PN   US2003203434-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 478
ID   ADE16726 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203435-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 479
ID   ADD73341 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203436-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 480
ID   ADD72699 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003194781-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 481
ID   ADE17350 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203433-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 482
ID   ADF47364 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195333-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 483
ID   ADG53121 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003216561-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 484
ID   ADG60441 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003206915-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 485
ID   ADI61201 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003077700-A1.
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PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 486
ID   ACD42858 standard; cDNA; 503 BP.
DE   Novel human secreted and transmembrane protein EST DNA42301.
PN   US2003050239-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 487
ID   ADE48858 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003104536-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 488
ID   ADE89959 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003130181-A1.
PD   10-JUL-2003.
PA   (ASHK/) ASHKENAZI A J.
PA   (BAKE/) BAKER K P.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GIRM/) GIRMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (KUOS/) KUO S S.
PA   (NAPI/) NAPIER M A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (SHEL/) SHELTON D L.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 489
ID   ADF61599 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195345-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            47.56%         Indels:        0
RESULT 490
ID   ADF40291 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003198994-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 491
ID   ADF46087 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195148-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 492
ID   ADF24483 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003204055-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 493
ID   ADF40915 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199021-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 494
ID   ADF23859 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003203402-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 495
ID   ADF33842 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003194780-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 496
ID   ADF27309 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199436-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 497
ID   ADF27945 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199437-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 498
ID   ADF41539 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199435-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 499
ID   ADF33218 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003211091-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 500
ID   ADF25584 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003211092-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 501
ID   ADF26685 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003199674-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 502
ID   ADF34474 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003194410-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 503
ID   ADF46711 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003195344-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 504
ID   ADG50697 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003207803-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 505
ID   ADG50073 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003215905-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            47.56%        Indels:        0
RESULT 506
ID   ADG51945 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003215908-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
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Query Match:             47.56%          Indels:         0
RESULT 507
ID   ADG49449 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003216305-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             47.56%          Indels:         0
RESULT 508
ID   ADG48825 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2003216560-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             47.56%          Indels:         0
RESULT 509
ID   ADG51321 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004005312-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             47.56%          Indels:         0
RESULT 510
ID   ADG59265 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004005657-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             47.56%          Indels:         0
RESULT 511
ID   ADG62721 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004006219-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             47.56%          Indels:         0
RESULT 512
ID   ADH25746 standard; cDNA; 503 BP.
DE   Human DNA42301 expressed sequence tag (EST) SEQ ID NO:524.
PN   EP1386931-A1.
PD   04-FEB-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             47.56%          Indels:         0
RESULT 513
ID   ADM17523 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004048332-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             47.56%          Indels:         0
RESULT 514
ID   ADL07357 standard; cDNA; 503 BP.
DE   Human EST from secreted/transmembrane protein, PRO337.
PN   US2004063921-A1.
PD   01-APR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%         Conservative:   0
Best Local Similarity:   100.00%         Mismatches:     0
Query Match:             47.56%          Indels:         0
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RESULT 515
ID   ABT17405 standard; DNA; 898 BP.
DE   Human IG gene related nucleic acid SEQ ID No 31.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:      74.65%          Conservative:   55
Best Local Similarity:   55.56%          Mismatches:     71
Query Match:             47.12%          Indels:         2
RESULT 516
ID   ABQ82337 standard; cDNA; 1196 BP.
DE   Human NOV12a encoding cDNA SEQ ID NO:23.
PN   WO200262999-A2.
PD   15-AUG-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:      67.18%          Conservative:   63
Best Local Similarity:   47.85%          Mismatches:     105
Query Match:             45.57%          Indels:         2
RESULT 517
ID   ADI28059 standard; cDNA; 1327 BP.
DE   ECMCAD gene clone 7087904CB1.
PN   WO200202634-A2.
PD   10-JAN-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:      67.18%          Conservative:   63
Best Local Similarity:   47.85%          Mismatches:     105
Query Match:             45.57%          Indels:         2
RESULT 518
ID   AAC87055 standard; cDNA; 4834 BP.
DE   Nucleotide sequence of human polypeptide PRO6004.
PN   WO200077037-A2.
PD   21-DEC-2000.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      67.18%          Conservative:   63
Best Local Similarity:   47.85%          Mismatches:     105
Query Match:             45.57%          Indels:         2
RESULT 519
ID   ABK33536 standard; cDNA; 4834 BP.
DE   cDNA encoding human PRO protein, Seq ID No 1.
PN   WO200208288-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      67.18%          Conservative:   63
Best Local Similarity:   47.85%          Mismatches:     105
Query Match:             45.57%          Indels:         2
RESULT 520
ID   ACA05014 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003032063-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      67.18%          Conservative:   63
Best Local Similarity:   47.85%          Mismatches:     105
Query Match:             45.57%          Indels:         2
RESULT 521
ID   ACA60544 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2002177165-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      67.18%          Conservative:   63
Best Local Similarity:   47.85%          Mismatches:     105
Query Match:             45.57%          Indels:         2
RESULT 522
ID   ACA04534 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 DNA.
PN   US2003032062-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      67.18%          Conservative:   63
Best Local Similarity:   47.85%          Mismatches:     105
Query Match:             45.57%          Indels:         2
RESULT 523
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ID   ACA68497 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088063-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 524
ID   ACA65675 standard; cDNA; 4834 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO6004.
PN   US2003032057-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 525
ID   ABT44226 standard; cDNA; 4834 BP.
DE   Human PRO6004 cDNA.
PN   US2003050448-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 526
ID   ADA47301 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003044844-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 527
ID   ABT44509 standard; cDNA; 4834 BP.
DE   Human PRO6004 cDNA.
PN   US2003027988-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 528
ID   ACD82176 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO 6004 cDNA.
PN   US2003044934-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 529
ID   ACD30291 standard; cDNA; 4834 BP.
DE   Human cDNA encoding Pro6004.
PN   US2003044902-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 530
ID   ABT43882 standard; cDNA; 4834 BP.
DE   Human membrane bound receptor/protein PRO6004 cDNA sequence.
PN   US2003065147-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 531
ID   ADB83491 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 532
ID   ADB80597 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088068-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 533
ID   ADB73138 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096968-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 534
ID   ADB78220 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092889-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 535
ID   ADB84868 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003073817-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 536
ID   ADB77974 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092886-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 537
ID   ADB87040 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003088067-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 538
ID   ADB84622 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003092890-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    67.18%        Conservative:  63
Best Local Similarity:  47.85%        Mismatches:    105
Query Match:           45.57%        Indels:        2
RESULT 539
ID   ADB83737 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
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PN   US2003069397-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 540
ID   ADB72892 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092887-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 541
ID   ADC36730 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003088065-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 542
ID   ADC21720 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 543
ID   ADC49751 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088064-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 544
ID   ADC48950 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088070-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 545
ID   ADC49467 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088071-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 546
ID   ADC47328 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088072-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 547
ID   ADC47073 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105288-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 548
ID   ADC77948 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096972-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 549
ID   ADD06183 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003073816-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 550
ID   ADC77702 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003088066-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 551
ID   ADD50665 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105291-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 552
ID   ADD50911 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 553
ID   ADD50392 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096971-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 554
ID   ADD50146 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096970-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 555
ID   ADD51157 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003105289-A1.
PD   05-JUN-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 556
ID   ADG63810 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003170721-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 557
ID   ACA66841 standard; cDNA; 4834 BP.
DE   cDNA encoding human PRO polypeptide #1.
PN   US2003036635-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 558
ID   ACD42405 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003040014-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 559
ID   ACD68593 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003045687-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 560
ID   ADC48704 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003092888-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 561
ID   ADE20875 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100735-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 562
ID   ADE05719 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100728-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 563
ID   ADD74948 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100712-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 564
ID   ADD75694 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100717-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 565
ID   ADD84926 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100722-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 566
ID   ADD86752 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100738-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 567
ID   ADE20629 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100734-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 568
ID   ADE38926 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096362-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 569
ID   ADE05473 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100727-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 570
ID   ADD73458 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100711-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 571
ID   ADD78298 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100737-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
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Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 572
ID   ADE21121 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100736-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 573
ID   ADD77236 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100732-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 574
ID   ADE20383 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100733-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 575
ID   ADD75448 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100064-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 576
ID   ADD73964 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100708-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 577
ID   ADD74210 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100709-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 578
ID   ADD75940 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100718-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 579
ID   ADD85432 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100721-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
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Query Match:            45.57%          Indels:        2
RESULT 580
ID   ADE04981 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100726-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 581
ID   ADD75194 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 582
ID   ADD76738 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 583
ID   ADD86506 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 584
ID   ADE41224 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003104558-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 585
ID   ADD77974 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 586
ID   ADD77482 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
RESULT 587
ID   ADD77728 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100730-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%          Conservative:  63
Best Local Similarity:  47.85%          Mismatches:    105
Query Match:            45.57%          Indels:        2
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RESULT 588
ID   ADD85186 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100725-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 589
ID   ADD73718 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 590
ID   ADD74456 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 591
ID   ADD76984 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100716-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 592
ID   ADD85678 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003100720-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 593
ID   ADE05227 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100723-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 594
ID   ADD74702 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003100724-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 595
ID   ADG05514 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096959-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 596
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ID   ADG27068 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096962-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 597
ID   ADG11131 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 598
ID   ADG11910 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 599
ID   ADF94467 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 600
ID   ADG06563 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2003096966-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 601
ID   ADH38907 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096965-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 602
ID   ADG63658 standard; cDNA; 4834 BP.
DE   Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN   US2003180796-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 603
ID   ADG33997 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2004006206-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:  63
Best Local Similarity:  47.85%         Mismatches:    105
Query Match:            45.57%         Indels:        2
RESULT 604
ID   ADI33467 standard; cDNA; 4834 BP.
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DE   Human PRO polynucleotide #1.
PN   US2003096960-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:   63
Best Local Similarity:  47.85%         Mismatches:     105
Query Match:            45.57%         Indels:         2
RESULT 605
ID   ADH69561 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2004019183-A1.
PD   29-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:   63
Best Local Similarity:  47.85%         Mismatches:     105
Query Match:            45.57%         Indels:         2
RESULT 606
ID   ADI29722 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2003096961-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:   63
Best Local Similarity:  47.85%         Mismatches:     105
Query Match:            45.57%         Indels:         2
RESULT 607
ID   ADM27119 standard; cDNA; 4834 BP.
DE   Novel human secreted and transmembrane protein PRO6004 cDNA.
PN   US2004044179-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:   63
Best Local Similarity:  47.85%         Mismatches:     105
Query Match:            45.57%         Indels:         2
RESULT 608
ID   ADK66477 standard; cDNA; 4834 BP.
DE   Human PRO polynucleotide #1.
PN   US2004044180-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     67.18%         Conservative:   63
Best Local Similarity:  47.85%         Mismatches:     105
Query Match:            45.57%         Indels:         2
RESULT 609
ID   ADS82049 standard; DNA; 4891 BP.
DE   Human cancer-associated protein coding sequence #5.
PN   WO2004035789-A1.
PD   29-APR-2004.
PA   (GLDS ) LG LIFE SCI LTD.
Percent Similarity:     67.18%         Conservative:   63
Best Local Similarity:  47.85%         Mismatches:     105
Query Match:            45.57%         Indels:         2
RESULT 610
ID   ABN85384 standard; DNA; 1119 BP.
DE   Human NOV6, KILON-like protein, coding sequence.
PN   WO200255704-A2.
PD   18-JUL-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     67.18%         Conservative:   63
Best Local Similarity:  47.85%         Mismatches:     105
Query Match:            45.51%         Indels:         2
RESULT 611
ID   ADB62841 standard; cDNA; 2383 BP.
DE   Human cDNA encoding clone OCBBF20110210.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity:     66.87%         Conservative:   62
Best Local Similarity:  47.85%         Mismatches:     106
Query Match:            45.40%         Indels:         2
RESULT 612
ID   ABQ82338 standard; cDNA; 1165 BP.
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DE   Human NOV12b encoding cDNA SEQ ID NO:25.
PN   WO200262999-A2.
PD   15-AUG-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     68.45%         Conservative:   63
Best Local Similarity:  48.58%         Mismatches:     98
Query Match:            45.35%         Indels:         2
RESULT 613
ID   ABT17401 standard; DNA; 1809 BP.
DE   Human IG gene related nucleic acid SEQ ID No 27.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     67.06%         Conservative:   66
Best Local Similarity:  47.48%         Mismatches:     101
Query Match:            45.13%         Indels:         10
RESULT 614
ID   AAC78596 standard; cDNA; 2840 BP.
DE   Human PRO4993 nucleotide sequence SEQ ID NO:611.
PN   WO200053756-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:   63
Best Local Similarity:  47.55%         Mismatches:     106
Query Match:            45.13%         Indels:         2
RESULT 615
ID   ACA63979 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
PN   US2002192706-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:   63
Best Local Similarity:  47.55%         Mismatches:     106
Query Match:            45.13%         Indels:         2
RESULT 616
ID   ACA72143 standard; cDNA; 2840 BP.
DE   Human secreted and transmembrane PRO polypeptide #39 cDNA.
PN   US2002177553-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:   63
Best Local Similarity:  47.55%         Mismatches:     106
Query Match:            45.13%         Indels:         2
RESULT 617
ID   ABX92783 standard; cDNA; 2840 BP.
DE   cDNA encoding human PRO4993 polypeptide.
PN   US2002169284-A1.
PD   14-NOV-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:   63
Best Local Similarity:  47.55%         Mismatches:     106
Query Match:            45.13%         Indels:         2
RESULT 618
ID   ACA66524 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO4993.
PN   US2003004102-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:   63
Best Local Similarity:  47.55%         Mismatches:     106
Query Match:            45.13%         Indels:         2
RESULT 619
ID   ADA25149 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
PN   US2003050241-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:   63
Best Local Similarity:  47.55%         Mismatches:     106
Query Match:            45.13%         Indels:         2
RESULT 620
ID   ACD30125 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
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PN   US2003050240-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 621
ID   ADA12811 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO4993.
PN   US2003055216-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 622
ID   ACD29540 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane polypeptide cDNA #139.
PN   US2003049633-A1.
PD   13-MAR-2003.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 623
ID   ADB74117 standard; cDNA; 2840 BP.
DE   Human PRO polynucleotide sequence #139.
PN   US2003045462-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 624
ID   ADB76833 standard; cDNA; 2840 BP.
DE   Human PRO polynucleotide sequence #139.
PN   US2003083248-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 625
ID   ADC44259 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003054986-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 626
ID   ADC62019 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003049684-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 627
ID   ADC63983 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003054405-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 628
ID   ADC67083 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003060406-A1.
PD   27-MAR-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 629
ID   ADC69207 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003064407-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 630
ID   ADC63267 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003068648-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 631
ID   ADC68332 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003069178-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 632
ID   ADC41652 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003072745-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 633
ID   ADC67707 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003073131-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 634
ID   ADC62643 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003073624-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 635
ID   ADC42276 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003104998-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 636
ID   ADE49645 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003096744-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 637
ID   ADE35699 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203434-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 638
ID   ADE16813 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203435-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 639
ID   ADD73428 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203436-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 640
ID   ADD72786 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003194781-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 641
ID   ADE17437 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203433-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 642
ID   ADF47451 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195333-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 643
ID   ADG53208 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003216561-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 644
ID   ADG60528 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003206915-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 645
ID   ADI61288 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003077700-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 646
ID   ACD42944 standard; cDNA; 2840 BP.
DE   Novel human secreted and transmembrane protein PRO4993 cDNA.
PN   US2003050239-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 647
ID   ADE48945 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003104536-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 648
ID   ADE90046 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003130181-A1.
PD   10-JUL-2003.
PA   (ASHK/) ASHKENAZI A J.
PA   (BAKE/) BAKER K P.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GIRM/) GIRMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (KUOS/) KUO S S.
PA   (NAPI/) NAPIER M A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (SHEL/) SHELTON D L.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
RESULT 649
ID   ADF61686 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195345-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%         Conservative:  63
Best Local Similarity:  47.55%         Mismatches:    106
Query Match:            45.13%         Indels:        2
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RESULT 650
ID   ADF40378 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003198994-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 651
ID   ADF46174 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195148-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 652
ID   ADF24570 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003204055-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 653
ID   ADF41002 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199021-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 654
ID   ADF23946 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003203402-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 655
ID   ADF33929 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003194780-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 656
ID   ADF27396 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199436-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 657
ID   ADF28032 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199437-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 658
ID   ADF41626 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199435-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 659
ID   ADF33305 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003211091-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 660
ID   ADF25671 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003211092-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 661
ID   ADF26772 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003199674-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 662
ID   ADF34561 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003194410-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 663
ID   ADF46798 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003195344-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 664
ID   ADG50784 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003207803-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 665
ID   ADG50160 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003215905-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     66.87%          Conservative:  63
Best Local Similarity:  47.55%          Mismatches:    106
Query Match:            45.13%          Indels:        2
RESULT 666
ID   ADG52032 standard; cDNA; 2840 BP.
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DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003215908-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    66.87%         Conservative:  63
Best Local Similarity: 47.55%         Mismatches:    106
Query Match:           45.13%         Indels:        2
RESULT 667
ID   ADG49536 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003216305-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    66.87%         Conservative:  63
Best Local Similarity: 47.55%         Mismatches:    106
Query Match:           45.13%         Indels:        2
RESULT 668
ID   ADG48912 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2003216560-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    66.87%         Conservative:  63
Best Local Similarity: 47.55%         Mismatches:    106
Query Match:           45.13%         Indels:        2
RESULT 669
ID   ADG51408 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004005312-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    66.87%         Conservative:  63
Best Local Similarity: 47.55%         Mismatches:    106
Query Match:           45.13%         Indels:        2
RESULT 670
ID   ADG59352 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004005657-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    66.87%         Conservative:  63
Best Local Similarity: 47.55%         Mismatches:    106
Query Match:           45.13%         Indels:        2
RESULT 671
ID   ADG62808 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004006219-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    66.87%         Conservative:  63
Best Local Similarity: 47.55%         Mismatches:    106
Query Match:           45.13%         Indels:        2
RESULT 672
ID   ADM17610 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004048332-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    66.87%         Conservative:  63
Best Local Similarity: 47.55%         Mismatches:    106
Query Match:           45.13%         Indels:        2
RESULT 673
ID   ADL07444 standard; cDNA; 2840 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN   US2004063921-A1.
PD   01-APR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:    66.87%         Conservative:  63
Best Local Similarity: 47.55%         Mismatches:    106
Query Match:           45.13%         Indels:        2
RESULT 674
ID   AAT42094 standard; cDNA to mRNA; 756 BP.
DE   Human LAMP residues 46-294 coding sequence.
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PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:    76.68%         Conservative:  50
Best Local Similarity: 56.92%         Mismatches:    58
Query Match:           44.10%         Indels:        1
RESULT 675
ID   AAT42095 standard; cDNA to mRNA; 756 BP.
DE   Rat LAMP residues 46-294 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:    76.68%         Conservative:  50
Best Local Similarity: 56.92%         Mismatches:    58
Query Match:           44.05%         Indels:        1
RESULT 676
ID   ADH71417 standard; DNA; 1030 BP.
DE   Human gene of the invention NOV11q SEQ ID NO:313.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    64.20%         Conservative:  44
Best Local Similarity: 50.62%         Mismatches:    104
Query Match:           42.25%         Indels:        12
RESULT 677
ID   ADH71411 standard; DNA; 1033 BP.
DE   Human gene of the invention NOV11n SEQ ID NO:307.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    64.20%         Conservative:  44
Best Local Similarity: 50.62%         Mismatches:    104
Query Match:           42.25%         Indels:        12
RESULT 678
ID   ADH71413 standard; DNA; 1035 BP.
DE   Human gene of the invention NOV11o SEQ ID NO:309.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    64.20%         Conservative:  44
Best Local Similarity: 50.62%         Mismatches:    104
Query Match:           42.25%         Indels:        12
RESULT 679
ID   ABS76364 standard; DNA; 1427 BP.
DE   DNA encoding human immunoglobulin superfamily protein IGSFP-9.
PN   WO200272794-A2.
PD   19-SEP-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:    64.20%         Conservative:  44
Best Local Similarity: 50.62%         Mismatches:    104
Query Match:           42.25%         Indels:        12
RESULT 680
ID   AAD47371 standard; DNA; 2653 BP.
DE   Human LP289 DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
Percent Similarity:    64.20%         Conservative:  44
Best Local Similarity: 50.62%         Mismatches:    104
Query Match:           42.25%         Indels:        12
RESULT 681
ID   ADH71395 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11f SEQ ID NO:291.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    64.40%         Conservative:  45
Best Local Similarity: 50.46%         Mismatches:    103
Query Match:           42.19%         Indels:        12
RESULT 682
ID   ADH71389 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11c SEQ ID NO:285.
PN   WO2003102155-A2.
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PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    64.40%        Conservative:  45
Best Local Similarity: 50.46%        Mismatches:    103
Query Match:           42.19%        Indels:        12
RESULT 683
ID   ADH71401 standard; DNA; 926 BP.
DE   Human gene of the invention NOV11i SEQ ID NO:297.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 684
ID   ADH71405 standard; DNA; 927 BP.
DE   Human gene of the invention NOV11k SEQ ID NO:301.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 685
ID   ADH71409 standard; DNA; 946 BP.
DE   Human gene of the invention NOV11m SEQ ID NO:305.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 686
ID   ADH71393 standard; DNA; 946 BP.
DE   Human gene of the invention NOV11e SEQ ID NO:289.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 687
ID   ADH71415 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11p SEQ ID NO:311.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 688
ID   ADH71397 standard; DNA; 976 BP.
DE   Human gene of the invention NOV11g SEQ ID NO:293.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 689
ID   ABS71699 standard; DNA; 1017 BP.
DE   DNA encoding human NOV5b protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 690
ID   ADL35978 standard; cDNA; 1017 BP.
DE   Human NOVX cDNA #12.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 691
ID   ABS71698 standard; DNA; 1018 BP.
DE   DNA encoding human NOV5a protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 692
ID   ADL35976 standard; cDNA; 1018 BP.
DE   Human NOVX cDNA #11.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 693
ID   ADH71399 standard; DNA; 1018 BP.
DE   Human gene of the invention NOV11h SEQ ID NO:295.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 694
ID   ADH71387 standard; DNA; 1033 BP.
DE   Human gene of the invention NOV11b SEQ ID NO:283.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    66.11%        Conservative:  41
Best Local Similarity: 52.49%        Mismatches:    94
Query Match:           42.14%        Indels:        8
RESULT 695
ID   ADH71385 standard; DNA; 1271 BP.
DE   Human gene of the invention NOV11a SEQ ID NO:281.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:    63.89%        Conservative:  43
Best Local Similarity: 50.62%        Mismatches:    105
Query Match:           42.08%        Indels:        12
RESULT 696
ID   ADH71421 standard; DNA; 1271 BP.
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DE   Human gene of the invention NOV11s SEQ ID NO:317.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     63.89%        Conservative:  43
Best Local Similarity:  50.62%        Mismatches:    105
Query Match:            42.08%        Indels:        12
RESULT 697
ID   ABS71700 standard; DNA; 1136 BP.
DE   DNA encoding human NOV5c protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     65.78%        Conservative:  40
Best Local Similarity:  52.49%        Mismatches:    95
Query Match:            41.92%        Indels:        8
RESULT 698
ID   ADH71403 standard; DNA; 1171 BP.
DE   Human gene of the invention NOV11j SEQ ID NO:299.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     65.78%        Conservative:  40
Best Local Similarity:  52.49%        Mismatches:    95
Query Match:            41.92%        Indels:        8
RESULT 699
ID   ADH71419 standard; DNA; 1271 BP.
DE   Human gene of the invention NOV11r SEQ ID NO:315.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     63.89%        Conservative:  44
Best Local Similarity:  50.31%        Mismatches:    105
Query Match:            41.92%        Indels:        12
RESULT 700
ID   ADP28685 standard; DNA; 834 BP.
DE   Human secreted protein encoding sequence SEQ ID #683.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity:     68.33%        Conservative:  40
Best Local Similarity:  54.09%        Mismatches:    84
Query Match:            41.67%        Indels:        5
RESULT 701
ID   ABK35606 standard; DNA; 1011 BP.
DE   Gene encoding novel human secreted or membrane-associated protein #25.
PN   WO200204600-A2.
PD   17-JAN-2002.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
Percent Similarity:     65.12%        Conservative:  44
Best Local Similarity:  50.50%        Mismatches:    97
Query Match:            40.20%        Indels:        8
RESULT 702
ID   ABS71701 standard; DNA; 1169 BP.
DE   DNA encoding human NOV5d protein.
PN   WO200266643-A2.
PD   29-AUG-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     64.78%        Conservative:  43
Best Local Similarity:  50.50%        Mismatches:    98
Query Match:            39.92%        Indels:        8
RESULT 703
ID   ADH71407 standard; DNA; 1169 BP.
DE   Human gene of the invention NOV11l SEQ ID NO:303.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     64.78%        Conservative:  43
Best Local Similarity:  50.50%        Mismatches:    98
Query Match:            39.92%        Indels:        8
RESULT 704
ID   ABA06475 standard; cDNA; 2813 BP.
DE   Human cDNA SEQ ID NO: 141.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity:     70.45%        Conservative:  53
Best Local Similarity:  50.38%        Mismatches:    77
Query Match:            39.89%        Indels:        1
RESULT 705
ID   ABV83812 standard; cDNA; 2813 BP.
DE   Human polynucleotide SEQ ID NO 141.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
Percent Similarity:     70.45%        Conservative:  53
Best Local Similarity:  50.38%        Mismatches:    77
Query Match:            39.89%        Indels:        1
RESULT 706
ID   AAD47374 standard; DNA; 2601 BP.
DE   Human LP319b DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
Percent Similarity:     65.12%        Conservative:  44
Best Local Similarity:  50.50%        Mismatches:    97
Query Match:            39.04%        Indels:        9
RESULT 707
ID   ACH15238 standard; cDNA; 437 BP.
DE   Human adult brain cDNA #2450.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
Percent Similarity:     99.25%        Conservative:  0
Best Local Similarity:  99.25%        Mismatches:    1
Query Match:            38.21%        Indels:        0
RESULT 708
ID   ADH71391 standard; DNA; 760 BP.
DE   Human gene of the invention NOV11d SEQ ID NO:287.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     68.40%        Conservative:  32
Best Local Similarity:  55.60%        Mismatches:    74
Query Match:            38.07%        Indels:        5
RESULT 709
ID   ADL35982 standard; cDNA; 1168 BP.
DE   Human NOVX cDNA #14.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
Percent Similarity:     64.24%        Conservative:  43
Best Local Similarity:  50.00%        Mismatches:    99
Query Match:            37.76%        Indels:        10
RESULT 710
ID   ABK35605 standard; DNA; 1056 BP.
DE   Gene encoding novel human secreted or membrane-associated protein #24.
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PN   WO200204600-A2.
PD   17-JAN-2002.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
Percent Similarity:      64.26%         Conservative:  36
Best Local Similarity:   51.89%         Mismatches:    86
Query Match:             37.74%         Indels:        19
RESULT 711
ID   ADL35980 standard; cDNA; 1133 BP.
DE   Human NOVX cDNA #13.
PN   US2003207800-A1.
PD   06-NOV-2003.
PA   (MALY/) MALYANKAR U M.
PA   (SHEN/) SHENOY S G.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (GUOX/) GUO X.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (LILL/) LI L.
PA   (PADI/) PADIGARU M.
Percent Similarity:      64.78%         Conservative:  41
Best Local Similarity:   51.16%         Mismatches:    98
Query Match:             37.71%         Indels:        11
RESULT 712
ID   AAS28811 standard; cDNA; 4656 BP.
DE   Human immunoglobulin encoding cDNA SEQ ID No 57.
PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity:      69.81%         Conservative:  54
Best Local Similarity:   49.43%         Mismatches:    78
Query Match:             37.35%         Indels:        3
RESULT 713
ID   ADB31536 standard; cDNA; 4656 BP.
DE   Human cDNA encoding a novel protein SEQ ID NO 57.
PN   US2003077606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity:      69.81%         Conservative:  54
Best Local Similarity:   49.43%         Mismatches:    78
Query Match:             37.35%         Indels:        3
RESULT 714
ID   AAD47373 standard; DNA; 2597 BP.
DE   Human LP319a DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
Percent Similarity:      59.57%         Conservative:  45
Best Local Similarity:   45.90%         Mismatches:    106
Query Match:             36.68%         Indels:        28
RESULT 715
ID   ABL99899 standard; cDNA; 5666 BP.
DE   Human secretory polynucleotide (sptm) 154.
PN   WO200220756-A2.
PD   14-MAR-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:      63.61%         Conservative:  66
Best Local Similarity:   44.08%         Mismatches:    109
Query Match:             36.10%         Indels:        14
RESULT 716
ID   AAC91321 standard; cDNA; 537 BP.
DE   Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 21.
PN   WO200073509-A2.
PD   07-DEC-2000.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:      97.54%         Conservative:  0
Best Local Similarity:   97.54%         Mismatches:    3
Query Match:             34.99%         Indels:        0
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RESULT 717
ID   AAD47372 standard; DNA; 754 BP.
DE   Human LP289 splice variant (LP343) DNA.
PN   WO200274906-A2.
PD   26-SEP-2002.
PA   (ELIL ) LILLY & CO ELI.
Percent Similarity:      69.27%         Conservative:  29
Best Local Similarity:   55.96%         Mismatches:    62
Query Match:             33.58%         Indels:        5
RESULT 718
ID   AAS78035 standard; cDNA; 484 BP.
DE   DNA encoding novel human diagnostic protein #13839.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:      90.30%         Conservative:  5
Best Local Similarity:   86.57%         Mismatches:    13
Query Match:             33.22%         Indels:        0
RESULT 719
ID   ADP28686 standard; DNA; 666 BP.
DE   Human secreted protein encoding sequence SEQ ID #684.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity:      67.70%         Conservative:  31
Best Local Similarity:   53.98%         Mismatches:    68
Query Match:             33.19%         Indels:        5
RESULT 720
ID   ACH46276 standard; cDNA; 409 BP.
DE   Human infant brain cDNA #339.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
Percent Similarity:      95.87%         Conservative:  2
Best Local Similarity:   94.21%         Mismatches:    5
Query Match:             32.06%         Indels:        0
RESULT 721
ID   AAF93346 standard; cDNA; 452 BP.
DE   Spinal cord tissue cDNA encoding SRT protein SEQ ID 167.
PN   WO200107611-A2.
PD   01-FEB-2001.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:   100.00%        Mismatches:    0
Query Match:             32.00%         Indels:        0
RESULT 722
ID   AAS78034 standard; cDNA; 443 BP.
DE   DNA encoding novel human diagnostic protein #13838.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:      88.89%         Conservative:  0
Best Local Similarity:   88.89%         Mismatches:    3
Query Match:             31.53%         Indels:        11
RESULT 723
ID   ADQ83739 standard; cDNA; 919 BP.
DE   Human tumour-associated antigenic target (TAT) cDNA sequence #553.
PN   WO2004060270-A2.
PD   22-JUL-2004.
PA   (GETH ) GENENTECH INC.
PA   (WUTD/) WU T D.
PA   (ZHOU/) ZHOU Y.
Percent Similarity:      64.96%         Conservative:  35
Best Local Similarity:   50.00%         Mismatches:    74
Query Match:             30.79%         Indels:        8
RESULT 724
ID   AAC19214 standard; cDNA; 333 BP.
DE   Human secreted protein 5' EST, SEQ ID NO: 23289.
PN   EP1033401-A2.
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PD   06-SEP-2000.
PA   (GEST ) GENSET.
Percent Similarity:     95.50%         Conservative:  1
Best Local Similarity:  94.59%         Mismatches:    4
Query Match:            30.18%         Indels:        1
RESULT 725
ID   AAS78003 standard; cDNA; 2883 BP.
DE   DNA encoding novel human diagnostic protein #13807.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     56.58%         Conservative:  31
Best Local Similarity:  45.55%         Mismatches:    74
Query Match:            29.10%         Indels:        50
RESULT 726
ID   ADE08816 standard; DNA; 2883 BP.
DE   Novel DNA-related contig nucleotide sequence #60.
PN   WO2003054152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     56.58%         Conservative:  31
Best Local Similarity:  45.55%         Mismatches:    74
Query Match:            29.10%         Indels:        50
RESULT 727
ID   AAF93597 standard; cDNA; 585 BP.
DE   Umbilical vein endothelial cell cDNA encoding SRT protein SEQ ID 418.
PN   WO200107611-A2.
PD   01-FEB-2001.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     71.58%         Conservative:  40
Best Local Similarity:  50.53%         Mismatches:    50
Query Match:            27.16%         Indels:        4
RESULT 728
ID   ABS52769 standard; cDNA; 408 BP.
DE   Murine tuberous sclerosis complex 8 (TSC8) DNA.
PN   WO200246475-A2.
PD   13-JUN-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     75.00%         Conservative:  26
Best Local Similarity:  55.88%         Mismatches:    33
Query Match:            22.18%         Indels:        1
RESULT 729
ID   ADG63283 standard; DNA; 540 BP.
DE   Human OBCAM gene exon 2.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity:     78.38%         Conservative:  10
Best Local Similarity:  69.37%         Mismatches:    11
Query Match:            21.68%         Indels:        13
RESULT 730
ID   AAC02777 standard; cDNA; 352 BP.
DE   Human secreted protein 5' EST, SEQ ID NO: 2775.
PN   EP1033401-A2.
PD   06-SEP-2000.
PA   (GEST ) GENSET.
Percent Similarity:     82.80%         Conservative:  9
Best Local Similarity:  73.12%         Mismatches:    16
Query Match:            19.05%         Indels:        1
RESULT 731
ID   ABL25337 standard; DNA; 1242 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 27484.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     42.93%         Conservative:  55
Best Local Similarity:  27.99%         Mismatches:    147
Query Match:            18.74%         Indels:        63
RESULT 732
ID   ABL17651 standard; DNA; 948 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 4426.
PN   WO200171042-A2.
PD   27-SEP-2001.
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PA   (PEKE ) PE CORP NY.
Percent Similarity:     50.17%         Conservative:  54
Best Local Similarity:  31.86%         Mismatches:    125
Query Match:            18.44%         Indels:        22
RESULT 733
ID   ABL11515 standard; cDNA; 2010 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 29027.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     47.64%         Conservative:  56
Best Local Similarity:  28.72%         Mismatches:    125
Query Match:            16.97%         Indels:        30
RESULT 734
ID   ABX71182 standard; cDNA; 913 BP.
DE   Novel human cDNA sequence #407.
PN   WO200281731-A2.
PD   17-OCT-2002.
PA   (HYSE-) HYSEQ INC.
PA   (GOOD/) GOODRICH R W.
Percent Similarity:     66.13%         Conservative:  24
Best Local Similarity:  46.77%         Mismatches:    41
Query Match:            16.75%         Indels:        1
RESULT 735
ID   ABL04261 standard; cDNA; 1110 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 7265.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     44.37%         Conservative:  43
Best Local Similarity:  29.69%         Mismatches:    136
Query Match:            16.47%         Indels:        27
RESULT 736
ID   ABL04260 standard; cDNA; 3426 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 7262.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     44.37%         Conservative:  43
Best Local Similarity:  29.69%         Mismatches:    136
Query Match:            16.47%         Indels:        27
RESULT 737
ID   ABX56303 standard; DNA; 8243 BP.
DE   Human NOV25b CG93858-02 DNA SEQ ID 85.
PN   WO200281625-A2.
PD   17-OCT-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     42.47%         Conservative:  36
Best Local Similarity:  30.14%         Mismatches:    105
Query Match:            16.47%         Indels:        63
RESULT 738
ID   ADK60477 standard; DNA; 8546 BP.
DE   Angiogenesis differentially expressed gene GS-N52.
PN   FR2836687-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
Percent Similarity:     42.12%         Conservative:  36
Best Local Similarity:  29.79%         Mismatches:    106
Query Match:            16.09%         Indels:        63
RESULT 739
ID   ADK60778 standard; DNA; 8546 BP.
DE   Angiogenesis differentially expressed gene GS-N52.
PN   FR2836686-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
Percent Similarity:     42.12%         Conservative:  36
Best Local Similarity:  29.79%         Mismatches:    106
Query Match:            16.09%         Indels:        63
RESULT 740
ID   ADP73100 standard; DNA; 8546 BP.
DE   Angiogenesis inhibitor human DNA sequence, GS-N52.
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PN   FR2843753-A1.
PD   27-FEB-2004.
PA   (GENE/) GENE S.
PA   (ALMS/) AL M S.
Percent Similarity:     42.12%         Conservative:  36
Best Local Similarity:  29.79%         Mismatches:    106
Query Match:            16.09%         Indels:        63
RESULT 741
ID   ADS09799 standard; DNA; 8546 BP.
DE   Human therapeutic DNA - SEQ ID 36.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
Percent Similarity:     42.12%         Conservative:  36
Best Local Similarity:  29.79%         Mismatches:    106
Query Match:            16.09%         Indels:        63
RESULT 742
ID   ADO08272 standard; cDNA; 15659 BP.
DE   Human NOVX polynucleotide #10.
PN   US2004018594-A1.
PD   29-JAN-2004.
PA   (ALSO/) ALSOBROOK J P.
PA   (ANDE/) ANDERSON D W.
PA   (BOLD/) BOLDOG F L.
PA   (BURG/) BURGESS C E.
PA   (CASM/) CASMAN S J.
PA   (CHAP/) CHAPOVAL A.
PA   (EDIN/) EDINGER S R.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (GUNT/) GUNTHER E.
PA   (GUOX/) GUO X S.
PA   (KEKU/) KEKUDA R.
PA   (LEPL/) LEPLEY D M.
PA   (LILL/) LI L.
PA   (LIUX/) LIU X.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLER C E.
PA   (MILL/) MILLET I.
PA   (PADI/) PADIGARU M.
PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
PA   (RIEG/) RIEGER D K.
PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (SPYT/) SPYTEK K A.
PA   (TAUP/) TAUPIER R J.
PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
PA   (ZERH/) ZERHUSEN B D.
Percent Similarity:     42.12%         Conservative:  36
Best Local Similarity:  29.79%         Mismatches:    106
Query Match:            16.09%         Indels:        63
RESULT 743
ID   ACA10120 standard; cDNA; 15660 BP.
DE   Human NOVX polynucleotide #10.
PN   WO200290504-A2.
PD   14-NOV-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     42.12%         Conservative:  36
Best Local Similarity:  29.79%         Mismatches:    106
Query Match:            16.09%         Indels:        63
RESULT 744
ID   ADH72105 standard; DNA; 15660 BP.
DE   Human gene of the invention NOV43c SEQ ID NO:1001.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     42.12%         Conservative:  36
Best Local Similarity:  29.79%         Mismatches:    106
Query Match:            16.09%         Indels:        63
RESULT 745
ID   ADK60455 standard; DNA; 18207 BP.
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DE   Angiogenesis differentially expressed gene GS-N29.
PN   FR2836687-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
Percent Similarity:     42.56%         Conservative:  33
Best Local Similarity:  31.14%         Mismatches:    109
Query Match:            16.09%         Indels:        57
RESULT 746
ID   ADK60756 standard; DNA; 18207 BP.
DE   Angiogenesis differentially expressed gene GS-N29.
PN   FR2836686-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
Percent Similarity:     42.56%         Conservative:  33
Best Local Similarity:  31.14%         Mismatches:    109
Query Match:            16.09%         Indels:        57
RESULT 747
ID   ADP73078 standard; DNA; 18207 BP.
DE   Angiogenesis inhibitor human DNA sequence, GS-N29.
PN   FR2843753-A1.
PD   27-FEB-2004.
PA   (GENE/) GENE S.
PA   (ALMS/) AL M S.
Percent Similarity:     42.56%         Conservative:  33
Best Local Similarity:  31.14%         Mismatches:    109
Query Match:            16.09%         Indels:        57
RESULT 748
ID   ADH72103 standard; DNA; 2136 BP.
DE   Human gene of the invention NOV43b SEQ ID NO:999.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.36%         Conservative:  35
Best Local Similarity:  31.12%         Mismatches:    111
Query Match:            15.97%         Indels:        51
RESULT 749
ID   ACA10119 standard; cDNA; 2153 BP.
DE   Human NOVX polynucleotide #9.
PN   WO200290504-A2.
PD   14-NOV-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.36%         Conservative:  35
Best Local Similarity:  31.12%         Mismatches:    111
Query Match:            15.97%         Indels:        51
RESULT 750
ID   ADH72101 standard; DNA; 2153 BP.
DE   Human gene of the invention NOV43a SEQ ID NO:997.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.36%         Conservative:  35
Best Local Similarity:  31.12%         Mismatches:    111
Query Match:            15.97%         Indels:        51
RESULT 751
ID   ADO08270 standard; cDNA; 2153 BP.
DE   Human NOVX polynucleotide #9.
PN   US2004018594-A1.
PD   29-JAN-2004.
PA   (ALSO/) ALSOBROOK J P.
PA   (ANDE/) ANDERSON D W.
PA   (BOLD/) BOLDOG F L.
PA   (BURG/) BURGESS C E.
PA   (CASM/) CASMAN S J.
PA   (CHAP/) CHAPOVAL A.
PA   (EDIN/) EDINGER S R.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (GUNT/) GUNTHER E.
PA   (GUOX/) GUO X S.
PA   (KEKU/) KEKUDA R.
PA   (LEPL/) LEPLEY D M.
PA   (LILL/) LI L.
PA   (LIUX/) LIU X.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLER C E.
PA   (MILL/) MILLET I.
PA   (PADI/) PADIGARU M.
PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
PA   (RIEG/) RIEGER D K.
PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (SPYT/) SPYTEK K A.
PA   (TAUP/) TAUPIER R J.
PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
PA   (ZERH/) ZERHUSEN B D.
Percent Similarity:     43.36%         Conservative:  35
Best Local Similarity:  31.12%         Mismatches:    111
Query Match:            15.97%         Indels:        51
RESULT 752
ID   ACD03633 standard; cDNA; 2916 BP.
DE   Novel human GPCR related protein NOV9b cDNA.
PN   WO200299116-A2.
PD   12-DEC-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.97%         Conservative:  38
Best Local Similarity:  30.50%         Mismatches:    117
Query Match:            15.97%         Indels:        41
RESULT 753
ID   AAS68120 standard; cDNA; 3910 BP.
DE   DNA encoding novel human diagnostic protein #3924.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     43.36%         Conservative:  35
Best Local Similarity:  31.12%         Mismatches:    111
Query Match:            15.97%         Indels:        51
RESULT 754
ID   AAI72024 standard; cDNA; 4073 BP.
DE   Human thrombospondin protein, BTL.012, coding sequence.
PN   WO200174852-A2.
PD   11-OCT-2001.
PA   (FARB ) BAYER CORP.
Percent Similarity:     43.36%         Conservative:  35
Best Local Similarity:  31.12%         Mismatches:    111
Query Match:            15.97%         Indels:        51
RESULT 755
ID   ADL93996 standard; cDNA; 5877 BP.
DE   Human G-coupled protein receptor-related gene #44.
PN   US2004006205-A1.
PD   08-JAN-2004.
PA   (LILL/) LI L.
PA   (GERL/) GERLACH V.
PA   (LIUX/) LIU X.
PA   (MILL/) MILLER C E.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PENA/) PENA C E A.
PA   (SHEN/) SHENOY S G.
PA   (ZHON/) ZHONG H.
PA   (SMIT/) SMITHSON G.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (VOSS/) VOSS E Z.
PA   (VERN/) VERNET C A.
PA   (MACD/) MACDOUGALL J R.
PA   (RAST/) RASTELLI L.
PA   (ANDE/) ANDERSON D W.
PA   (ZHON/) ZHONG M.
PA   (MEZE/) MEZES P S.
PA   (FURT/) FURTAK K.
PA   (PATT/) PATTURAJAN M.
PA   (BURG/) BURGESS C E.
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PA   (MALY/) MALYANKAR U M.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (EDIN/) EDINGER S.
PA   (MAZU/) MAZUR A.
Percent Similarity:     43.36%         Conservative:  35
Best Local Similarity:  31.12%         Mismatches:    111
Query Match:            15.97%         Indels:        51
RESULT 756
ID   ADE16057 standard; DNA; 5935 BP.
DE   G-coupled protein receptor related polypeptide DNA, SEQ ID No 87.
PN   WO200283841-A2.
PD   24-OCT-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.36%         Conservative:  35
Best Local Similarity:  31.12%         Mismatches:    111
Query Match:            15.97%         Indels:        51
RESULT 757
ID   ABX56304 standard; DNA; 6343 BP.
DE   Human NOV25c CG56914-03 DNA SEQ ID 87.
PN   WO200281625-A2.
PD   17-OCT-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.36%         Conservative:  35
Best Local Similarity:  31.12%         Mismatches:    111
Query Match:            15.97%         Indels:        51
RESULT 758
ID   ADH72107 standard; DNA; 6343 BP.
DE   Human gene of the invention NOV43d SEQ ID NO:1003.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.36%         Conservative:  35
Best Local Similarity:  31.12%         Mismatches:    111
Query Match:            15.97%         Indels:        51
RESULT 759
ID   ABQ86156 standard; DNA; 16908 BP.
DE   Novel human gene. SEQ ID 27.
PN   WO200250105-A1.
PD   27-JUN-2002.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
Percent Similarity:     43.36%         Conservative:  35
Best Local Similarity:  31.12%         Mismatches:    111
Query Match:            15.97%         Indels:        51
RESULT 760
ID   ADQ22570 standard; DNA; 18248 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5390.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity:     43.77%         Conservative:  38
Best Local Similarity:  30.25%         Mismatches:    117
Query Match:            15.92%         Indels:        41
RESULT 761
ID   ADM93822 standard; DNA; 2916 BP.
DE   DNA encoding human NOV protein #21.
PN   US2004009480-A1.
PD   15-JAN-2004.
PA   (ANDE/) ANDERSON D W.
PA   (BAUM/) BAUMGARTNER J C.
PA   (BOLD/) BOLDOG F L.
PA   (CASM/) CASMAN S J.
PA   (EDIN/) EDINGER S R.
PA   (GANG/) GANGOLLI E A.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (GUOX/) GUO X S.
PA   (HJAL/) HJALT T.
PA   (KEKU/) KEKUDA R.
PA   (LILL/) LI L.
PA   (MACD/) MACDOUGALL J R.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLET I.
PA   (PADI/) PADIGARU M.
PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
PA   (RAST/) RASTELLI L.
PA   (SHIM/) SHIMKETS R A.
PA   (STON/) STONE D J.
PA   (SPYT/) SPYTEK K A.
PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
PA   (ZERH/) ZERHUSEN B D.
Percent Similarity:     43.01%          Conservative:  37
Best Local Similarity:  30.07%          Mismatches:    114
Query Match:            15.86%          Indels:        49
RESULT 762
ID   ABL12455 standard; cDNA; 1710 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 31847.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     43.10%          Conservative:  59
Best Local Similarity:  26.15%          Mismatches:    159
Query Match:            15.75%          Indels:        39
RESULT 763
ID   ADB53259 standard; DNA; 3170 BP.
DE   Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3801.
PN   WO2003065993-A2.
PD   14-AUG-2003.
PA   (GENE-) GENE LOGIC INC.
Percent Similarity:     42.52%          Conservative:  50
Best Local Similarity:  25.51%          Mismatches:    132
Query Match:            15.37%          Indels:        37
RESULT 764
ID   ADI24496 standard; cDNA; 2960 BP.
DE   Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:46.
PN   WO2004004785-A1.
PD   15-JAN-2004.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     43.31%          Conservative:  50
Best Local Similarity:  25.70%          Mismatches:    133
Query Match:            15.28%          Indels:        28
RESULT 765
ID   ADA53985 standard; cDNA; 3309 BP.
DE   Human coding sequence, SEQ ID 1553.
PN   EP1293569-A2.
PD   19-MAR-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity:     43.31%          Conservative:  50
Best Local Similarity:  25.70%          Mismatches:    133
Query Match:            15.28%          Indels:        28
RESULT 766
ID   AAH98595 standard; cDNA; 4710 BP.
DE   Human EST-derived coding sequence SEQ ID NO: 452.
PN   WO200154477-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     43.31%          Conservative:  50
Best Local Similarity:  25.70%          Mismatches:    133
Query Match:            15.28%          Indels:        28
RESULT 767
ID   AAH98610 standard; cDNA; 4710 BP.
DE   Human EST-derived coding sequence SEQ ID NO: 467.
PN   WO200154477-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     43.31%          Conservative:  50
Best Local Similarity:  25.70%          Mismatches:    133
Query Match:            15.28%          Indels:        28
RESULT 768
ID   AAD14203 standard; DNA; 8513 BP.
DE   MESVR/EGFP/IRESNCAMPro(ori) vector.
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PN   WO200155371-A1.
PD   02-AUG-2001.
PA   (SCRI ) SCRIPPS RES INST.
Percent Similarity:     43.31%          Conservative:  50
Best Local Similarity:  25.70%          Mismatches:    133
Query Match:            15.28%          Indels:        28
RESULT 769
ID   ADD25618 standard; DNA; 2633 BP.
DE   Binding domain-immunoglobulin fusion protein-associated DNA #93.
PN   US2003118592-A1.
PD   26-JUN-2003.
PA   (GENE-) GENECRAFT INC.
Percent Similarity:     43.31%          Conservative:  50
Best Local Similarity:  25.70%          Mismatches:    133
Query Match:            15.23%          Indels:        28
RESULT 770
ID   ADI31624 standard; cDNA; 2633 BP.
DE   Human cDNA #950.
PN   US6607879-B1.
PD   19-AUG-2003.
PA   (INCY-) INCYTE CORP.
Percent Similarity:     43.31%          Conservative:  50
Best Local Similarity:  25.70%          Mismatches:    133
Query Match:            15.23%          Indels:        28
RESULT 771
ID   ADL12516 standard; cDNA; 5807 BP.
DE   Human steroid-induced C3A liver cell cDNA #245.
PN   US6673549-B1.
PD   06-JAN-2004.
PA   (INCY-) INCYTE CORP.
Percent Similarity:     43.31%          Conservative:  50
Best Local Similarity:  25.70%          Mismatches:    133
Query Match:            15.17%          Indels:        28
RESULT 772
ID   AAD56185 standard; DNA; 6801 BP.
DE   Human LRRCAPS DNA #2.
PN   WO2003035831-A2.
PD   01-MAY-2003.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     39.58%          Conservative:  35
Best Local Similarity:  29.17%          Mismatches:    147
Query Match:            15.17%          Indels:        56
RESULT 773
ID   ADH48823 standard; DNA; 7097 BP.
DE   NOV45B coding sequence, SEQ ID 107.
PN   WO200268652-A2.
PD   06-SEP-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     41.99%          Conservative:  43
Best Local Similarity:  29.00%          Mismatches:    165
Query Match:            15.14%          Indels:        28
RESULT 774
ID   ADH48821 standard; DNA; 4321 BP.
DE   NOV45A coding sequence, SEQ ID 105.
PN   WO200268652-A2.
PD   06-SEP-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     41.74%          Conservative:  41
Best Local Similarity:  28.97%          Mismatches:    152
Query Match:            15.03%          Indels:        36
RESULT 775
ID   AAL62047 standard; cDNA; 3360 BP.
DE   Human cell adhesion and extracellular matrix protein (CADECM)-35 cDNA.
PN   WO2003047526-A2.
PD   12-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:     41.84%          Conservative:  50
Best Local Similarity:  24.83%          Mismatches:    133
Query Match:            15.01%          Indels:        38
RESULT 776
ID   ABL23499 standard; DNA; 2190 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 21970.
PN   WO200171042-A2.
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PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     41.18%        Conservative:  49
Best Local Similarity:  26.01%        Mismatches:    131
Query Match:            14.95%        Indels:        60
RESULT 777
ID   ADQ89919 standard; DNA; 4491 BP.
DE   Antagonist of cell cycle progression nucleotide sequence #175.
PN   WO2004063362-A2.
PD   29-JUL-2004.
PA   (CYCL-) CYCLACEL LTD.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 778
ID   ADQ89913 standard; DNA; 4491 BP.
DE   Antagonist of cell cycle progression nucleotide sequence #172.
PN   WO2004063362-A2.
PD   29-JUL-2004.
PA   (CYCL-) CYCLACEL LTD.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 779
ID   AAZ51671 standard; cDNA; 5510 BP.
DE   Human p53 target molecule, PRG2 cDNA.
PN   WO200012526-A1.
PD   09-MAR-2000.
PA   (UYPR-) UNIV PRINCETON.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 780
ID   ABK83723 standard; cDNA; 5510 BP.
DE   Human cDNA differentially expressed in granulocytic cells #294.
PN   WO200228999-A2.
PD   11-APR-2002.
PA   (GENE-) GENE LOGIC INC.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 781
ID   ABN95260 standard; DNA; 5510 BP.
DE   Gene #1758 used to diagnose liver cancer.
PN   WO200229103-A2.
PD   11-APR-2002.
PA   (GENE-) GENE LOGIC INC.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 782
ID   ADD89099 standard; cDNA; 5510 BP.
DE   Encoding sequence TAT264.
PN   WO2003057160-A2.
PD   17-JUL-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 783
ID   ABX08782 standard; cDNA; 5510 BP.
DE   Angiogenesis-associated human polynucleotide sequence #44.
PN   WO200279492-A2.
PD   10-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 784
ID   ADQ18901 standard; DNA; 5510 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 1720.
PN   WO2004048938-A2.
PD   10-JUN-2004.
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PA   (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 785
ID   ABA08831 standard; cDNA; 5530 BP.
DE   Human peroxidasin homologue-encoding cDNA, SEQ ID NO:607.
PN   WO200157188-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 786
ID   ACD05839 standard; cDNA; 5530 BP.
DE   Novel human contig #13.
PN   WO2003023013-A2.
PD   20-MAR-2003.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 787
ID   ADL35716 standard; DNA; 6807 BP.
DE   Human peroxidasin-melanoma antigen-related DNA.
PN   WO2004019893-A2.
PD   11-MAR-2004.
PA   (RIGE-) RIGEL PHARM INC.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 788
ID   AAV99922 standard; cDNA; 6847 BP.
DE   Melanoma associated antigen MG50 gene.
PN   WO9855133-A1.
PD   10-DEC-1998.
PA   (REGC ) UNIV CALIFORNIA.
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 789
ID   ABQ88160 standard; cDNA; 6847 BP.
DE   Human osteoblast differentiation related cDNA SEQ ID NO 67.
PN   WO200250301-A2.
PD   27-JUN-2002.
PA   (GENE-) GENE LOGIC INC.
PA   (PROC ) PROCTER & GAMBLE CO.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 790
ID   ADR66609 standard; DNA; 6847 BP.
DE   Human prostatic carcinoma derived DNA SEQ ID 121 #3.
PN   WO2004076614-A2.
PD   10-SEP-2004.
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (ROSE/) ROSENTHAL A.
PA   (HERM/) HERMANN K.
PA   (PILA/) PILARSKY C.
Percent Similarity:     38.70%        Conservative:  32
Best Local Similarity:  28.79%        Mismatches:    147
Query Match:            14.87%        Indels:        51
RESULT 791
ID   ADR65865 standard; DNA; 6847 BP.
DE   Human prostatic carcinoma derived DNA SEQ ID 61 #1.
PN   WO2004076614-A2.
PD   10-SEP-2004.
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (ROSE/) ROSENTHAL A.
PA   (HERM/) HERMANN K.
PA   (PILA/) PILARSKY C.
Percent Similarity:     38.70%          Conservative:  32
Best Local Similarity:  28.79%          Mismatches:    147
Query Match:            14.87%          Indels:        51
RESULT 792
ID   ADR66267 standard; DNA; 6847 BP.
DE   Human prostatic carcinoma derived DNA SEQ ID 121 #2.
PN   WO2004076614-A2.
PD   10-SEP-2004.
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (ROSE/) ROSENTHAL A.
PA   (HERM/) HERMANN K.
PA   (PILA/) PILARSKY C.
Percent Similarity:     38.70%          Conservative:  32
Best Local Similarity:  28.79%          Mismatches:    147
Query Match:            14.87%          Indels:        51
RESULT 793
ID   ADR66768 standard; DNA; 6847 BP.
DE   Human prostatic carcinoma derived DNA SEQ ID 61 #4.
PN   WO2004076614-A2.
PD   10-SEP-2004.
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (ROSE/) ROSENTHAL A.
PA   (HERM/) HERMANN K.
PA   (PILA/) PILARSKY C.
Percent Similarity:     38.70%          Conservative:  32
Best Local Similarity:  28.79%          Mismatches:    147
Query Match:            14.87%          Indels:        51
RESULT 794
ID   ADF81722 standard; DNA; 6939 BP.
DE   Leukaemia-related DNA sequence #2278.
PN   WO2003039443-A2.
PD   15-MAY-2003.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA   (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA   (HAFE/) HAFERLACH T.
PA   (SCHO/) SCHOCH C.
PA   (KERN/) KERN W.
Percent Similarity:     38.70%          Conservative:  32
Best Local Similarity:  28.79%          Mismatches:    147
Query Match:            14.87%          Indels:        51
RESULT 795
ID   ADF81721 standard; DNA; 6939 BP.
DE   Leukaemia-related DNA sequence #2277.
PN   WO2003039443-A2.
PD   15-MAY-2003.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA   (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA   (HAFE/) HAFERLACH T.
PA   (SCHO/) SCHOCH C.
PA   (KERN/) KERN W.
Percent Similarity:     38.70%          Conservative:  32
Best Local Similarity:  28.79%          Mismatches:    147
Query Match:            14.87%          Indels:        51
RESULT 796
ID   ABL17650 standard; DNA; 3060 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 4423.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     44.74%          Conservative:  54
Best Local Similarity:  28.53%          Mismatches:    124
Query Match:            14.78%          Indels:        62
RESULT 797
ID   ABS70409 standard; cDNA; 6814 BP.
DE   Human bone remodelling gene #66.
PN   US6426186-B1.
PD   30-JUL-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:     38.39%          Conservative:  32
Best Local Similarity:  28.48%          Mismatches:    148
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Query Match:            14.59%          Indels:        51
RESULT 798
ID   ABX63089 standard; cDNA; 4978 BP.
DE   Human cDNA #89 differentially expressed in activated vascular tissue.
PN   US2002137081-A1.
PD   26-SEP-2002.
PA   (BAND/) BANDMAN O.
Percent Similarity:     43.15%          Conservative:  50
Best Local Similarity:  26.03%          Mismatches:    133
Query Match:            14.56%          Indels:        33
RESULT 799
ID   AAX55767 standard; cDNA; 4188 BP.
DE   Drosophila Robo 1 polypeptde encoding cDNA.
PN   WO9925833-A1.
PD   27-MAY-1999.
PA   (REGC ) UNIV CALIFORNIA.
Percent Similarity:     42.16%          Conservative:  49
Best Local Similarity:  26.14%          Mismatches:    127
Query Match:            14.45%          Indels:        50
RESULT 800
ID   AAX57250 standard; cDNA; 4188 BP.
DE   Drosophila sp. ROBO1 cDNA.
PN   WO9920764-A1.
PD   29-APR-1999.
PA   (REGC ) UNIV CALIFORNIA.
Percent Similarity:     42.16%          Conservative:  49
Best Local Similarity:  26.14%          Mismatches:    127
Query Match:            14.45%          Indels:        50
RESULT 801
ID   ABL10471 standard; cDNA; 2113 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 25895.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     42.34%          Conservative:  58
Best Local Similarity:  26.18%          Mismatches:    134
Query Match:            14.42%          Indels:        73
RESULT 802
ID   ABL22881 standard; DNA; 4355 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 20116.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     42.16%          Conservative:  49
Best Local Similarity:  26.14%          Mismatches:    127
Query Match:            14.40%          Indels:        50
RESULT 803
ID   ABX13540 standard; DNA; 93801 BP.
DE   Human RGS11 DNA.
PN   WO2002103355-A1.
PD   27-DEC-2002.
PA   (TAKE ) TAKEDA CHEM IND LTD.
Percent Similarity:     42.96%          Conservative:  37
Best Local Similarity:  29.60%          Mismatches:    132
Query Match:            14.34%          Indels:        26
RESULT 804
ID   ADQ89963 standard; DNA; 103052 BP.
DE   Antagonist of cell cycle progression nucleotide sequence #197.
PN   WO2004063362-A2.
PD   29-JUL-2004.
PA   (CYCL-) CYCLACEL LTD.
Percent Similarity:     42.96%          Conservative:  37
Best Local Similarity:  29.60%          Mismatches:    132
Query Match:            14.34%          Indels:        26
RESULT 805
ID   ADM74170 standard; DNA; 1140 BP.
DE   Human NOV3A gene sequence SeqID9.
PN   WO2004015079-A2.
PD   19-FEB-2004.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.38%          Conservative:  52
Best Local Similarity:  27.38%          Mismatches:    123
Query Match:            14.31%          Indels:        61
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RESULT 806
ID   AAZ06640 standard; cDNA; 1335 BP.
DE   Beta-secretase polynucleotide.
PN   US5942400-A.
PD   24-AUG-1999.
PA   (ELAN-) ELAN PHARM INC.
Percent Similarity:     42.39%        Conservative:  58
Best Local Similarity:  26.63%        Mismatches:    137
Query Match:            14.17%        Indels:        76
RESULT 807
ID   AAC85809 standard; cDNA; 1335 BP.
DE   Beta-secretase cDNA.
PN   US6221645-B1.
PD   24-APR-2001.
PA   (ELAN-) ELAN PHARM INC.
Percent Similarity:     42.39%        Conservative:  58
Best Local Similarity:  26.63%        Mismatches:    137
Query Match:            14.17%        Indels:        76
RESULT 808
ID   ABL14207 standard; cDNA; 2131 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 37103.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     39.78%        Conservative:  53
Best Local Similarity:  24.93%        Mismatches:    131
Query Match:            14.17%        Indels:        84
RESULT 809
ID   ADM74176 standard; DNA; 918 BP.
DE   Human NOV3D gene sequence SeqID15.
PN   WO2004015079-A2.
PD   19-FEB-2004.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.38%        Conservative:  53
Best Local Similarity:  27.08%        Mismatches:    123
Query Match:            14.04%        Indels:        61
RESULT 810
ID   ABT17377 standard; DNA; 1216 BP.
DE   Human IG gene related nucleic acid SEQ ID No 3.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     43.60%        Conservative:  55
Best Local Similarity:  26.83%        Mismatches:    124
Query Match:            14.04%        Indels:        61
RESULT 811
ID   ABT17376 standard; DNA; 1242 BP.
DE   Human IG gene related nucleic acid SEQ ID No 2.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     43.06%        Conservative:  57
Best Local Similarity:  26.91%        Mismatches:    137
Query Match:            14.04%        Indels:        65
RESULT 812
ID   ADI19787 standard; DNA; 2113 BP.
DE   Human NOV12 DNA.
PN   US2004002134-A1.
PD   01-JAN-2004.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.06%        Conservative:  57
Best Local Similarity:  26.91%        Mismatches:    137
Query Match:            14.04%        Indels:        65
RESULT 813
ID   AAF27862 standard; cDNA; 2116 BP.
DE   Human NOV12 cDNA.
PN   WO200075321-A2.
PD   14-DEC-2000.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.06%        Conservative:  57
Best Local Similarity:  26.91%        Mismatches:    137
Query Match:            14.04%        Indels:        65
RESULT 814
ID   ABT17375 standard; DNA; 2116 BP.
DE   Human IG gene related nucleic acid SEQ ID No 1.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     43.06%        Conservative:  57
Best Local Similarity:  26.91%        Mismatches:    137
Query Match:            14.04%        Indels:        65
RESULT 815
ID   ACD40265 standard; DNA; 2116 BP.
DE   Human breast tumour associated protein 47-like polypeptide NOV12 DNA.
PN   US2003027158-A1.
PD   06-FEB-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.06%        Conservative:  57
Best Local Similarity:  26.91%        Mismatches:    137
Query Match:            14.04%        Indels:        65
RESULT 816
ID   ADM56388 standard; cDNA; 2116 BP.
DE   Human cDNA encoding cell adhesion molecule NOV12.
PN   US2003082554-A1.
PD   01-MAY-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.06%        Conservative:  57
Best Local Similarity:  26.91%        Mismatches:    137
Query Match:            14.04%        Indels:        65
RESULT 817
ID   ADF66750 standard; cDNA; 2116 BP.
DE   cDNA encoding novel human protein NOV12.
PN   US2003199103-A1.
PD   23-OCT-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.06%        Conservative:  57
Best Local Similarity:  26.91%        Mismatches:    137
Query Match:            14.04%        Indels:        65
RESULT 818
ID   ADO60260 standard; DNA; 2116 BP.
DE   Human NOV12 DNA.
PN   US2003134430-A1.
PD   17-JUL-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     43.06%        Conservative:  57
Best Local Similarity:  26.91%        Mismatches:    137
Query Match:            14.04%        Indels:        65
RESULT 819
ID   ABK94901 standard; cDNA; 2422 BP.
DE   Human novel polynucleotide #12.
PN   WO200244340-A2.
PD   06-JUN-2002.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     43.06%        Conservative:  57
Best Local Similarity:  26.91%        Mismatches:    137
Query Match:            14.04%        Indels:        65
RESULT 820
ID   AAS86623 standard; cDNA; 16421 BP.
DE   DNA encoding novel human diagnostic protein #22427.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     42.86%        Conservative:  42
Best Local Similarity:  26.19%        Mismatches:    115
Query Match:            14.04%        Indels:        29
RESULT 821
ID   ADO47373 standard; DNA; 1761 BP.
DE   Human neurotrimin-like protein-related DNA SeqID8.
PN   WO2004039942-A2.
PD   13-MAY-2004.
PA   (NUVE-) NUVELO.
Percent Similarity:     43.97%        Conservative:  51
Best Local Similarity:  27.36%        Mismatches:    132
Query Match:            14.01%        Indels:        40
RESULT 822
ID   ABL54191 standard; cDNA; 2196 BP.
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DE   Neurotrimin-like protein splice variant coding sequence.
PN   WO200157175-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     43.97%          Conservative:  51
Best Local Similarity:  27.36%          Mismatches:    132
Query Match:            14.01%          Indels:        40
RESULT 823
ID   ADO47371 standard; DNA; 2196 BP.
DE   Human neurotrimin-like protein-related gene SeqID6.
PN   WO2004039942-A2.
PD   13-MAY-2004.
PA   (NUVE-) NUVELO.
Percent Similarity:     43.97%          Conservative:  51
Best Local Similarity:  27.36%          Mismatches:    132
Query Match:            14.01%          Indels:        40
RESULT 824
ID   ABL09371 standard; cDNA; 2658 BP.
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 22595.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     42.56%          Conservative:  54
Best Local Similarity:  26.49%          Mismatches:    122
Query Match:            13.87%          Indels:        71
RESULT 825
ID   ABL54189 standard; cDNA; 1124 BP.
DE   Neurotrimin-like protein partial coding sequence.
PN   WO200157175-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 826
ID   ADO47367 standard; DNA; 1124 BP.
DE   Human neurotrimin-like protein-related gene SeqID2.
PN   WO2004039942-A2.
PD   13-MAY-2004.
PA   (NUVE-) NUVELO.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 827
ID   ADO47370 standard; cDNA; 1377 BP.
DE   Human neurotrimin-like protein-related cDNA SeqID5.
PN   WO2004039942-A2.
PD   13-MAY-2004.
PA   (NUVE-) NUVELO.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 828
ID   ABL54190 standard; cDNA; 1699 BP.
DE   Neurotrimin-like protein coding sequence.
PN   WO200157175-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 829
ID   ADO47368 standard; cDNA; 1699 BP.
DE   Human neurotrimin-like protein-related cDNA SeqID3.
PN   WO2004039942-A2.
PD   13-MAY-2004.
PA   (NUVE-) NUVELO.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 830
ID   ADS09923 standard; DNA; 1699 BP.
DE   Human therapeutic DNA - SEQ ID 160.
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PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 831
ID   ADO47384 standard; DNA; 2868 BP.
DE   Human neurotrimin-like protein-related DNA SeqID12.
PN   WO2004039942-A2.
PD   13-MAY-2004.
PA   (NUVE-) NUVELO.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 832
ID   AAL62046 standard; cDNA; 3257 BP.
DE   Human cell adhesion and extracellular matrix protein (CADECM)-34 cDNA.
PN   WO2003047526-A2.
PD   12-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 833
ID   ADO47382 standard; DNA; 3312 BP.
DE   Human neurotrimin-like protein-related gene SeqID17.
PN   WO2004039942-A2.
PD   13-MAY-2004.
PA   (NUVE-) NUVELO.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 834
ID   ADS09924 standard; DNA; 3312 BP.
DE   Human therapeutic DNA - SEQ ID 161.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 835
ID   ADS10423 standard; DNA; 3386 BP.
DE   Human therapeutic DNA - SEQ ID 660.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 836
ID   AAS76287 standard; cDNA; 3868 BP.
DE   DNA encoding novel human diagnostic protein #12091.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 837
ID   ADH72133 standard; DNA; 4141 BP.
DE   Human gene of the invention NOV46f SEQ ID NO:1029.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     44.89%          Conservative:  47
Best Local Similarity:  27.74%          Mismatches:    123
Query Match:            13.84%          Indels:        28
RESULT 838
ID   ABX70427 standard; DNA; 4169 BP.
DE   DNA encoding human GPCR related protein NOV13a.
PN   WO200279398-A2.
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PD   10-OCT-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     44.89%        Conservative:  47
Best Local Similarity:  27.74%        Mismatches:    123
Query Match:            13.84%        Indels:        28
RESULT 839
ID   ADH72137 standard; DNA; 4169 BP.
DE   Human gene of the invention NOV46h SEQ ID NO:1033.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     44.89%        Conservative:  47
Best Local Similarity:  27.74%        Mismatches:    123
Query Match:            13.84%        Indels:        28
RESULT 840
ID   ADL24006 standard; cDNA; 4169 BP.
DE   Human NOVX cDNA #26.
PN   US2004002120-A1.
PD   01-JAN-2004.
PA   (KEKU/) KEKUDA R.
PA   (TCHE/) TCHERNEV V T.
PA   (LIUX/) LIU X.
PA   (SPYT/) SPYTEK K A.
PA   (PATT/) PATTURAJAN M.
PA   (BURG/) BURGESS C E.
PA   (VERN/) VERNET C A M.
PA   (LILL/) LI L.
PA   (GORM/) GORMAN L.
PA   (MALY/) MALYANKAR U M.
PA   (BOLD/) BOLDOG F L.
PA   (GUOX/) GUO X.
PA   (SHEN/) SHENOY S G.
PA   (PADI/) PADIGARU M.
PA   (TAUP/) TAUPIER R J.
PA   (MILL/) MILLER C E.
PA   (CASM/) CASMAN S J.
PA   (PENA/) PENA C E A.
PA   (GANG/) GANGOLLI E A.
PA   (GUSE/) GUSEV V Y.
PA   (SMIT/) SMITHSON G.
PA   (ZERH/) ZERHUSEN B D.
PA   (GERL/) GERLACH V.
PA   (POCH/) POCHART P F.
PA   (FERN/) FERNANDES E R.
PA   (SHIM/) SHIMKETS R A.
PA   (RAST/) RASTELLI L.
PA   (SPAD/) SPADERNA S K.
PA   (LARO/) LAROCHELLE W J.
PA   (ZHON/) ZHONG M.
PA   (KHRA/) KHRAMTSOV N V.
PA   (VOSS/) VOSS E Z.
PA   (HERR/) HERRMANN J L.
Percent Similarity:     44.89%        Conservative:  47
Best Local Similarity:  27.74%        Mismatches:    123
Query Match:            13.84%        Indels:        28
RESULT 841
ID   ABX70420 standard; DNA; 4295 BP.
DE   DNA encoding human GPCR related protein NOV12a.
PN   WO200279398-A2.
PD   10-OCT-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     44.89%        Conservative:  47
Best Local Similarity:  27.74%        Mismatches:    123
Query Match:            13.84%        Indels:        28
RESULT 842
ID   ADL23992 standard; cDNA; 4295 BP.
DE   Human NOVX cDNA #19.
PN   US2004002120-A1.
PD   01-JAN-2004.
PA   (KEKU/) KEKUDA R.
PA   (TCHE/) TCHERNEV V T.
PA   (LIUX/) LIU X.
PA   (SPYT/) SPYTEK K A.
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PA   (PATT/) PATTURAJAN M.
PA   (BURG/) BURGESS C E.
PA   (VERN/) VERNET C A M.
PA   (LILL/) LI L.
PA   (GORM/) GORMAN L.
PA   (MALY/) MALYANKAR U M.
PA   (BOLD/) BOLDOG F L.
PA   (GUOX/) GUO X.
PA   (SHEN/) SHENOY S G.
PA   (PADI/) PADIGARU M.
PA   (TAUP/) TAUPIER R J.
PA   (MILL/) MILLER C E.
PA   (CASM/) CASMAN S J.
PA   (PENA/) PENA C E A.
PA   (GANG/) GANGOLLI E A.
PA   (GUSE/) GUSEV V Y.
PA   (SMIT/) SMITHSON G.
PA   (ZERH/) ZERHUSEN B D.
PA   (GERL/) GERLACH V.
PA   (POCH/) POCHART P F.
PA   (FERN/) FERNANDES E R.
PA   (SHIM/) SHIMKETS R A.
PA   (RAST/) RASTELLI L.
PA   (SPAD/) SPADERNA S K.
PA   (LARO/) LAROCHELLE W J.
PA   (ZHON/) ZHONG M.
PA   (KHRA/) KHRAMTSOV N V.
PA   (VOSS/) VOSS E Z.
PA   (HERR/) HERRMANN J L.
Percent Similarity:     44.89%        Conservative:  47
Best Local Similarity:  27.74%        Mismatches:    123
Query Match:            13.84%        Indels:        28
RESULT 843
ID   ABD33040 standard; cDNA; 3588 BP.
DE   Human cancer-associated cDNA HR22-025.1.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity:     40.70%        Conservative:  40
Best Local Similarity:  26.67%        Mismatches:    110
Query Match:            13.82%        Indels:        59
RESULT 844
ID   AAI64283 standard; DNA; 4548 BP.
DE   Human transient axonal glycoprotein (tag-1) DNA.
PN   WO200188546-A2.
PD   22-NOV-2001.
PA   (UNMI ) UNIV MICHIGAN.
Percent Similarity:     40.70%        Conservative:  40
Best Local Similarity:  26.67%        Mismatches:    110
Query Match:            13.82%        Indels:        59
RESULT 845
ID   ABD33041 standard; cDNA; 6137 BP.
DE   Human cancer-associated cDNA HR22-025.2.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity:     40.70%        Conservative:  40
Best Local Similarity:  26.67%        Mismatches:    110
Query Match:            13.82%        Indels:        59
RESULT 846
ID   ADQ23368 standard; DNA; 7625 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 6188.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity:     40.70%        Conservative:  40
Best Local Similarity:  26.67%        Mismatches:    110
Query Match:            13.82%        Indels:        59
RESULT 847
ID   ADQ24513 standard; DNA; 7625 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.
PN   WO2004048938-A2.
PD   10-JUN-2004.
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PA   (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity:     40.70%         Conservative:  40
Best Local Similarity:  26.67%         Mismatches:    110
Query Match:            13.82%         Indels:        59
RESULT 848
ID   ADO28580 standard; cDNA; 7650 BP.
DE   Human axonin-1 precursor (AXO1) encoding cDNA SEQ ID NO:9.
PN   WO2004044178-A2.
PD   27-MAY-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     40.70%         Conservative:  40
Best Local Similarity:  26.67%         Mismatches:    110
Query Match:            13.82%         Indels:        59
RESULT 849
ID   ADA53286 standard; cDNA; 1880 BP.
DE   Human coding sequence, SEQ ID 854.
PN   EP1293569-A2.
PD   19-MAR-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity:     44.31%         Conservative:  58
Best Local Similarity:  26.46%         Mismatches:    126
Query Match:            13.76%         Indels:        55
RESULT 850
ID   ABL24131 standard; DNA; 1404 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 23866.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     42.08%         Conservative:  38
Best Local Similarity:  27.41%         Mismatches:    72
Query Match:            13.73%         Indels:        78
RESULT 851
ID   ABK94709 standard; DNA; 3314 BP.
DE   Neurodegenerative disease associated polynucleotide #18.
PN   WO200240996-A2.
PD   23-MAY-2002.
PA   (MITO-) MITOKOR.
Percent Similarity:     41.85%         Conservative:  54
Best Local Similarity:  24.60%         Mismatches:    133
Query Match:            13.65%         Indels:        49
RESULT 852
ID   ABK94710 standard; DNA; 3335 BP.
DE   Neurodegenerative disease associated polynucleotide #19.
PN   WO200240996-A2.
PD   23-MAY-2002.
PA   (MITO-) MITOKOR.
Percent Similarity:     41.85%         Conservative:  54
Best Local Similarity:  24.60%         Mismatches:    133
Query Match:            13.65%         Indels:        49
RESULT 853
ID   AAQ74440 standard; cDNA; 3360 BP.
DE   Human contactin cDNA (EMBL Accession #Z21488).
PN   EP618293-A1.
PD   05-OCT-1994.
PA   (BECT ) BECTON DICKINSON CO.
Percent Similarity:     41.85%         Conservative:  54
Best Local Similarity:  24.60%         Mismatches:    133
Query Match:            13.65%         Indels:        49
RESULT 854
ID   ABL64109 standard; DNA; 3360 BP.
DE   Breast cancer related gene sequence SEQ ID NO:2446.
PN   WO200194629-A2.
PD   13-DEC-2001.
PA   (AVAL-) AVALON PHARM.
Percent Similarity:     41.85%         Conservative:  54
Best Local Similarity:  24.60%         Mismatches:    133
Query Match:            13.65%         Indels:        49
RESULT 855
ID   ABL63715 standard; DNA; 3360 BP.
DE   Breast cancer related gene sequence SEQ ID NO:2052.
PN   WO200194629-A2.
PD   13-DEC-2001.
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PA   (AVAL-) AVALON PHARM.
Percent Similarity:     41.85%         Conservative:  54
Best Local Similarity:  24.60%         Mismatches:    133
Query Match:            13.65%         Indels:        49
RESULT 856
ID   ABK94708 standard; DNA; 3360 BP.
DE   Neurodegenerative disease associated polynucleotide #17.
PN   WO200240996-A2.
PD   23-MAY-2002.
PA   (MITO-) MITOKOR.
Percent Similarity:     41.85%         Conservative:  54
Best Local Similarity:  24.60%         Mismatches:    133
Query Match:            13.65%         Indels:        49
RESULT 857
ID   ADE71112 standard; DNA; 3360 BP.
DE   Contactin gene, SEQ ID 66.
PN   WO2003070889-A2.
PD   28-AUG-2003.
PA   (IDEC-) IDEC PHARM CORP.
Percent Similarity:     41.85%         Conservative:  54
Best Local Similarity:  24.60%         Mismatches:    133
Query Match:            13.65%         Indels:        49
RESULT 858
ID   ADJ75287 standard; DNA; 3360 BP.
DE   Marker gene SEQ ID NO:539.
PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (GENO-) GENOX RES INC.
Percent Similarity:     41.85%         Conservative:  54
Best Local Similarity:  24.60%         Mismatches:    133
Query Match:            13.65%         Indels:        49
RESULT 859
ID   AAT07313 standard; cDNA; 3395 BP.
DE   Human contactin coding sequence.
PN   WO9535373-A2.
PD   28-DEC-1995.
PA   (LJOL-) LA JOLLA CANCER RES FOUND.
Percent Similarity:     41.85%         Conservative:  54
Best Local Similarity:  24.60%         Mismatches:    133
Query Match:            13.65%         Indels:        49
RESULT 860
ID   ADO28658 standard; cDNA; 3427 BP.
DE   Human CONT encoding cDNA SEQ ID NO:87.
PN   WO2004044178-A2.
PD   27-MAY-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     41.85%         Conservative:  54
Best Local Similarity:  24.60%         Mismatches:    133
Query Match:            13.65%         Indels:        49
RESULT 861
ID   ADR66243 standard; DNA; 4015 BP.
DE   Human prostatic carcinoma derived DNA SEQ ID 97 #2.
PN   WO2004076614-A2.
PD   10-SEP-2004.
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (ROSE/) ROSENTHAL A.
PA   (HERM/) HERMANN K.
PA   (PILA/) PILARSKY C.
Percent Similarity:     39.04%         Conservative:  40
Best Local Similarity:  27.03%         Mismatches:    146
Query Match:            13.62%         Indels:        57
RESULT 862
ID   ADR66585 standard; DNA; 4015 BP.
DE   Human prostatic carcinoma derived DNA SEQ ID 97 #3.
PN   WO2004076614-A2.
PD   10-SEP-2004.
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (ROSE/) ROSENTHAL A.
PA   (HERM/) HERMANN K.
PA   (PILA/) PILARSKY C.
Percent Similarity:     39.04%         Conservative:  40
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Best Local Similarity:  27.03%          Mismatches:    146
Query Match:            13.62%          Indels:        57
RESULT 863
ID   AAS67246 standard; cDNA; 2678 BP.
DE   DNA encoding novel human diagnostic protein #3050.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     45.21%          Conservative:  60
Best Local Similarity:  27.25%          Mismatches:    99
Query Match:            13.43%          Indels:        87
RESULT 864
ID   AAS71723 standard; cDNA; 2678 BP.
DE   DNA encoding novel human diagnostic protein #7527.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     45.21%          Conservative:  60
Best Local Similarity:  27.25%          Mismatches:    99
Query Match:            13.43%          Indels:        87
RESULT 865
ID   AAS64445 standard; cDNA; 3131 BP.
DE   DNA encoding novel human diagnostic protein #249.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     45.21%          Conservative:  60
Best Local Similarity:  27.25%          Mismatches:    99
Query Match:            13.43%          Indels:        87
RESULT 866
ID   AAS64798 standard; cDNA; 3131 BP.
DE   DNA encoding novel human diagnostic protein #602.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     45.21%          Conservative:  60
Best Local Similarity:  27.25%          Mismatches:    99
Query Match:            13.43%          Indels:        87
RESULT 867
ID   ABK90037 standard; cDNA; 7764 BP.
DE   Human OCP cDNA.
PN   WO200246364-A2.
PD   13-JUN-2002.
PA   (QUAR-) QUARK BIOTECH INC.
Percent Similarity:     40.47%          Conservative:  46
Best Local Similarity:  26.98%          Mismatches:    129
Query Match:            13.40%          Indels:        74
RESULT 868
ID   ABK90051 standard; cDNA; 7770 BP.
DE   Coding sequence of human OCP protein.
PN   WO200246364-A2.
PD   13-JUN-2002.
PA   (QUAR-) QUARK BIOTECH INC.
Percent Similarity:     40.47%          Conservative:  46
Best Local Similarity:  26.98%          Mismatches:    129
Query Match:            13.40%          Indels:        74
RESULT 869
ID   ADL02243 standard; cDNA; 7770 BP.
DE   Human OCP cDNA #5.
PN   US2004053301-A1.
PD   18-MAR-2004.
PA   (QUAR-) QUARK BIOTECH INC.
Percent Similarity:     40.47%          Conservative:  46
Best Local Similarity:  26.98%          Mismatches:    129
Query Match:            13.40%          Indels:        74
RESULT 870
ID   AAT15929 standard; cDNA; 2178 BP.
DE   Neural cell adhesion molecule splice variant cDNA.
PN   WO9604396-A1.
PD   15-FEB-1996.
PA   (SYST-) SYSTEMIX INC.
Percent Similarity:     41.98%          Conservative:  57
Best Local Similarity:  24.38%          Mismatches:    157
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Query Match:            13.37%          Indels:        31
RESULT 871
ID   AAT15928 standard; cDNA; 2450 BP.
DE   Neural cell adhesion molecule full-length DNA.
PN   WO9604396-A1.
PD   15-FEB-1996.
PA   (SYST-) SYSTEMIX INC.
Percent Similarity:     41.98%          Conservative:  57
Best Local Similarity:  24.38%          Mismatches:    157
Query Match:            13.37%          Indels:        31
RESULT 872
ID   ADJ76119 standard; DNA; 3843 BP.
DE   Marker gene SEQ ID NO:1371.
PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (GENO-) GENOX RES INC.
Percent Similarity:     41.85%          Conservative:  55
Best Local Similarity:  24.28%          Mismatches:    133
Query Match:            13.37%          Indels:        49
RESULT 873
ID   ADA53434 standard; cDNA; 3870 BP.
DE   Human coding sequence, SEQ ID 1002.
PN   EP1293569-A2.
PD   19-MAR-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity:     44.33%          Conservative:  48
Best Local Similarity:  27.84%          Mismatches:    109
Query Match:            13.37%          Indels:        53
RESULT 874
ID   ADI24497 standard; cDNA; 4723 BP.
DE   Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:47.
PN   WO2004004785-A1.
PD   15-JAN-2004.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     41.67%          Conservative:  55
Best Local Similarity:  24.69%          Mismatches:    158
Query Match:            13.37%          Indels:        31
RESULT 875
ID   ABZ11468 standard; cDNA; 6599 BP.
DE   Human polynucleotide SEQ ID NO 350.
PN   WO200270539-A2.
PD   12-SEP-2002.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     42.60%          Conservative:  44
Best Local Similarity:  26.71%          Mismatches:    131
Query Match:            13.34%          Indels:        28
RESULT 876
ID   ADM43986 standard; cDNA; 6599 BP.
DE   Novel human arginine-rich protein cDNA #350.
PN   US2004053250-A1.
PD   18-MAR-2004.
PA   (TANG/) TANG Y T.
PA   (XUEA/) XUE A.
PA   (DRMA/) DRMANAC R T.
Percent Similarity:     42.60%          Conservative:  44
Best Local Similarity:  26.71%          Mismatches:    131
Query Match:            13.34%          Indels:        28
RESULT 877
ID   AAD04326 standard; DNA; 2766 BP.
DE   Human nuclear cell adhesion molecule homologue, NCAM_c_2 DNA.
PN   WO200129215-A2.
PD   26-APR-2001.
PA   (COMP-) COMPUGEN LTD.
Percent Similarity:     41.28%          Conservative:  52
Best Local Similarity:  25.38%          Mismatches:    109
Query Match:            13.21%          Indels:        83
RESULT 878
ID   AAD04325 standard; DNA; 2771 BP.
DE   Human cell adhesion molecule homologue (CAM-H) DNA #2.
PN   WO200129215-A2.
PD   26-APR-2001.
PA   (COMP-) COMPUGEN LTD.
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Percent Similarity:     41.28%          Conservative:  52
Best Local Similarity:  25.38%          Mismatches:    109
Query Match:            13.21%          Indels:        83
RESULT 879
ID   AAD04327 standard; DNA; 2771 BP.
DE   Human nuclear cell adhesion molecule homologue, NCAM_c_1 DNA.
PN   WO200129215-A2.
PD   26-APR-2001.
PA   (COMP-) COMPUGEN LTD.
Percent Similarity:     41.28%          Conservative:  52
Best Local Similarity:  25.38%          Mismatches:    109
Query Match:            13.21%          Indels:        83
RESULT 880
ID   AAD04328 standard; DNA; 3060 BP.
DE   Human nuclear cell adhesion molecule homologue, NCAM_d_2 DNA.
PN   WO200129215-A2.
PD   26-APR-2001.
PA   (COMP-) COMPUGEN LTD.
Percent Similarity:     41.28%          Conservative:  52
Best Local Similarity:  25.38%          Mismatches:    109
Query Match:            13.21%          Indels:        83
RESULT 881
ID   AAD04324 standard; DNA; 3065 BP.
DE   Human cell adhesion molecule homologue (CAM-H) DNA #1.
PN   WO200129215-A2.
PD   26-APR-2001.
PA   (COMP-) COMPUGEN LTD.
Percent Similarity:     41.28%          Conservative:  52
Best Local Similarity:  25.38%          Mismatches:    109
Query Match:            13.21%          Indels:        83
RESULT 882
ID   ADJ56383 standard; cDNA; 6829 BP.
DE   C_elegans cDNA differentially expressed in MYCN activated cells SeqID189.
PN   US2003119009-A1.
PD   26-JUN-2003.
PA   (STUA/) STUART S G.
PA   (NUCH/) NUCHTERN J G.
PA   (PLON/) PLON S E.
PA   (SHOH/) SHOHET J M.
Percent Similarity:     38.39%          Conservative:  32
Best Local Similarity:  28.48%          Mismatches:    148
Query Match:            13.18%          Indels:        52
RESULT 883
ID   ABS54189 standard; cDNA; 8180 BP.
DE   Human osteoclast protein (OCP) cDNA 5+3 corrected.
PN   US2002086825-A1.
PD   04-JUL-2002.
PA   (EINA/) EINAT P.
PA   (SEGE/) SEGEV O.
PA   (SKAL/) SKALITER R.
PA   (FEIN/) FEINSTEIN E.
PA   (FAER/) FAERMAN A.
Percent Similarity:     40.64%          Conservative:  47
Best Local Similarity:  26.90%          Mismatches:    128
Query Match:            13.15%          Indels:        75
RESULT 884
ID   ADL02228 standard; cDNA; 8180 BP.
DE   Human OCP cDNA #3.
PN   US2004053301-A1.
PD   18-MAR-2004.
PA   (QUAR-) QUARK BIOTECH INC.
Percent Similarity:     40.64%          Conservative:  47
Best Local Similarity:  26.90%          Mismatches:    128
Query Match:            13.15%          Indels:        75
RESULT 885
ID   ABK90038 standard; cDNA; 8262 BP.
DE   Human 5+3 corrected OCP cDNA.
PN   WO200246364-A2.
PD   13-JUN-2002.
PA   (QUAR-) QUARK BIOTECH INC.
Percent Similarity:     40.64%          Conservative:  47
Best Local Similarity:  26.90%          Mismatches:    128
Query Match:            13.15%          Indels:        75
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RESULT 886
ID   AAI72586 standard; cDNA; 8262 BP.
DE   Human OCP cDNA.
PN   US2002022026-A1.
PD   21-FEB-2002.
PA   (EINA/) EINAT P.
PA   (SEGE/) SEGEV O.
PA   (SKAL/) SKALITER R.
PA   (FEIN/) FEINSTEIN E.
PA   (FAER/) FAERMAN A.
Percent Similarity:     40.64%          Conservative:  47
Best Local Similarity:  26.90%          Mismatches:    128
Query Match:            13.15%          Indels:        75
RESULT 887
ID   ABS54187 standard; cDNA; 8262 BP.
DE   Human osteoclast protein (OCP) cDNA.
PN   US2002086825-A1.
PD   04-JUL-2002.
PA   (EINA/) EINAT P.
PA   (SEGE/) SEGEV O.
PA   (SKAL/) SKALITER R.
PA   (FEIN/) FEINSTEIN E.
PA   (FAER/) FAERMAN A.
Percent Similarity:     40.64%          Conservative:  47
Best Local Similarity:  26.90%          Mismatches:    128
Query Match:            13.15%          Indels:        75
RESULT 888
ID   ADL02226 standard; cDNA; 8262 BP.
DE   Human OCP cDNA #2.
PN   US2004053301-A1.
PD   18-MAR-2004.
PA   (QUAR-) QUARK BIOTECH INC.
Percent Similarity:     40.64%          Conservative:  47
Best Local Similarity:  26.90%          Mismatches:    128
Query Match:            13.15%          Indels:        75
RESULT 889
ID   AAT42088 standard; cDNA to mRNA; 219 BP.
DE   Human LAMP residues 46-118 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     77.78%          Conservative:  14
Best Local Similarity:  58.33%          Mismatches:    16
Query Match:            13.12%          Indels:        0
RESULT 890
ID   AAT42089 standard; cDNA to mRNA; 219 BP.
DE   Rat LAMP residues 46-118 coding sequence.
PN   WO9630052-A1.
PD   03-OCT-1996.
PA   (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity:     77.78%          Conservative:  14
Best Local Similarity:  58.33%          Mismatches:    16
Query Match:            13.12%          Indels:        0
RESULT 891
ID   ADR07797 standard; cDNA; 2451 BP.
DE   Full length human cDNA useful for treating neurological disease Seq 1303.
PN   EP1447413-A2.
PD   18-AUG-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity:     40.83%          Conservative:  34
Best Local Similarity:  29.07%          Mismatches:    133
Query Match:            13.07%          Indels:        39
RESULT 892
ID   ADH71831 standard; DNA; 2902 BP.
DE   Human gene of the invention NOV29af SEQ ID NO:727.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.59%          Conservative:  46
Best Local Similarity:  27.06%          Mismatches:    127
Query Match:            13.04%          Indels:        75
RESULT 893
ID   ADH71817 standard; DNA; 2902 BP.
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DE   Human gene of the invention NOV29y SEQ ID NO:713.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.59%         Conservative:  46
Best Local Similarity:  27.06%         Mismatches:    127
Query Match:            13.04%         Indels:        75
RESULT 894
ID   ABK90046 standard; DNA; 3518 BP.
DE   Middle fragment (B) comprising central region of human OCP DNA.
PN   WO200246364-A2.
PD   13-JUN-2002.
PA   (QUAR-) QUARK BIOTECH INC.
Percent Similarity:     40.64%         Conservative:  47
Best Local Similarity:  26.90%         Mismatches:    128
Query Match:            13.04%         Indels:        75
RESULT 895
ID   ADL02247 standard; cDNA; 3518 BP.
DE   Human OCP cDNA #7.
PN   US2004053301-A1.
PD   18-MAR-2004.
PA   (QUAR-) QUARK BIOTECH INC.
Percent Similarity:     40.64%         Conservative:  47
Best Local Similarity:  26.90%         Mismatches:    128
Query Match:            13.04%         Indels:        75
RESULT 896
ID   ADR07921 standard; cDNA; 4086 BP.
DE   Full length human cDNA useful for treating neurological disease Seq 1427.
PN   EP1447413-A2.
PD   18-AUG-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity:     40.64%         Conservative:  47
Best Local Similarity:  26.90%         Mismatches:    128
Query Match:            13.04%         Indels:        75
RESULT 897
ID   ADL02251 standard; cDNA; 7872 BP.
DE   Human OCP cDNA #10.
PN   US2004053301-A1.
PD   18-MAR-2004.
PA   (QUAR-) QUARK BIOTECH INC.
Percent Similarity:     40.64%         Conservative:  47
Best Local Similarity:  26.90%         Mismatches:    128
Query Match:            13.04%         Indels:        75
RESULT 898
ID   ADS09892 standard; DNA; 7996 BP.
DE   Human therapeutic DNA - SEQ ID 129.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
Percent Similarity:     40.64%         Conservative:  47
Best Local Similarity:  26.90%         Mismatches:    128
Query Match:            13.04%         Indels:        75
RESULT 899
ID   ADS09893 standard; DNA; 8782 BP.
DE   Human therapeutic DNA - SEQ ID 130.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
Percent Similarity:     40.64%         Conservative:  47
Best Local Similarity:  26.90%         Mismatches:    128
Query Match:            13.04%         Indels:        75
RESULT 900
ID   ADB62179 standard; cDNA; 2420 BP.
DE   Human cDNA encoding clone CTONG20036990.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity:     43.35%         Conservative:  44
Best Local Similarity:  26.62%         Mismatches:    103
Query Match:            12.96%         Indels:        46
RESULT 901
ID   ABL88109 standard; cDNA; 1427 BP.
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DE   Human PRO7261 cDNA sequence SEQ ID NO:75.
PN   WO200200690-A2.
PD   03-JAN-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     39.45%         Conservative:  42
Best Local Similarity:  24.91%         Mismatches:    132
Query Match:            12.93%         Indels:        43
RESULT 902
ID   ABL95598 standard; cDNA; 1427 BP.
DE   Human angiogenesis related cDNA PRO7261 SEQ ID NO: 75.
PN   WO200208284-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     39.45%         Conservative:  42
Best Local Similarity:  24.91%         Mismatches:    132
Query Match:            12.93%         Indels:        43
RESULT 903
ID   ADD10364 standard; cDNA; 1427 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #38.
PN   US2003105011-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     39.45%         Conservative:  42
Best Local Similarity:  24.91%         Mismatches:    132
Query Match:            12.93%         Indels:        43
RESULT 904
ID   ADD11324 standard; cDNA; 1427 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #38.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     39.45%         Conservative:  42
Best Local Similarity:  24.91%         Mismatches:    132
Query Match:            12.93%         Indels:        43
RESULT 905
ID   ADD37117 standard; cDNA; 1427 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #38.
PN   US2003105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     39.45%         Conservative:  42
Best Local Similarity:  24.91%         Mismatches:    132
Query Match:            12.93%         Indels:        43
RESULT 906
ID   ADE41325 standard; cDNA; 1427 BP.
DE   Human secreted/transmembrane PRO polypeptide cDNA #38.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     39.45%         Conservative:  42
Best Local Similarity:  24.91%         Mismatches:    132
Query Match:            12.93%         Indels:        43
RESULT 907
ID   ADH43508 standard; cDNA; 1427 BP.
DE   Human PRO polynucleotide #38.
PN   US2003224984-A1.
PD   04-DEC-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     39.45%        Conservative:  42
Best Local Similarity:  24.91%        Mismatches:    132
Query Match:            12.93%        Indels:        43
RESULT 908
ID   ADK82853 standard; cDNA; 1427 BP.
DE   Human PRO polynucleotide #38.
PN   US2004043927-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     39.45%        Conservative:  42
Best Local Similarity:  24.91%        Mismatches:    132
Query Match:            12.93%        Indels:        43
RESULT 909
ID   ADR67151 standard; DNA; 3904 BP.
DE   Human bladder cancer associated nucleotide sequence.
PN   WO2004076613-A2.
PD   10-SEP-2004.
PA   (HERR/) HERR A.
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (STAU/) STAUB E.
PA   (PILA/) PILARSKY C.
PA   (SPEC/) SPECHT T.
Percent Similarity:     39.45%        Conservative:  42
Best Local Similarity:  24.91%        Mismatches:    132
Query Match:            12.93%        Indels:        43
RESULT 910
ID   ABL22880 standard; DNA; 8410 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 20113.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     38.84%        Conservative:  49
Best Local Similarity:  23.85%        Mismatches:    121
Query Match:            12.93%        Indels:        79
RESULT 911
ID   ADH71829 standard; DNA; 2902 BP.
DE   Human gene of the invention NOV29ae SEQ ID NO:725.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.71%        Conservative:  47
Best Local Similarity:  26.84%        Mismatches:    126
Query Match:            12.87%        Indels:        75
RESULT 912
ID   ADH71815 standard; DNA; 2902 BP.
DE   Human gene of the invention NOV29x SEQ ID NO:711.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.71%        Conservative:  47
Best Local Similarity:  26.84%        Mismatches:    126
Query Match:            12.87%        Indels:        75
RESULT 913
ID   ADH71819 standard; DNA; 7831 BP.
DE   Human gene of the invention NOV29z SEQ ID NO:715.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 914
ID   ABS51089 standard; cDNA; 7876 BP.
DE   cDNA encoding human NOV12a protein.
PN   WO200250277-A2.
PD   27-JUN-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 915
ID   ADJ83054 standard; DNA; 7876 BP.
DE   Human NOVX NOV12a DNA.
PN   US2003170630-A1.
PD   11-SEP-2003.
PA   (ALSO/) ALSOBROOK J P.
PA   (TCHE/) TCHERNEV V T.
PA   (LIUX/) LIU X.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (LEPL/) LEPLEY D M.
PA   (BURG/) BURGESS C E.
PA   (SHIM/) SHIMKETS R A.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERES E S.
PA   (VERN/) VERNET C A M.
PA   (LILL/) LI L.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (GORM/) GORMAN L.
PA   (GANG/) GANGOLLI E A.
PA   (FERN/) FERNANDES E R.
PA   (RIEG/) RIEGER D K.
PA   (EDIN/) EDINGER S R.
PA   (GUNT/) GUNTHER E.
PA   (MILL/) MILLET I.
PA   (SCIO/) SCIORE P.
PA   (ELLE/) ELLERMAN K.
PA   (MACD/) MACDOUGALL J R.
PA   (SMIT/) SMITHSON G.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 916
ID   ADH71843 standard; DNA; 7876 BP.
DE   Human gene of the invention NOV29al SEQ ID NO:739.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 917
ID   ADH71769 standard; DNA; 7876 BP.
DE   Human gene of the invention NOV29a SEQ ID NO:665.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 918
ID   ADH71839 standard; DNA; 7876 BP.
DE   Human gene of the invention NOV29aj SEQ ID NO:735.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 919
ID   ADH71847 standard; DNA; 7876 BP.
DE   Human gene of the invention NOV29an SEQ ID NO:743.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 920
ID   ADH71853 standard; DNA; 7876 BP.
DE   Human gene of the invention NOV29aq SEQ ID NO:749.
PN   WO2003102155-A2.
PD   11-DEC-2003.
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PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 921
ID   ADH71841 standard; DNA; 7876 BP.
DE   Human gene of the invention NOV29ak SEQ ID NO:737.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 922
ID   ADH71845 standard; DNA; 7876 BP.
DE   Human gene of the invention NOV29am SEQ ID NO:741.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 923
ID   ADH71849 standard; DNA; 7876 BP.
DE   Human gene of the invention NOV29ao SEQ ID NO:745.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 924
ID   ADH71835 standard; DNA; 7876 BP.
DE   Human gene of the invention NOV29ah SEQ ID NO:731.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 925
ID   ADH71851 standard; DNA; 7876 BP.
DE   Human gene of the invention NOV29ap SEQ ID NO:747.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 926
ID   ADH71837 standard; DNA; 7877 BP.
DE   Human gene of the invention NOV29ai SEQ ID NO:733.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 927
ID   ABS51094 standard; cDNA; 8270 BP.
DE   cDNA encoding human NOV12f protein.
PN   WO200250277-A2.
PD   27-JUN-2002.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 928
ID   ADJ83064 standard; DNA; 8270 BP.
DE   Human NOVX NOV12f DNA.
PN   US2003170630-A1.
PD   11-SEP-2003.
PA   (ALSO/) ALSOBROOK J P.
PA   (TCHE/) TCHERNEV V T.
PA   (LIUX/) LIU X.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (LEPL/) LEPLEY D M.
PA   (BURG/) BURGESS C E.
PA   (SHIM/) SHIMKETS R A.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERES E S.
PA   (VERN/) VERNET C A M.
PA   (LILL/) LI L.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (GORM/) GORMAN L.
PA   (GANG/) GANGOLLI E A.
PA   (FERN/) FERNANDES E R.
PA   (RIEG/) RIEGER D K.
PA   (EDIN/) EDINGER S R.
PA   (GUNT/) GUNTHER E.
PA   (MILL/) MILLET I.
PA   (SCIO/) SCIORE P.
PA   (ELLE/) ELLERMAN K.
PA   (MACD/) MACDOUGALL J R.
PA   (SMIT/) SMITHSON G.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 929
ID   ADH71821 standard; DNA; 8270 BP.
DE   Human gene of the invention NOV29aa SEQ ID NO:717.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     40.35%        Conservative:  46
Best Local Similarity:  26.90%        Mismatches:    132
Query Match:            12.85%        Indels:        72
RESULT 930
ID   ABX10231 standard; cDNA; 11796 BP.
DE   Human cDNA encoding protein NOV9.
PN   WO200285922-A2.
PD   31-OCT-2002.
PA   (CURA-) CURAGEN CORP.
PA   (MILL-) MILLENNIUM PHARM INC.
Percent Similarity:     39.55%        Conservative:  35
Best Local Similarity:  28.30%        Mismatches:    128
Query Match:            12.85%        Indels:        60
RESULT 931
ID   AAV40528 standard; cDNA; 3442 BP.
DE   Homo sapiens DL185_1 clone secreted protein coding region.
PN   WO9830695-A2.
PD   16-JUL-1998.
PA   (GEMY ) GENETICS INST INC.
Percent Similarity:     42.01%        Conservative:  44
Best Local Similarity:  26.74%        Mismatches:    135
Query Match:            12.79%        Indels:        32
RESULT 932
ID   ADQ38613 standard; DNA; 13650 BP.
DE   Human SNP containing myocardial infarction-associated gene, SEQ ID 276.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Percent Similarity:     38.91%        Conservative:  40
Best Local Similarity:  26.05%        Mismatches:    148
Query Match:            12.79%        Indels:        42
RESULT 933
ID   ADQ38612 standard; DNA; 13711 BP.
DE   Human SNP containing myocardial infarction-associated gene, SEQ ID 275.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Percent Similarity:     38.91%        Conservative:  40
Best Local Similarity:  26.05%        Mismatches:    148
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Query Match:             12.79%          Indels:        42
RESULT 934
ID   ADQ38614 standard; DNA; 13793 BP.
DE   Human SNP containing myocardial infarction-associated gene, SEQ ID 277.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Percent Similarity:      38.91%          Conservative:  40
Best Local Similarity:   26.05%          Mismatches:    148
Query Match:             12.79%          Indels:        42
RESULT 935
ID   ADQ38611 standard; DNA; 14194 BP.
DE   Human SNP containing myocardial infarction-associated gene, SEQ ID 274.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Percent Similarity:      38.91%          Conservative:  40
Best Local Similarity:   26.05%          Mismatches:    148
Query Match:             12.79%          Indels:        42
RESULT 936
ID   AAT87074 standard; cDNA; 2869 BP.
DE   Rat Dmk receptor cDNA.
PN   US5656473-A.
PD   12-AUG-1997.
PA   (REGE-) REGENERON PHARM INC.
Percent Similarity:      39.13%          Conservative:  45
Best Local Similarity:   25.16%          Mismatches:    145
Query Match:             12.76%          Indels:        51
RESULT 937
ID   AAT90472 standard; cDNA; 2869 BP.
DE   Rat muscle-specific kinase (MuSK) cDNA.
PN   WO9721811-A2.
PD   19-JUN-1997.
PA   (REGE-) REGENERON PHARM INC.
Percent Similarity:      39.13%          Conservative:  45
Best Local Similarity:   25.16%          Mismatches:    145
Query Match:             12.76%          Indels:        51
RESULT 938
ID   ABD33038 standard; cDNA; 8455 BP.
DE   Mouse cancer-associated cDNA MR22-025.1.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity:      38.78%          Conservative:  39
Best Local Similarity:   25.51%          Mismatches:    103
Query Match:             12.76%          Indels:        77
RESULT 939
ID   ABD32650 standard; cDNA; 10976 BP.
DE   Human cancer-associated cDNA HR13-036.1.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity:      36.96%          Conservative:  50
Best Local Similarity:   24.30%          Mismatches:    134
Query Match:             12.76%          Indels:        116
RESULT 940
ID   AAT87073 standard; DNA; 2610 BP.
DE   Human Dmk receptor gene.
PN   US5656473-A.
PD   12-AUG-1997.
PA   (REGE-) REGENERON PHARM INC.
Percent Similarity:      39.88%          Conservative:  44
Best Local Similarity:   26.17%          Mismatches:    138
Query Match:             12.74%          Indels:        55
RESULT 941
ID   AAT90473 standard; cDNA; 2610 BP.
DE   Human muscle-specific kinase (MuSK) cDNA.
PN   WO9721811-A2.
PD   19-JUN-1997.
PA   (REGE-) REGENERON PHARM INC.
Percent Similarity:      39.88%          Conservative:  44
Best Local Similarity:   26.17%          Mismatches:    138
Query Match:             12.74%          Indels:        55
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RESULT 942
ID   ADQ89843 standard; DNA; 2610 BP.
DE   Antagonist of cell cycle progression nucleotide sequence #137.
PN   WO2004063362-A2.
PD   29-JUL-2004.
PA   (CYCL-) CYCLACEL LTD.
Percent Similarity:      39.88%          Conservative:  44
Best Local Similarity:   26.17%          Mismatches:    138
Query Match:             12.74%          Indels:        55
RESULT 943
ID   ADL13698 standard; DNA; 13182 BP.
DE   Osteoarthritis-associated polymorphic nucleotide #230.
PN   WO2003054166-A2.
PD   03-JUL-2003.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:      38.91%          Conservative:  40
Best Local Similarity:   26.05%          Mismatches:    148
Query Match:             12.74%          Indels:        42
RESULT 944
ID   ADL13697 standard; DNA; 13793 BP.
DE   Osteoarthritis-associated polymorphic nucleotide #229.
PN   WO2003054166-A2.
PD   03-JUL-2003.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:      38.91%          Conservative:  40
Best Local Similarity:   26.05%          Mismatches:    148
Query Match:             12.74%          Indels:        42
RESULT 945
ID   ADL35757 standard; DNA; 13793 BP.
DE   Human perlecan (heparan sulphate proteoglycan 2; HSPG2) DNA.
PN   WO2004019893-A2.
PD   11-MAR-2004.
PA   (RIGE-) RIGEL PHARM INC.
Percent Similarity:      38.91%          Conservative:  40
Best Local Similarity:   26.05%          Mismatches:    148
Query Match:             12.74%          Indels:        42
RESULT 946
ID   AAS87452 standard; cDNA; 14586 BP.
DE   DNA encoding novel human diagnostic protein #23256.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:      38.91%          Conservative:  40
Best Local Similarity:   26.05%          Mismatches:    148
Query Match:             12.74%          Indels:        42
RESULT 947
ID   ADM03329 standard; cDNA; 2004 BP.
DE   Human cDNA of the invention SEQ ID NO:2014.
PN   EP1347046-A1.
PD   24-SEP-2003.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity:      37.60%          Conservative:  36
Best Local Similarity:   27.58%          Mismatches:    146
Query Match:             12.71%          Indels:        78
RESULT 948
ID   ACN42337 standard; cDNA; 6144 BP.
DE   Human diagnostic and therapeutic polynucleotide SEQ ID NO:1212.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
Percent Similarity:      39.74%          Conservative:  44
Best Local Similarity:   25.64%          Mismatches:    139
Query Match:             12.71%          Indels:        49
RESULT 949
ID   ADL16583 standard; cDNA; 6487 BP.
DE   Human 282P1G3 polynucleotide #16.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:      39.74%          Conservative:  44
Best Local Similarity:   25.64%          Mismatches:    139
Query Match:             12.71%          Indels:        49
RESULT 950
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ID   ADL16581 standard; cDNA; 6487 BP.
DE   Human 282P1G3 polynucleotide #14.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 951
ID   ADL16430 standard; cDNA; 6487 BP.
DE   Human 282P1G3 polynucleotide #4.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 952
ID   ADL16587 standard; cDNA; 7329 BP.
DE   Human 282P1G3 polynucleotide #17.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 953
ID   ADL16432 standard; cDNA; 7329 BP.
DE   Human 282P1G3 polynucleotide #5.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 954
ID   ADL16589 standard; cDNA; 7329 BP.
DE   Human 282P1G3 polynucleotide #19.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 955
ID   ADL16601 standard; cDNA; 7527 BP.
DE   Human 282P1G3 polynucleotide #25.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 956
ID   ADL16436 standard; cDNA; 7527 BP.
DE   Human 282P1G3 polynucleotide #7.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 957
ID   ADL16599 standard; cDNA; 7527 BP.
DE   Human 282P1G3 polynucleotide #23.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 958
ID   ADL16442 standard; cDNA; 7570 BP.
DE   Human 282P1G3 polynucleotide #10.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 959
ID   ADL16617 standard; cDNA; 7570 BP.
DE   Human 282P1G3 polynucleotide #32.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 960
ID   ADL16619 standard; cDNA; 7570 BP.
DE   Human 282P1G3 polynucleotide #34.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 961
ID   ADL16434 standard; cDNA; 7602 BP.
DE   Human 282P1G3 polynucleotide #6.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 962
ID   ADL16593 standard; cDNA; 7602 BP.
DE   Human 282P1G3 polynucleotide #20.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 963
ID   ADL16595 standard; cDNA; 7602 BP.
DE   Human 282P1G3 polynucleotide #22.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 964
ID   ADL16576 standard; cDNA; 7650 BP.
DE   Human 282P1G3 polynucleotide #12.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 965
ID   ADL16582 standard; cDNA; 7650 BP.
DE   Human 282P1G3 polynucleotide #15.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 966
ID   ADL16612 standard; cDNA; 7650 BP.
DE   Human 282P1G3 polynucleotide #30.
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PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 967
ID   ADL16426 standard; cDNA; 7650 BP.
DE   Human 282P1G3 polynucleotide #2.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 968
ID   ADL16594 standard; cDNA; 7650 BP.
DE   Human 282P1G3 polynucleotide #21.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 969
ID   ADL16588 standard; cDNA; 7650 BP.
DE   Human 282P1G3 polynucleotide #18.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 970
ID   ADL16618 standard; cDNA; 7650 BP.
DE   Human 282P1G3 polynucleotide #33.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 971
ID   ADL16600 standard; cDNA; 7650 BP.
DE   Human 282P1G3 polynucleotide #24.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 972
ID   ADL16606 standard; cDNA; 7650 BP.
DE   Human 282P1G3 polynucleotide #27.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 973
ID   ADL16631 standard; cDNA; 7651 BP.
DE   Human 282P1G3 polynucleotide #35.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.74%        Conservative:  44
Best Local Similarity:  25.64%        Mismatches:    139
Query Match:            12.71%        Indels:        49
RESULT 974
ID   ADQ97818 standard; DNA; 109661 BP.
DE   Human cancer associated sequence HD11-002, SEQ ID 795.
PN   WO2004060304-A2.
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PD   22-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity:     39.94%        Conservative:  48
Best Local Similarity:  26.15%        Mismatches:    130
Query Match:            12.71%        Indels:        79
RESULT 975
ID   ADG39785 standard; cDNA; 11796 BP.
DE   Human cDNA encoding NOV9.
PN   US2003203843-A1.
PD   30-OCT-2003.
PA   (PENA/) PENA C E A.
PA   (GUOX/) GUO X.
PA   (SHIM/) SHIMKETS R A.
PA   (PADI/) PADIGARU M.
PA   (KEKU/) KEKUDA R.
PA   (SPYT/) SPYTEK K A.
PA   (MEHR/) MEHRABAN F.
PA   (TOPP/) TOPPER J N.
PA   (MALY/) MALYANKAR U M.
PA   (WASS/) WASSERMAN S M.
PA   (EDIN/) EDINGER S R.
PA   (SMIT/) SMITHSON G.
PA   (GUNT/) GUNTHER E.
PA   (KOMU/) KOMUVES L.
Percent Similarity:     39.55%        Conservative:  36
Best Local Similarity:  27.97%        Mismatches:    128
Query Match:            12.68%        Indels:        60
RESULT 976
ID   AAS92794 standard; cDNA; 4452 BP.
DE   DNA encoding novel human diagnostic protein #28598.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     33.24%        Conservative:  33
Best Local Similarity:  24.10%        Mismatches:    137
Query Match:            12.62%        Indels:        104
RESULT 977
ID   AAS80523 standard; cDNA; 4452 BP.
DE   DNA encoding novel human diagnostic protein #16327.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     33.24%        Conservative:  33
Best Local Similarity:  24.10%        Mismatches:    137
Query Match:            12.62%        Indels:        104
RESULT 978
ID   ABN59991 standard; cDNA; 4009 BP.
DE   Novel human coding sequence SEQ ID NO: 402.
PN   WO200222660-A2.
PD   21-MAR-2002.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     39.43%        Conservative:  48
Best Local Similarity:  25.71%        Mismatches:    146
Query Match:            12.57%        Indels:        66
RESULT 979
ID   ABT17394 standard; DNA; 4045 BP.
DE   Human IG gene related nucleic acid SEQ ID No 20.
PN   WO200299040-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     39.43%        Conservative:  48
Best Local Similarity:  25.71%        Mismatches:    146
Query Match:            12.57%        Indels:        66
RESULT 980
ID   ACN37528 standard; cDNA; 4045 BP.
DE   Tumour-associated antigenic target (TAT) cDNA DNA323962, SEQ ID NO:476.
PN   WO2004030615-A2.
PD   15-APR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     39.43%        Conservative:  48
Best Local Similarity:  25.71%        Mismatches:    146
Query Match:            12.57%        Indels:        66
RESULT 981
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ID   AAT16350 standard; cDNA; 1581 BP.
DE   Mouse muscle-localized protein-tyrosine-kinase receptor 5' fragment.
PN   WO9602644-A1.
PD   01-FEB-1996.
PA   (GEMY ) GENETICS INST INC.
Percent Similarity:     38.82%         Conservative:  45
Best Local Similarity:  24.84%         Mismatches:    146
Query Match:            12.49%         Indels:        51
RESULT 982
ID   AAT16349 standard; cDNA; 2604 BP.
DE   Mouse muscle-localised protein-tyrosine-kinase receptor-2 isoform.
PN   WO9602644-A1.
PD   01-FEB-1996.
PA   (GEMY ) GENETICS INST INC.
Percent Similarity:     38.82%         Conservative:  45
Best Local Similarity:  24.84%         Mismatches:    146
Query Match:            12.49%         Indels:        51
RESULT 983
ID   ABT11196 standard; DNA; 3562 BP.
DE   Human secreted protein (SECP) coding sequence #18.
PN   WO200270669-A2.
PD   12-SEP-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:     43.00%         Conservative:  28
Best Local Similarity:  29.47%         Mismatches:    71
Query Match:            12.49%         Indels:        47
RESULT 984
ID   AAF85337 standard; DNA; 2607 BP.
DE   Nucleotide sequence of a human MuSK-R polypeptide.
PN   WO200136659-A2.
PD   25-MAY-2001.
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Percent Similarity:     39.56%         Conservative:  44
Best Local Similarity:  25.86%         Mismatches:    139
Query Match:            12.46%         Indels:        55
RESULT 985
ID   AAH78836 standard; cDNA; 2607 BP.
DE   Coding sequence of muscle specific tyrosine kinase receptor (hMuSK-R).
PN   WO200172834-A1.
PD   04-OCT-2001.
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Percent Similarity:     39.56%         Conservative:  44
Best Local Similarity:  25.86%         Mismatches:    139
Query Match:            12.46%         Indels:        55
RESULT 986
ID   ADI02582 standard; cDNA; 13559 BP.
DE   Human cDNA differentially expressed in the vascular endothelium #123.
PN   US2003166903-A1.
PD   04-SEP-2003.
PA   (ASTR/) ASTROMOFF A.
PA   (BAND/) BANDMAN O.
PA   (COCK/) COCKS B G.
Percent Similarity:     38.91%         Conservative:  41
Best Local Similarity:  25.72%         Mismatches:    148
Query Match:            12.46%         Indels:        42
RESULT 987
ID   AAF54724 standard; DNA; 14327 BP.
DE   Nucleotide sequence of a human polynucleotide sequence.
PN   WO200105422-A2.
PD   25-JAN-2001.
PA   (INMR ) BIOMERIEUX STELHYS.
Percent Similarity:     38.91%         Conservative:  41
Best Local Similarity:  25.72%         Mismatches:    148
Query Match:            12.46%         Indels:        42
RESULT 988
ID   ADR06784 standard; cDNA; 3960 BP.
DE   Full length human cDNA useful for treating neurological disease Seq 290.
PN   EP1447413-A2.
PD   18-AUG-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity:     39.42%         Conservative:  44
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Best Local Similarity:  25.32%         Mismatches:    140
Query Match:            12.43%         Indels:        49
RESULT 989
ID   ADP28189 standard; DNA; 4752 BP.
DE   Human secreted protein encoding sequence SEQ ID #187.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity:     35.35%         Conservative:  52
Best Local Similarity:  22.22%         Mismatches:    145
Query Match:            12.43%         Indels:        111
RESULT 990
ID   ADP28123 standard; DNA; 4752 BP.
DE   Human secreted protein encoding sequence SEQ ID #121.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity:     35.35%         Conservative:  52
Best Local Similarity:  22.22%         Mismatches:    145
Query Match:            12.43%         Indels:        111
RESULT 991
ID   AAS84195 standard; cDNA; 5298 BP.
DE   DNA encoding novel human diagnostic protein #19999.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     35.35%         Conservative:  52
Best Local Similarity:  22.22%         Mismatches:    145
Query Match:            12.43%         Indels:        111
RESULT 992
ID   AAS86818 standard; cDNA; 5298 BP.
DE   DNA encoding novel human diagnostic protein #22622.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     35.35%         Conservative:  52
Best Local Similarity:  22.22%         Mismatches:    145
Query Match:            12.43%         Indels:        111
RESULT 993
ID   AAS76204 standard; cDNA; 6040 BP.
DE   DNA encoding novel human diagnostic protein #12008.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     35.35%         Conservative:  52
Best Local Similarity:  22.22%         Mismatches:    145
Query Match:            12.43%         Indels:        111
RESULT 994
ID   ADL16575 standard; cDNA; 7491 BP.
DE   Human 282P1G3 polynucleotide #11.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.42%         Conservative:  44
Best Local Similarity:  25.32%         Mismatches:    140
Query Match:            12.43%         Indels:        49
RESULT 995
ID   ADL16577 standard; cDNA; 7491 BP.
DE   Human 282P1G3 polynucleotide #13.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.42%         Conservative:  44
Best Local Similarity:  25.32%         Mismatches:    140
Query Match:            12.43%         Indels:        49
RESULT 996
ID   ADL16428 standard; cDNA; 7491 BP.
DE   Human 282P1G3 polynucleotide #3.
PN   WO2004016734-A2.
PD   26-FEB-2004.
PA   (AGEN-) AGENSYS INC.
Percent Similarity:     39.42%         Conservative:  44
Best Local Similarity:  25.32%         Mismatches:    140
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Query Match:             12.43%         Indels:        49
RESULT 997
ID   ADL15033 standard; DNA; 7642 BP.
DE   Human neural cell adhesion molecule DNA for cancer treatment.
PN   WO2003068268-A2.
PD   21-AUG-2003.
PA   (BIOI-) BIOINVENT INT AB.
Percent Similarity:      39.42%         Conservative:  44
Best Local Similarity:   25.32%         Mismatches:    140
Query Match:             12.43%         Indels:        49
RESULT 998
ID   ADJ75061 standard; DNA; 7642 BP.
DE   Marker gene SEQ ID NO:313.
PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (GENO-) GENOX RES INC.
Percent Similarity:      39.42%         Conservative:  44
Best Local Similarity:   25.32%         Mismatches:    140
Query Match:             12.43%         Indels:        49
RESULT 999
ID   ADN04061 standard; cDNA; 7642 BP.
DE   Antipsoriatic cDNA sequence #230.
PN   WO2004028479-A2.
PD   08-APR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      39.42%         Conservative:  44
Best Local Similarity:   25.32%         Mismatches:    140
Query Match:             12.43%         Indels:        49
RESULT 1000
ID   ADQ19765 standard; DNA; 7642 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 2584.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity:      39.42%         Conservative:  44
Best Local Similarity:   25.32%         Mismatches:    140
Query Match:             12.43%         Indels:        49
RESULT 1001
ID   ADQ23905 standard; DNA; 7642 BP.
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 6725.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity:      39.42%         Conservative:  44
Best Local Similarity:   25.32%         Mismatches:    140
Query Match:             12.43%         Indels:        49
RESULT 1002
ID   ADR14750 standard; DNA; 7642 BP.
DE   Nucleotide sequence of human MAPCAX orthologue #8.
PN   WO2004066948-A2.
PD   12-AUG-2004.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:      39.42%         Conservative:  44
Best Local Similarity:   25.32%         Mismatches:    140
Query Match:             12.43%         Indels:        49
RESULT 1003
ID   ADI61707 standard; cDNA; 7647 BP.
DE   Human cDNA downregulated in Alzheimer's disease, INCYTE 334247.2.
PN   US6682888-B1.
PD   27-JAN-2004.
PA   (INCY-) INCYTE CORP.
Percent Similarity:      39.42%         Conservative:  44
Best Local Similarity:   25.32%         Mismatches:    140
Query Match:             12.43%         Indels:        49
RESULT 1004
ID   AAS66304 standard; cDNA; 1464 BP.
DE   DNA encoding novel human diagnostic protein #2108.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:      37.25%         Conservative:  41
Best Local Similarity:   25.50%         Mismatches:    137
Query Match:             12.40%         Indels:        82
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RESULT 1005
ID   AAS90766 standard; cDNA; 1464 BP.
DE   DNA encoding novel human diagnostic protein #26570.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:      37.25%         Conservative:  41
Best Local Similarity:   25.50%         Mismatches:    137
Query Match:             12.40%         Indels:        82
RESULT 1006
ID   AAS72490 standard; cDNA; 1802 BP.
DE   DNA encoding novel human diagnostic protein #8294.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:      37.25%         Conservative:  41
Best Local Similarity:   25.50%         Mismatches:    137
Query Match:             12.40%         Indels:        82
RESULT 1007
ID   AAS66206 standard; cDNA; 2214 BP.
DE   DNA encoding novel human diagnostic protein #2010.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:      37.25%         Conservative:  41
Best Local Similarity:   25.50%         Mismatches:    137
Query Match:             12.40%         Indels:        82
RESULT 1008
ID   AAK94785 standard; cDNA; 2500 BP.
DE   Human full-length cDNA, SEQ ID NO: 3892.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
Percent Similarity:      37.90%         Conservative:  44
Best Local Similarity:   23.89%         Mismatches:    127
Query Match:             12.40%         Indels:        68
RESULT 1009
ID   ADL31859 standard; cDNA; 2500 BP.
DE   Full length human cDNA clone SeqID 3892.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity:      37.90%         Conservative:  44
Best Local Similarity:   23.89%         Mismatches:    127
Query Match:             12.40%         Indels:        68
RESULT 1010
ID   AAX37725 standard; cDNA; 3598 BP.
DE   Human PRO335 DNA fragment #2.
PN   WO9914241-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:   20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1011
ID   AAX52264 standard; DNA; 3662 BP.
DE   Protein PRO335 cDNA clone DNA41388-1234.
PN   WO9914328-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:   20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1012
ID   AAZ52206 standard; cDNA; 3662 BP.
DE   Human PRO335 protein encoding cDNA, UNQ287V.
PN   WO200015797-A2.
PD   23-MAR-2000.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:   20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1013
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ID   ADC78601 standard; cDNA; 3662 BP.
DE   Human PRO335 cDNA.
PN   WO200015796-A2.
PD   23-MAR-2000.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     37.90%        Conservative:  44
Best Local Similarity:  23.89%        Mismatches:    127
Query Match:            12.40%        Indels:        68
RESULT 1014
ID   AAF72422 standard; cDNA; 3662 BP.
DE   Human PRO335 cDNA.
PN   WO200104311-A1.
PD   18-JAN-2001.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1015
ID   AAS00161 standard; cDNA; 3662 BP.
DE   Human cDNA clone DNA41388-1234 encoding PRO335 (UNQ287).
PN   WO200119991-A1.
PD   22-MAR-2001.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1016
ID   ACA60239 standard; cDNA; 3662 BP.
DE   Human cDNA for secreted/transmembrane protein PRO335.
PN   US2003003530-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1017
ID   ACD07639 standard; cDNA; 3662 BP.
DE   Novel human secreted and transmembrane protein PRO335 cDNA.
PN   US2002197671-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1018
ID   ABX71687 standard; cDNA; 3662 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO335.
PN   US2002132240-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1019
ID   ACH07019 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane polypeptide PRO335 cDNA.
PN   US2003044839-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1020
ID   ABX96256 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #52.
PN   US2002160374-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1021
ID   ACA05577 standard; cDNA; 3662 BP.
DE   cDNA encoding human secreted protein PRO335.
PN   US2003023054-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1022
ID   ACD20244 standard; cDNA; 3662 BP.
DE   Human secreted / transmembrane polypeptide PRO335 cDNA.
PN   US2003036060-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1023
ID   ACA55047 standard; cDNA; 3662 BP.
DE   Novel human secreted and transmembrane protein PRO335 cDNA.
PN   US2003017463-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1024
ID   ACD19882 standard; cDNA; 3662 BP.
DE   Human secreted / transmembrane polypeptide PRO335 cDNA.
PN   US2003027143-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1025
ID   ADB29494 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003092002-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1026
ID   ADA18350 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003039971-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1027
ID   ACD67029 standard; cDNA; 3662 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO335.
PN   US2003045693-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1028
ID   ACD83190 standard; cDNA; 3662 BP.
DE   Human PRO polynucleotide #50.
PN   US2003044793-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1029
ID   ADA16325 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
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PN   US2003049621-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1030
ID   ADA42470 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003054401-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1031
ID   ACD23368 standard; cDNA; 3662 BP.
DE   Human PRO polynucleotide #50.
PN   US2003064367-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1032
ID   ADA16749 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003039969-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1033
ID   ADA13178 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003049622-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1034
ID   ADA42046 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003082540-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1035
ID   ADA17393 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003017498-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1036
ID   ADA42896 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003054351-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1037
ID   ACD23730 standard; cDNA; 3662 BP.
DE   Human PRO polynucleotide #50.
PN   US2003064923-A1.
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PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1038
ID   ADB77815 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003077654-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1039
ID   ADB74951 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003082542-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1040
ID   ADC28597 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003059772-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1041
ID   ADC39797 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003059828-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1042
ID   ADC40311 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003059829-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1043
ID   ADC19135 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003036061-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1044
ID   ADC34435 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003036094-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1045
ID   ADC29490 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003049676-A1.
PD   13-MAR-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1046
ID   ADC29021 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003049677-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1047
ID   ADC40906 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003054400-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1048
ID   ADC19563 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003054441-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1049
ID   ADC34011 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003073077-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1050
ID   ADC13081 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003073079-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1051
ID   ADC12533 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003082541-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1052
ID   ADD05088 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003104469-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1053
ID   ADD04094 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003104381-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1054
ID   ADD03670 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003108983-A1.
PD   12-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1055
ID   ADE34922 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003077583-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1056
ID   ADH59405 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003039972-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1057
ID   ADI38184 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003054352-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1058
ID   ACA59135 standard; cDNA; 3662 BP.
DE   Human PRO polynucleotide #50.
PN   US2002146709-A1.
PD   10-OCT-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1059
ID   ACA58532 standard; cDNA; 3662 BP.
DE   cDNA encoding human PRO polypeptide #50.
PN   US2002192659-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1060
ID   ADJ26452 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003054349-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1061
ID   ADE79367 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003135025-A1.
PD   17-JUL-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
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Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1062
ID   ADE79791 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003130489-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1063
ID   ADE73467 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003129592-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1064
ID   ADE74002 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003148370-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1065
ID   ADE99556 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003211576-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1066
ID   ADE98675 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003211569-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1067
ID   ADE99102 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003211568-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1068
ID   ADG40572 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003225253-A1.
PD   04-DEC-2003.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1069
ID   ADF73966 standard; cDNA; 3662 BP.
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DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003180312-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1070
ID   ADF73542 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003166051-A1.
PD   04-SEP-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1071
ID   ADG92385 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003027145-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1072
ID   ADG92812 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003027146-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1073
ID   ADH20601 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2004005553-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1074
ID   ADH07456 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2004006211-A1.
PD   08-JAN-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1075
ID   ADH60001 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003215904-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1076
ID   ADH07029 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2004005665-A1.
PD   08-JAN-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1077
ID   ADI18771 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003152999-A1.
PD   14-AUG-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1078
ID   ADI37750 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003096340-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1079
ID   ADH97550 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003190610-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1080
ID   ADI65918 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003148371-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1081
ID   ADH60661 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2004023331-A1.
PD   05-FEB-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1082
ID   ADJ99718 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003187238-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1083
ID   ADL08911 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003186358-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1084
ID   ADM25252 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003096233-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1085
ID   ADM30002 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003190611-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1086
ID   ADO06324 standard; cDNA; 3662 BP.
DE   Human PRO polynucleotide #52.
PN   US6686451-B1.
PD   03-FEB-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1087
ID   ADR11176 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2004137561-A1.
PD   15-JUL-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1088
ID   ADR18085 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2004147017-A1.
PD   29-JUL-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI C J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (MATH/) MATHER J P.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
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RESULT 1089
ID   ADT03761 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2003152922-A1.
PD   14-AUG-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1090
ID   ADS74724 standard; cDNA; 3662 BP.
DE   Human secreted/transmembrane cDNA #54.
PN   US2004185531-A1.
PD   23-SEP-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI C J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (MATH/) MATHER J P.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1091
ID   AAX37743 standard; cDNA; 3807 BP.
DE   Human PRO326 DNA fragment #2.
PN   WO9914241-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1092
ID   AAX52266 standard; DNA; 4053 BP.
DE   Protein PRO326 cDNA clone DNA37140-1234.
PN   WO9914328-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1093
ID   AAZ52208 standard; cDNA; 4053 BP.
DE   Human PRO326 protein encoding cDNA, UNQ287.
PN   WO200015797-A2.
PD   23-MAR-2000.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1094
ID   AAF72424 standard; cDNA; 4053 BP.
DE   Human PRO326 cDNA.
PN   WO200104311-A1.
PD   18-JAN-2001.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1095
ID   AAC84422 standard; cDNA; 4053 BP.
DE   Human PRO326 polypeptide encoding cDNA.
PN   WO200075316-A1.
PD   14-DEC-2000.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1096
ID   AAS00163 standard; cDNA; 4053 BP.
DE   Human cDNA clone DNA37140-1234 encoding PRO326 (UNQ287).
PN   WO200119991-A1.
PD   22-MAR-2001.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1097
ID   AAS21419 standard; cDNA; 4053 BP.
DE   Human cDNA sequence encoding for PRO326 polypeptide.
PN   WO200140466-A2.
PD   07-JUN-2001.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1098
ID   ACA60241 standard; cDNA; 4053 BP.
DE   Human cDNA for secreted/transmembrane protein PRO326.
PN   US2003003530-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1099
ID   ACD07641 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2002197671-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1100
ID   ACA03778 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003036180-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1101
ID   ABX71689 standard; cDNA; 4053 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO326.
PN   US2002132240-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1102
ID   ACH07021 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane polypeptide PRO326 cDNA.
PN   US2003044839-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1103
ID   ABX89316 standard; cDNA; 4053 BP.
DE   DNA encoding novel secreted and transmembrane protein PRO326.
PN   US2003017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1104
ID   ACD41970 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #176.
PN   US2003036179-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1105
ID   ABX96258 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #54.
PN   US2002160374-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1106
ID   ACA05579 standard; cDNA; 4053 BP.
DE   cDNA encoding human secreted protein PRO326.
PN   US2003023054-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1107
ID   ACD20246 standard; cDNA; 4053 BP.
DE   Human secreted / transmembrane polypeptide PRO326 cDNA.
PN   US2003036060-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1108
ID   ACA04199 standard; cDNA; 4053 BP.
DE   Human cDNA encoding a secreted/transmembrane protein, SEQ ID 351.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1109
ID   ACA55049 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003017463-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1110
ID   ACD19884 standard; cDNA; 4053 BP.
DE   Human secreted / transmembrane polypeptide PRO326 cDNA.
PN   US2003027143-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1111
ID   ADA45870 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1112
ID   ADA76301 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1113
ID   ADB29498 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003092002-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1114
ID   ADA18951 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003054517-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1115
ID   ADA61574 standard; cDNA; 4053 BP.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1116
ID   ADB19359 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1117
ID   ADB27900 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1118
ID   ADA86379 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
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Query Match:             12.40%         Indels:        146
RESULT 1119
ID   ADB15943 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1120
ID   ADA47729 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1121
ID   ADA18354 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003039971-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1122
ID   ACD67031 standard; cDNA; 4053 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO326.
PN   US2003045693-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1123
ID   ADA67524 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1124
ID   ADB30531 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003068794-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1125
ID   ADA85827 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082693-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1126
ID   ADA97039 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082705-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1127
ID   ADA79343 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082763-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1128
ID   ADA87482 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087345-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1129
ID   ADB16684 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003087349-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1130
ID   ACD83192 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #52.
PN   US2003044793-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1131
ID   ADA16329 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003049621-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1132
ID   ADA91776 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082694-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1133
ID   ADB14839 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003087351-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1134
ID   ADB18800 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003073211-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:             12.40%         Indels:        146
RESULT 1135
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ID   ADA94015 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003077722-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1136
ID   ADB19911 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082691-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1137
ID   ADB13223 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082710-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1138
ID   ACD98599 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003044945-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1139
ID   ADA74477 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003068798-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1140
ID   ADA42474 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003054401-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1141
ID   ADB24710 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide SEQ ID NO 351.
PN   US2003077713-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1142
ID   ADA82234 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082701-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1143
ID   ADA75197 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003073216-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1144
ID   ADA85275 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082695-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1145
ID   ADA84723 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1146
ID   ACD23370 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #52.
PN   US2003064367-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1147
ID   ADB29979 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1148
ID   ADA80507 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1149
ID   ADA75749 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082703-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1150
ID   ADA46974 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003073210-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%        Conservative:  54
Best Local Similarity:  20.73%        Mismatches:    148
Query Match:            12.40%        Indels:        146
RESULT 1151
ID   ADB25270 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide SEQ ID NO 351.
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PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1152
ID   ADA93446 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003077721-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1153
ID   ADB26796 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1154
ID   ADB31083 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1155
ID   ADA61011 standard; cDNA; 4053 BP.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1156
ID   ADB24158 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide SEQ ID NO 351.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1157
ID   ADA96487 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082690-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1158
ID   ADA81059 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082702-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1159
ID   ADA95935 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1160
ID   ADB26244 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1161
ID   ADB21729 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1162
ID   ADA77508 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003068797-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1163
ID   ADB18248 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003077710-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1164
ID   ADA86931 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082709-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1165
ID   ADA16753 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003039969-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1166
ID   ADA13182 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003049622-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1167
ID   ADA42050 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003082540-A1.
PD   01-MAY-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1168
ID   ADA88034 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082700-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1169
ID   ADA46422 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003054516-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1170
ID   ADA17397 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003017498-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1171
ID   ADA42900 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003054351-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1172
ID   ADB28452 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003082699-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1173
ID   ADB29004 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003082706-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1174
ID   ADA76956 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003059909-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1175
ID   ADA88586 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003073213-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1176
ID   ADA97591 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082686-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1177
ID   ADB27348 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003022239-A1.
PD   30-JAN-2003.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1178
ID   ADB22281 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087344-A1.
PD   08-MAY-2003.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1179
ID   ACD23732 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #52.
PN   US2003064923-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1180
ID   ADA66972 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003068793-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1181
ID   ADB22833 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003077711-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1182
ID   ADB23606 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide SEQ ID NO 351.
PN   US2003077712-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1183
ID   ADA92328 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082712-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
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RESULT 1184
ID   ADB15391 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003087352-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1185
ID   ADB38643 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082766-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1186
ID   ADB38091 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087347-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1187
ID   ADB66563 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082689-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1188
ID   ADB89643 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082698-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1189
ID   ADB90375 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082762-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1190
ID   ADB77819 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003077654-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1191
ID   ADB39476 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082764-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1192
ID   ADB74955 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003082542-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1193
ID   ADB47099 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082687-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1194
ID   ADB86706 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003082697-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1195
ID   ADB77311 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082696-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1196
ID   ADB34468 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide SEQ ID NO 351.
PN   US2003077717-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1197
ID   ADB35572 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide SEQ ID NO 351.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1198
ID   ADB33916 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide SEQ ID NO 351.
PN   US2003077716-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1199
ID   ADB35020 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide SEQ ID NO 351.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1200
ID   ADB36124 standard; cDNA; 4053 BP.
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DE   Human PRO polynucleotide SEQ ID NO 351.
PN   US2003077720-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1201
ID   ADB46519 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003082692-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1202
ID   ADC28601 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003059772-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1203
ID   ADC39801 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003059828-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1204
ID   ADC40315 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003059829-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1205
ID   ADC19139 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003036061-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1206
ID   ADC34439 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003036094-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1207
ID   ADC29494 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003049676-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1208
ID   ADC29025 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003049677-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1209
ID   ADC40910 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003054400-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1210
ID   ADC19567 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003054441-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1211
ID   ADC34015 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003073077-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1212
ID   ADC13085 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003073079-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1213
ID   ADC50392 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003092106-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1214
ID   ADC71939 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1215
ID   ADC59918 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1216
ID   ADC52925 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID351.
PN   US2003087365-A1.
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PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1217
ID   ADC57279 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID351.
PN   US2003087366-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1218
ID   ADC60470 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1219
ID   ADC50945 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1220
ID   ADC65472 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1221
ID   ADC54570 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID351.
PN   US2003087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1222
ID   ADC53531 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID351.
PN   US2003087364-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1223
ID   ADC59054 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID351.
PN   US2003087359-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1224
ID   ADC55932 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID351.
PN   US2003087360-A1.
PD   08-MAY-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1225
ID   ADC58502 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein cDNA Seq ID351.
PN   US2003087346-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1226
ID   ADC12537 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003082541-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1227
ID   ADD03176 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003092104-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1228
ID   ADC90168 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087348-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1229
ID   ADC69587 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003194770-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1230
ID   ADC48476 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003194773-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1231
ID   ADD10005 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1232
ID   ADD04580 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1233
ID   ADC80536 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1234
ID   ADD11043 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1235
ID   ADC47924 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1236
ID   ADD05092 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003104469-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1237
ID   ADC79984 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1238
ID   ADD09453 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1239
ID   ADD04098 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003104381-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1240
ID   ADD03674 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003108983-A1.
PD   12-JUN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1241
ID   ADD41166 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1242
ID   ADD52305 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1243
ID   ADD53045 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1244
ID   ADD53597 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003203437-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1245
ID   ADD51753 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1246
ID   ADD02552 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003203431-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1247
ID   ADD01986 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003203430-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1248
ID   ADD54168 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003203432-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
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Query Match:             12.40%          Indels:         146
RESULT 1249
ID   ADD92485 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199030-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1250
ID   ADD91381 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199055-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1251
ID   ADE03995 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199057-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1252
ID   ADE32292 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003194765-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1253
ID   ADE22224 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003199056-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1254
ID   ADD79448 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003203428-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1255
ID   ADE41984 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003194772-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1256
ID   ADE17801 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199023-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
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RESULT 1257
ID   ADD91933 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199053-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1258
ID   ADE33396 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003194767-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1259
ID   ADE33948 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003194791-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1260
ID   ADD80000 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003207417-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1261
ID   ADD93037 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003194768-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1262
ID   ADE19457 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199025-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1263
ID   ADE34926 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003077583-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1264
ID   ADE18905 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199026-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:      33.03%          Conservative:   54
Best Local Similarity:   20.73%          Mismatches:     148
Query Match:             12.40%          Indels:         146
RESULT 1265
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ID   ADE43101 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1266
ID   ADD95890 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199059-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1267
ID   ADE22776 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1268
ID   ADD78894 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1269
ID   ADE32844 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1270
ID   ADE42536 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1271
ID   ADD80552 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1272
ID   ADD89580 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1273
ID   ADE40864 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1274
ID   ADE04663 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1275
ID   ADE92792 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003194777-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1276
ID   ADG21501 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1277
ID   ADG23142 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1278
ID   ADF97477 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1279
ID   ADG80541 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1280
ID   ADG79989 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1281
ID   ADH59409 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
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PN   US2003039972-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1282
ID   ADH55281 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207381-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1283
ID   ADH55833 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207379-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1284
ID   ADI38188 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003054352-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1285
ID   ADI64052 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207385-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1286
ID   ADI65001 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207386-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1287
ID   ADI63500 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207387-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1288
ID   ADH81914 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207388-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1289
ID   ADH81362 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207377-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1290
ID   ACA59137 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #52.
PN   US2002146709-A1.
PD   10-OCT-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1291
ID   ACD24028 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003032156-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1292
ID   ACA58534 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #52.
PN   US2002192659-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1293
ID   ACA67169 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003004311-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1294
ID   ADJ26456 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003054349-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1295
ID   ADM82531 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087355-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1296
ID   ADN15930 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087353-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1297
ID   ADN16559 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087385-A1.
PD   08-MAY-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1298
ID   ADN15378 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087356-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1299
ID   ADN14826 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003087357-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1300
ID   ADC81088 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003092115-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1301
ID   ADE79371 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003135025-A1.
PD   17-JUL-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1302
ID   ADD76536 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003100087-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1303
ID   ADD87900 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003092113-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1304
ID   ADD86304 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003203440-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1305
ID   ADE79795 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003130489-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1306
ID   ADE75752 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003211571-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1307
ID   ADE73471 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003129592-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1308
ID   ADE23328 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003092108-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1309
ID   ADE23880 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003092110-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1310
ID   ADE24523 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003092111-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1311
ID   ADD87348 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1312
ID   ADE89214 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1313
ID   ADE74006 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003148370-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
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Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1314
ID   ADE18353 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003194794-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1315
ID   ADE88662 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1316
ID   ADE99560 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003211576-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1317
ID   ADE94682 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003199027-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1318
ID   ADE91093 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1319
ID   ADE95234 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1320
ID   ADE93344 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1321
ID   ADF34925 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003199029-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
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Query Match:            12.40%         Indels:        146
RESULT 1322
ID   ADE98679 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003211569-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1323
ID   ADE92240 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1324
ID   ADE90541 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1325
ID   ADE91688 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1326
ID   ADE99106 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003211568-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1327
ID   ADG40576 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003225253-A1.
PD   04-DEC-2003.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1328
ID   ADF73970 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003180312-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1329
ID   ADG02267 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
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PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1330
ID   ADG22053 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1331
ID   ADG20123 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1332
ID   ADF98029 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1333
ID   ADG24246 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207426-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1334
ID   ADF98600 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1335
ID   ADG03431 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1336
ID   ADF99152 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1337
ID   ADG16737 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1338
ID   ADG05196 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1339
ID   ADG19463 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1340
ID   ADF73546 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003166051-A1.
PD   04-SEP-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1341
ID   ADG13300 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1342
ID   ADG08357 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1343
ID   ADG15527 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1344
ID   ADF96925 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1345
ID   ADG06110 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207374-A1.
PD   06-NOV-2003.
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PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1346
ID   ADG23694 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1347
ID   ADG03983 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1348
ID   ADG24884 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1349
ID   ADG07181 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1350
ID   ADG07733 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207356-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1351
ID   ADG55228 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1352
ID   ADG60892 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1353
ID   ADG61996 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1354
ID   ADG92389 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003027145-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1355
ID   ADG82197 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1356
ID   ADG57436 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1357
ID   ADG56884 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1358
ID   ADG55780 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1359
ID   ADG58540 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1360
ID   ADG70906 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1361
ID   ADG92816 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003027146-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
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Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1362
ID   ADG57988 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1363
ID   ADG53572 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1364
ID   ADG71458 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1365
ID   ADG81645 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003207805-A1.
PD   06-NOV-2003.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1366
ID   ADH30607 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1367
ID   ADH11974 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1368
ID   ADG52396 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1369
ID   ADG54124 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1370
ID   ADG81093 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1371
ID   ADG56332 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1372
ID   ADH12598 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1373
ID   ADG61444 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1374
ID   ADH28531 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1375
ID   ADG54676 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1376
ID   ADG59716 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1377
ID   ADH20605 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2004005553-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%          Conservative:  54
Best Local Similarity:  20.73%          Mismatches:    148
Query Match:            12.40%          Indels:        146
RESULT 1378
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ID   ADH07460 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2004006211-A1.
PD   08-JAN-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1379
ID   ADH60005 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003215904-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1380
ID   ADH07033 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2004005665-A1.
PD   08-JAN-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1381
ID   ADI81140 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003207361-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1382
ID   ADI18775 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003152999-A1.
PD   14-AUG-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1383
ID   ADI37754 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003096340-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1384
ID   ADG09883 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2004009548-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1385
ID   ADH97554 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003190610-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1386
ID   ADI15354 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207382-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1387
ID   ADG09231 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2004009547-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1388
ID   ADI65922 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003148371-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1389
ID   ADI14686 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207383-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1390
ID   ADH60665 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2004023331-A1.
PD   05-FEB-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1391
ID   ADI18281 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207349-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1392
ID   ADJ99722 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
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PN   US2003187238-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1393
ID   ADL08915 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003186358-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1394
ID   ADM25256 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003096233-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1395
ID   ADJ63562 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1396
ID   ADM30006 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003190611-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1397
ID   ADJ77457 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #176.
PN   US2004038336-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1398
ID   ADJ65579 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2004038335-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1399
ID   ADM27715 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2004048333-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1400
ID   ADM42439 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2004058424-A1.
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PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1401
ID   AD006328 standard; cDNA; 4053 BP.
DE   Human PRO polynucleotide #54.
PN   US6686451-B1.
PD   03-FEB-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1402
ID   ADM28301 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2004077064-A1.
PD   22-APR-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1403
ID   ADR11180 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2004137561-A1.
PD   15-JUL-2004.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1404
ID   ADR18089 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2004147017-A1.
PD   29-JUL-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI C J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (MATH/) MATHER J P.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1405
ID   ADI95783 standard; cDNA; 4053 BP.
DE   cDNA encoding human PRO polypeptide #176.
PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
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RESULT 1406
ID   ADI96335 standard; cDNA; 4053 BP.
DE   Novel human secreted and transmembrane protein PRO326 cDNA.
PN   US2003207354-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1407
ID   ADT03765 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane protein cDNA, #56.
PN   US2003152922-A1.
PD   14-AUG-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1408
ID   ADS74728 standard; cDNA; 4053 BP.
DE   Human secreted/transmembrane cDNA #56.
PN   US2004185531-A1.
PD   23-SEP-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI C J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (MATH/) MATHER J P.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Percent Similarity:     33.03%         Conservative:  54
Best Local Similarity:  20.73%         Mismatches:    148
Query Match:            12.40%         Indels:        146
RESULT 1409
ID   ABA06424 standard; cDNA; 2667 BP.
DE   Human cDNA SEQ ID NO: 90.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity:     37.92%         Conservative:  34
Best Local Similarity:  25.28%         Mismatches:    123
Query Match:            12.38%         Indels:        45
RESULT 1410
ID   ABV83761 standard; cDNA; 2667 BP.
DE   Human polynucleotide SEQ ID NO 90.
PN   US2002090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
Percent Similarity:     37.92%         Conservative:  34
Best Local Similarity:  25.28%         Mismatches:    123
Query Match:            12.38%         Indels:        45
RESULT 1411
ID   ABX34664 standard; cDNA; 1213 BP.
DE   Human mddt cDNA SEQ ID 225.
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PN   WO200279449-A2.
PD   10-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Percent Similarity:     38.94%         Conservative:  38
Best Local Similarity:  26.40%         Mismatches:    123
Query Match:            12.35%         Indels:        62
RESULT 1412
ID   AAZ33346 standard; cDNA; 1417 BP.
DE   Human secreted protein clone cw1000_2 nucleotide sequence SEQ ID NO:61.
PN   WO9957132-A1.
PD   11-NOV-1999.
PA   (GEMY ) GENETICS INST INC.
Percent Similarity:     42.25%         Conservative:  61
Best Local Similarity:  25.07%         Mismatches:    153
Query Match:            12.35%         Indels:        52
RESULT 1413
ID   ADR28012 standard; cDNA; 3540 BP.
DE   Long form full-length IGSF9 protein encoding cDNA.
PN   WO2004066933-A2.
PD   12-AUG-2004.
PA   (MCLA/) MCLACHLAN K.
PA   (GLAS/) GLASER S.
PA   (PEAC/) PEACH R J.
PA   (ROWE/) ROWE T.
Percent Similarity:     39.48%         Conservative:  51
Best Local Similarity:  24.78%         Mismatches:    144
Query Match:            12.35%         Indels:        66
RESULT 1414
ID   ADP28247 standard; DNA; 3018 BP.
DE   Human secreted protein encoding sequence SEQ ID #245.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity:     40.81%         Conservative:  49
Best Local Similarity:  25.55%         Mismatches:    142
Query Match:            12.29%         Indels:        48
RESULT 1415
ID   ADP28237 standard; DNA; 3018 BP.
DE   Human secreted protein encoding sequence SEQ ID #235.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity:     40.81%         Conservative:  49
Best Local Similarity:  25.55%         Mismatches:    142
Query Match:            12.29%         Indels:        48
RESULT 1416
ID   ADH72193 standard; DNA; 3333 BP.
DE   Human gene of the invention NOV51d SEQ ID NO:1089.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Percent Similarity:     39.25%         Conservative:  40
Best Local Similarity:  24.15%         Mismatches:    111
Query Match:            12.29%         Indels:        50
RESULT 1417
ID   ABL23498 standard; DNA; 7171 BP.
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 21967.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Percent Similarity:     36.66%         Conservative:  43
Best Local Similarity:  24.05%         Mismatches:    115
Query Match:            12.29%         Indels:        101
RESULT 1418
ID   AAA43911 standard; cDNA; 971 BP.
DE   Human secreted expressed sequence tag SEQ ID NO:486.
PN   WO200021991-A1.
PD   20-APR-2000.
PA   (GEMY ) GENETICS INST INC.
Percent Similarity:     42.34%         Conservative:  53
Best Local Similarity:  26.43%         Mismatches:    128
Query Match:            12.24%         Indels:        65
RESULT 1419
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ID   AAS86820 standard; cDNA; 2948 BP.
DE   DNA encoding novel human diagnostic protein #22624.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Percent Similarity:     37.77%        Conservative:  28
Best Local Similarity:  25.75%        Mismatches:    107
Query Match:            12.24%        Indels:        38
RESULT 1420
ID   AAV31988 standard; cDNA; 6413 BP.
DE   Human Down syndrome-cell adhesion molecule DS-CAM2 cDNA.
PN   WO9817795-A1.
PD   30-APR-1998.
PA   (CEDA-) CEDARS SINAI MEDICAL CENT.
Percent Similarity:     40.25%        Conservative:  28
Best Local Similarity:  28.63%        Mismatches:    122
Query Match:            12.24%        Indels:        22
RESULT 1421
ID   AAV31981 standard; cDNA; 6604 BP.
DE   Human Down syndrome-cell adhesion molecule DS-CAM1 cDNA.
PN   WO9817795-A1.
PD   30-APR-1998.
PA   (CEDA-) CEDARS SINAI MEDICAL CENT.
Percent Similarity:     40.25%        Conservative:  28
Best Local Similarity:  28.63%        Mismatches:    122
Query Match:            12.24%        Indels:        22
RESULT 1422
ID   ADK71086 standard; DNA; 6649 BP.
DE   Human MP21 polypeptide encoding DNA.
PN   WO2004015073-A2.
PD   19-FEB-2004.
PA   (EXEL-) EXELIXIS INC.
Percent Similarity:     40.25%        Conservative:  28
Best Local Similarity:  28.63%        Mismatches:    122
Query Match:            12.24%        Indels:        22
RESULT 1423
ID   ADR41293 standard; cDNA; 1153 BP.
DE   Human CD-like molecule HATCZ07 cDNA, SEQ ID NO:92.
PN   WO200226930-A2.
PD   04-APR-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity:     43.22%        Conservative:  54
Best Local Similarity:  26.18%        Mismatches:    135
Query Match:            12.21%        Indels:        45
RESULT 1424
ID   AAA80677 standard; cDNA; 1329 BP.
DE   Human secreted protein #11 nucleotide sequence SEQ ID #137.
PN   WO200029435-A1.
PD   25-MAY-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity:     43.22%        Conservative:  54
Best Local Similarity:  26.18%        Mismatches:    135
Query Match:            12.21%        Indels:        45
RESULT 1425
ID   ADA27145 standard; cDNA; 1329 BP.
DE   Human novel secreted protein from gene 11 cDNA #3.
PN   US2003055231-A1.
PD   20-MAR-2003.
PA   (NIJJ/) NI J.
PA   (YOUN/) YOUNG P E.
PA   (KENN/) KENNY J J.
PA   (OLSE/) OLSEN H S.
PA   (MOOR/) MOORE P A.
PA   (WEIY/) WEI Y.
PA   (GREE/) GREENE J M.
PA   (RUBE/) RUBEN S M.
PA   (LIUD/) LIU D.
PA   (CROC/) CROCKER P R.
Percent Similarity:     43.22%        Conservative:  54
Best Local Similarity:  26.18%        Mismatches:    135
Query Match:            12.21%        Indels:        45
RESULT 1426
ID   ADE86686 standard; cDNA; 1329 BP.
DE   Novel human secreted protein #11 associated cDNA #1.
PN   US2003129685-A1.
PD   10-JUL-2003.
PA   (NIJJ/) NI J.
PA   (YOUN/) YOUNG P E.
PA   (KENN/) KENNY J J.
PA   (OLSE/) OLSEN H S.
PA   (MOOR/) MOORE P A.
PA   (WEIY/) WEI Y.
PA   (GREE/) GREENE J M.
PA   (RUBE/) RUBEN S M.
Percent Similarity:     43.22%        Conservative:  54
Best Local Similarity:  26.18%        Mismatches:    135
Query Match:            12.21%        Indels:        45
RESULT 1427
ID   AAX80055 standard; cDNA; 1413 BP.
DE   Human PRO355 nucleotide sequence.
PN   WO9928462-A2.
PD   10-JUN-1999.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%        Conservative:  54
Best Local Similarity:  26.18%        Mismatches:    135
Query Match:            12.21%        Indels:        45
RESULT 1428
ID   AAA49563 standard; cDNA; 1413 BP.
DE   Human PRO355 cDNA.
PN   WO200032776-A2.
PD   08-JUN-2000.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%        Conservative:  54
Best Local Similarity:  26.18%        Mismatches:    135
Query Match:            12.21%        Indels:        45
RESULT 1429
ID   AAS45941 standard; cDNA; 1413 BP.
DE   Human DNA encoding PRO polypeptide sequence #17.
PN   WO200168848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%        Conservative:  54
Best Local Similarity:  26.18%        Mismatches:    135
Query Match:            12.21%        Indels:        45
RESULT 1430
ID   ACA89391 standard; cDNA; 1413 BP.
DE   cDNA encoding human PRO polypeptide #17.
PN   US2003036141-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%        Conservative:  54
Best Local Similarity:  26.18%        Mismatches:    135
Query Match:            12.21%        Indels:        45
RESULT 1431
ID   ACA73401 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003036146-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%        Conservative:  54
Best Local Similarity:  26.18%        Mismatches:    135
Query Match:            12.21%        Indels:        45
RESULT 1432
ID   ACA05716 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003036162-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%        Conservative:  54
Best Local Similarity:  26.18%        Mismatches:    135
Query Match:            12.21%        Indels:        45
RESULT 1433
ID   ACA66550 standard; cDNA; 1413 BP.
DE   cDNA encoding human PRO protein #17.
PN   US2003036137-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
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Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1434
ID   ACF20125 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003040063-A1.
PD   27-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1435
ID   ACF19511 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003040064-A1.
PD   27-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1436
ID   ACD21799 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003027267-A1.
PD   06-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1437
ID   ACF12964 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003036160-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1438
ID   ACD25067 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003044925-A1.
PD   06-MAR-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1439
ID   ACF00116 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003054474-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1440
ID   ABX96814 standard; cDNA; 1413 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO355.
PN   US2002173463-A1.
PD   21-NOV-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1441
ID   ACA72173 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003032114-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1442
ID   ACD04697 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003032101-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1443
ID   ACD18158 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003036124-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1444
ID   ACD08165 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003040054-A1.
PD   27-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1445
ID   ABX78468 standard; DNA; 1413 BP.
DE   DNA encoding Novel human secreted protein PRO355.
PN   US2002150976-A1.
PD   17-OCT-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1446
ID   ACA88599 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003036133-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1447
ID   ACA70041 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003036134-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1448
ID   ACD12263 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003022294-A1.
PD   30-JAN-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1449
ID   ACC74178 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003027275-A1.
PD   06-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1450
ID   ACD15806 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003027324-A1.
PD   06-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1451
ID   ACD25374 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003036118-A1.
```

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PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1452
ID   ACD17851 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003036123-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1453
ID   ACC88138 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003036148-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1454
ID   ACD21492 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003040060-A1.
PD   27-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1455
ID   ACD18559 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003044916-A1.
PD   06-MAR-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1456
ID   ABX77102 standard; cDNA; 1413 BP.
DE   cDNA encoding human PRO355 protein.
PN   US2002142958-A1.
PD   03-OCT-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1457
ID   ABX98169 standard; cDNA; 1413 BP.
DE   Human cDNA encoding a secreted/transmembrane protein, SEQ ID 33.
PN   US2003036156-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1458
ID   ACD13920 standard; cDNA; 1413 BP.
DE   Human PRO polynucleotide #17.
PN   US2003032117-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1459
ID   ACD09700 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003036128-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1460
ID   ACC88445 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003027266-A1.
PD   06-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1461
ID   ACD21185 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003054483-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1462
ID   ABX75557 standard; cDNA; 1413 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO355.
PN   US2003022298-A1.
PD   30-JAN-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1463
ID   ABX97760 standard; cDNA; 1413 BP.
DE   Human PRO polynucleotide #17.
PN   US2003032102-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1464
ID   ACA97236 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003036117-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1465
ID   ACA57699 standard; cDNA; 1413 BP.
DE   Human PRO355 cDNA.
PN   US2003036143-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1466
ID   ACD14227 standard; cDNA; 1413 BP.
DE   Human PRO polynucleotide #17.
PN   US2003032130-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1467
ID   ACC91010 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003032138-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1468
ID   ACC88752 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003036132-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1469
ID   ACD06949 standard; cDNA; 1413 BP.
```

```
DE   Human PRO polynucleotide #17.
PN   US2003008353-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1470
ID   ACA67400 standard; cDNA; 1413 BP.
DE   Human PRO polynucleotide #17.
PN   US2003017542-A1.
PD   23-JAN-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1471
ID   ACC81455 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003032137-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1472
ID   ACC89059 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003027269-A1.
PD   06-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1473
ID   ACC86415 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003027268-A1.
PD   06-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1474
ID   ACC89673 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003027274-A1.
PD   06-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1475
ID   ACC92852 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003032135-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1476
ID   ACA72480 standard; cDNA; 1413 BP.
DE   Human PRO polynucleotide #17.
PN   US2003022295-A1.
PD   30-JAN-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1477
ID   ACA88998 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003022297-A1.
PD   30-JAN-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1478
ID   ACA69734 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003032105-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1479
ID   ACA96877 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003032123-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1480
ID   ACA90873 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003032108-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1481
ID   ACA70655 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003032111-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1482
ID   ACA95165 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003032119-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1483
ID   ACC86108 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003027263-A1.
PD   06-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1484
ID   ACC89980 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003027271-A1.
PD   06-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1485
ID   ACD12588 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003036125-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1486
ID   ACF19818 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003040068-A1.
PD   27-FEB-2003.
Percent Similarity:     43.22%         Conservative:  54
Best Local Similarity:  26.18%         Mismatches:    135
Query Match:            12.21%         Indels:        45
RESULT 1487
```

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ID   ABX75933 standard; cDNA; 1413 BP.
DE   Human cDNA encoding secreted/transmembrane protein, PRO355.
PN   US2002132981-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1488
ID   ABX76762 standard; cDNA; 1413 BP.
DE   Human PRO polynucleotide #17.
PN   US2003027280-A1.
PD   06-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1489
ID   ACA73094 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003022300-A1.
PD   30-JAN-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1490
ID   ACA68637 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003036136-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1491
ID   ACA74481 standard; cDNA; 1413 BP.
DE   cDNA encoding human PRO polypeptide #17.
PN   US2003036138-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1492
ID   ACA70348 standard; cDNA; 1413 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #17.
PN   US2003032109-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1493
ID   ACD14534 standard; cDNA; 1413 BP.
DE   Human PRO polynucleotide #17.
PN   US2003040066-A1.
PD   27-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1494
ID   ABX89644 standard; cDNA; 1413 BP.
DE   cDNA encoding novel secreted and transmembrane protein PRO355.
PN   US2002168715-A1.
PD   14-NOV-2002.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1495
ID   ACA68206 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003032104-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1496
ID   ABX98671 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003036157-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1497
ID   ACC81148 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003032120-A1.
PD   13-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1498
ID   ACA95472 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003036155-A1.
PD   20-FEB-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1499
ID   ACD04390 standard; cDNA; 1413 BP.
DE   Novel human secreted and transmembrane protein PRO355 cDNA.
PN   US2003022296-A1.
PD   30-JAN-2003.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
RESULT 1500
ID   ACC87831 standard; cDNA; 1413 BP.
DE   Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN   US2003027281-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Percent Similarity:     43.22%          Conservative:  54
Best Local Similarity:  26.18%          Mismatches:    135
Query Match:            12.21%          Indels:        45
```

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                    GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:        June 16, 2005, 12:21:54 ; Search time 212 Seconds
                                          (without alignments)
                                          2655.091 Million cell updates/sec

Title:         US-10-017-084A-523
Perfect score: 1806
Sequence:      1 MKTIQPKMHNSISWAIFTGL..........RRAGCVWLLPLLVLHLLLKF 344

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext  0.5
               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched:      1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:      2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US10017084/runat_14062005_151230_18877/app_query.fasta_1.519
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=1500 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017084_@CGN_1_1_69_@runat_14062005_151230_18877 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :     Issued_Patents_NA:*
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               6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES
               %
Result         Query
  No.   Score  Match Length DB  ID                     Description
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    1    1806  100.0   1032  4  US-09-700-397-1          Sequence 1, Appli
    2    1806  100.0   1693  4  US-09-700-397-2          Sequence 2, Appli
    3    1642   90.9    939  4  US-09-700-397-5          Sequence 5, Appli
    4   931.5   51.6   1195  4  US-09-976-594-403        Sequence 403, App
    5   926.5   51.3   1014  2  US-08-414-657D-5         Sequence 5, Appli
    6   926.5   51.3   1014  3  US-09-135-080-7          Sequence 7, Appli
    7   926.5   51.3   1238  2  US-08-414-657D-3         Sequence 3, Appli
    8   926.5   51.3   1238  3  US-09-135-080-3          Sequence 3, Appli
    9   923.5   51.1    977  2  US-08-414-657D-1         Sequence 1, Appli
   10   923.5   51.1    977  3  US-09-135-080-1          Sequence 1, Appli
   11     908   50.3    924  2  US-08-414-657D-7         Sequence 7, Appli
   12     907   50.2    945  2  US-08-414-657D-8         Sequence 8, Appli
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   13     902   49.9    912  2  US-08-414-657D-6         Sequence 6, Appli
   14   886.5   49.1    861  2  US-08-414-657D-9         Sequence 9, Appli
   15   885.5   49.0    861  2  US-08-414-657D-10        Sequence 10, Appl
   16   796.5   44.1    756  2  US-08-414-657D-17        Sequence 17, Appl
   17   795.5   44.0    756  2  US-08-414-657D-18        Sequence 18, Appl
   18   742.5   41.1   1030  4  US-09-949-016-4587       Sequence 4587, Ap
   19     545   30.2    333  4  US-09-513-999C-23289     Sequence 23289, A
   20     344   19.0    352  4  US-09-513-999C-2775      Sequence 2775, Ap
   21     339   18.8 113538  4  US-09-949-016-16329      Sequence 16329, A
   22   302.5   16.7    913  4  US-09-774-528-410        Sequence 410, App
   23     276   15.3   2599  4  US-09-949-016-4676       Sequence 4676, Ap
   24     275   15.2   2633  4  US-09-023-655-950        Sequence 950, App
   25     274   15.2   5807  4  US-09-976-594-245        Sequence 245, App
   26   273.5   15.1   2118  4  US-09-270-767-11659      Sequence 11659, A
   27   263.5   14.6   6814  3  US-09-484-970B-66        Sequence 66, Appl
   28     256   14.2   1266  2  US-08-659-984A-2         Sequence 2, Appli
   29     256   14.2   1266  3  US-08-660-531-2          Sequence 2, Appli
   30     256   14.2   1335  2  US-08-659-984A-4         Sequence 4, Appli
   31     256   14.2   1335  3  US-08-660-531-4          Sequence 4, Appli
   32   249.5   13.8   4548  4  US-09-571-479C-5         Sequence 5, Appli
   33   246.5   13.6   3318  4  US-09-949-016-4450       Sequence 4450, Ap
   34   246.5   13.6   3360  1  US-08-408-093-5          Sequence 5, Appli
   35   246.5   13.6   3360  1  US-08-408-420A-5         Sequence 5, Appli
   36   246.5   13.6   3360  1  US-08-714-901-5          Sequence 5, Appli
   37   246.5   13.6   3360  3  US-08-040-741-5          Sequence 5, Appli
   38   241.5   13.4   4723  4  US-09-949-016-644        Sequence 644, App
   39     241   13.3   6599  4  US-09-799-451-350        Sequence 350, App
   40   237.5   13.2   4597  4  US-09-949-016-5173       Sequence 5173, Ap
   41     237   13.1    219  2  US-08-414-657D-11        Sequence 11, Appl
   42     237   13.1    219  2  US-08-414-657D-12        Sequence 12, Appl
   43   230.5   12.8   2869  1  US-08-374-834-2          Sequence 2, Appli
   44   230.5   12.8   2869  1  US-08-644-271-2          Sequence 2, Appli
   45   230.5   12.8   2869  3  US-09-077-955-2          Sequence 2, Appli
   46     230   12.7   2610  1  US-08-374-834-17         Sequence 17, Appl
   47     230   12.7   2610  1  US-08-644-271-28         Sequence 28, Appl
   48     230   12.7   2610  3  US-09-077-955-32         Sequence 32, Appl
   49   225.5   12.5   1581  5  PCT-US95-08493-14        Sequence 14, Appl
   50   225.5   12.5   2580  5  PCT-US95-08493-18        Sequence 18, Appl
   51   225.5   12.5   2604  5  PCT-US95-08493-20        Sequence 20, Appl
   52     225   12.5   2607  4  US-09-715-249-7          Sequence 7, Appli
   53   224.5   12.4   7647  4  US-09-566-921-75         Sequence 75, Appl
   54     224   12.4   3662  4  US-09-907-794A-289       Sequence 289, App
   55     224   12.4   3662  4  US-09-905-125A-289       Sequence 289, App
   56     224   12.4   3662  4  US-09-902-775A-289       Sequence 289, App
   57     224   12.4   3662  4  US-09-906-700-289        Sequence 289, App
   58     224   12.4   3662  4  US-09-903-603A-289       Sequence 289, App
   59     224   12.4   3662  4  US-09-904-920A-289       Sequence 289, App
   60     224   12.4   3662  4  US-09-909-064-289        Sequence 289, App
   61     224   12.4   3662  4  US-09-905-381A-289       Sequence 289, App
   62     224   12.4   3662  4  US-09-906-618-289        Sequence 289, App
   63     224   12.4   4053  4  US-09-907-794A-293       Sequence 293, App
   64     224   12.4   4053  4  US-09-905-125A-293       Sequence 293, App
   65     224   12.4   4053  4  US-09-902-775A-293       Sequence 293, App
   66     224   12.4   4053  4  US-09-906-700-293        Sequence 293, App
   67     224   12.4   4053  4  US-09-903-603A-293       Sequence 293, App
   68     224   12.4   4053  4  US-09-904-920A-293       Sequence 293, App
   69     224   12.4   4053  4  US-09-909-064-293        Sequence 293, App
   70     224   12.4   4053  4  US-09-905-381A-293       Sequence 293, App
   71     224   12.4   4053  4  US-09-906-618-293        Sequence 293, App
   72   220.5   12.2   1413  4  US-09-866-028-60         Sequence 60, Appl
   73   220.5   12.2   1413  4  US-09-944-457-60         Sequence 60, Appl
   74   220.5   12.2   1598  4  US-09-778-510-19         Sequence 19, Appl
   75   220.5   12.2   1935  4  US-09-778-510-21         Sequence 21, Appl
   76     219   12.1   4843  3  US-08-986-485-1          Sequence 1, Appli
   77   213.5   11.8   1685  4  US-09-907-794A-83        Sequence 83, Appl
   78   213.5   11.8   1685  4  US-09-905-125A-83        Sequence 83, Appl
   79   213.5   11.8   1685  4  US-09-902-775A-83        Sequence 83, Appl
   80   213.5   11.8   1685  4  US-09-906-700-83         Sequence 83, Appl
   81   213.5   11.8   1685  4  US-09-903-603A-83        Sequence 83, Appl
   82   213.5   11.8   1685  4  US-09-904-920A-83        Sequence 83, Appl
   83   213.5   11.8   1685  4  US-09-909-064-83         Sequence 83, Appl
   84   213.5   11.8   1685  4  US-09-905-381A-83        Sequence 83, Appl
   85   213.5   11.8   1685  4  US-09-906-618-83         Sequence 83, Appl
   86   213.5   11.8   1718  4  US-09-778-510-5          Sequence 5, Appli
   87     213   11.8    177  2  US-08-414-657D-13        Sequence 13, Appl
   88     212   11.7    177  2  US-08-414-657D-14        Sequence 14, Appl
   89   211.5   11.7   5506  4  US-09-976-594-530        Sequence 530, App
   90     211   11.7   1273  4  US-09-778-510-3          Sequence 3, Appli
c  91     210   11.6    577  4  US-09-270-767-1011       Sequence 1011, Ap
c  92     210   11.6    577  4  US-09-270-767-16293      Sequence 16293, A
   93     210   11.6   4078  4  US-09-016-434-1120       Sequence 1120, Ap
   94     210   11.6   5926  4  US-09-917-254-41         Sequence 41, Appl
   95     209   11.6   3093  4  US-09-949-016-4183       Sequence 4183, Ap
   96     209   11.6   3145  4  US-09-949-016-1149       Sequence 1149, Ap
   97   205.5   11.4   1542  4  US-09-205-258-123        Sequence 123, App
   98     205   11.4   1820  4  US-09-778-510-1          Sequence 1, Appli
   99   203.5   11.3   5824  4  US-09-620-312D-72        Sequence 72, Appl
  100     202   11.2   4059  4  US-09-799-451-560        Sequence 560, App
  101     201   11.1   3398  5  PCT-US95-08493-12        Sequence 12, Appl
  102     200   11.1   1967  3  US-09-383-586-22         Sequence 22, Appl
  103     200   11.1   1967  4  US-09-823-038A-22        Sequence 22, Appl
  104     199   11.0   4285  3  US-09-040-774-1          Sequence 1, Appli
  105     198   11.0   6718  4  US-09-949-016-4632       Sequence 4632, Ap
  106   197.5   10.9   4608  3  US-09-041-886-24         Sequence 24, Appl
  107   197.5   10.9   4608  5  PCT-US94-05277-1         Sequence 1, Appli
  108   196.5   10.9   5905  4  US-09-949-016-5625       Sequence 5625, Ap
  109   196.5   10.9   6218  4  US-09-949-016-706        Sequence 706, App
  110   196.5   10.9   6384  4  US-09-976-594-724        Sequence 724, App
c 111   196.5   10.9   6384  4  US-09-919-039-279        Sequence 279, App
  112     194   10.7   3783  3  US-08-506-296B-20        Sequence 20, Appl
  113   192.5   10.7   2481  3  US-09-877-730-15         Sequence 15, Appl
  114   192.5   10.7   2715  3  US-09-877-730-5          Sequence 5, Appli
  115   192.5   10.7   2724  3  US-09-877-730-19         Sequence 19, Appl
  116   192.5   10.7   2958  3  US-09-877-730-9          Sequence 9, Appli
  117   192.5   10.7   2976  3  US-09-877-730-11         Sequence 11, Appl
  118   192.5   10.7   3192  3  US-09-412-554A-1         Sequence 1, Appli
  119   192.5   10.7   3210  3  US-09-877-730-1          Sequence 1, Appli
  120   192.5   10.7   3219  3  US-09-877-730-17         Sequence 17, Appl
  121   192.5   10.7   3453  3  US-09-877-730-7          Sequence 7, Appli
  122   192.5   10.7   3874  3  US-09-877-730-31         Sequence 31, Appl
  123   192.5   10.7   3943  3  US-08-506-296B-27        Sequence 27, Appl
  124     192   10.6   2094  4  US-09-270-767-13304      Sequence 13304, A
c 125     191   10.6    601  4  US-09-949-016-163724     Sequence 163724,
  126     190   10.5   6055  4  US-09-953-318-10         Sequence 10, Appl
  127   187.5   10.4   3991  3  US-08-506-296B-3         Sequence 3, Appli
  128     186   10.3   3551  4  US-09-620-312D-760       Sequence 760, App
  129   185.5   10.3    957  2  US-08-633-148-3          Sequence 3, Appli
  130   185.5   10.3   1023  2  US-08-633-148-1          Sequence 1, Appli
  131   185.5   10.3   1215  4  US-09-949-016-5154       Sequence 5154, Ap
  132   185.5   10.3   2031  1  US-08-217-299-2          Sequence 2, Appli
  133   185.5   10.3   2097  2  US-08-602-725-35         Sequence 35, Appl
  134   185.5   10.3   2220  1  US-08-389-459A-16        Sequence 16, Appl
  135   185.5   10.3   2220  3  US-08-987-867A-16        Sequence 16, Appl
  136   185.5   10.3   2349  2  US-08-184-009-145        Sequence 145, App
  137   185.5   10.3   2349  2  US-08-458-356-145        Sequence 145, App
  138   185.5   10.3   2349  3  US-08-460-736-145        Sequence 145, App
  139   185.5   10.3   2349  4  US-09-535-370-145        Sequence 145, App
  140   185.5   10.3   2349  4  US-09-663-667-145        Sequence 145, App
  141   185.5   10.3   2434  2  US-08-184-009-144        Sequence 144, App
  142   185.5   10.3   2434  2  US-08-458-356-144        Sequence 144, App
  143   185.5   10.3   2434  3  US-08-460-736-144        Sequence 144, App
  144   185.5   10.3   2434  4  US-09-535-370-144        Sequence 144, App
  145   185.5   10.3   2434  4  US-09-663-667-144        Sequence 144, App
  146   185.5   10.3   2974  4  US-09-949-016-613        Sequence 613, App
  147   185.5   10.3   2976  4  US-09-949-016-2297       Sequence 2297, Ap
  148   184.5   10.2    198  2  US-08-414-657D-15        Sequence 15, Appl
  149   184.5   10.2    198  2  US-08-414-657D-16        Sequence 16, Appl
  150   184.5   10.2   1391  4  US-09-638-649-4          Sequence 4, Appli
  151   184.5   10.2   1391  4  US-09-638-648-4          Sequence 4, Appli
  152     182   10.1   2346  4  US-09-949-016-1979       Sequence 1979, Ap
  153     182   10.1   2350  4  US-09-949-016-342        Sequence 342, App
  154   179.5    9.9   2839  3  US-08-468-856B-5         Sequence 5, Appli
  155   179.5    9.9   2839  3  US-08-468-859A-5         Sequence 5, Appli
c 156     174    9.6    785  4  US-09-270-767-1269       Sequence 1269, Ap
c 157     174    9.6    785  4  US-09-270-767-16551      Sequence 16551, A
  158   173.5    9.6   2550  1  US-08-245-295-10         Sequence 10, Appl

  159   173.5    9.6   2550  1  US-08-481-130-10         Sequence 10, Appl
  160   173.5    9.6   2550  1  US-08-656-984A-10        Sequence 10, Appl
  161   173.5    9.6   2550  1  US-08-485-604-10         Sequence 10, Appl
  162   173.5    9.6   2550  2  US-08-487-595-10         Sequence 10, Appl
  163   173.5    9.6   2988  1  US-08-245-295-1          Sequence 1, Appli
  164   173.5    9.6   2988  1  US-08-481-130-1          Sequence 1, Appli
  165   173.5    9.6   2988  1  US-08-656-984A-1         Sequence 1, Appli
  166   173.5    9.6   2988  1  US-08-485-604-1          Sequence 1, Appli
  167   173.5    9.6   2988  2  US-08-487-595-1          Sequence 1, Appli
  168     173    9.6   3189  2  US-08-427-497E-3         Sequence 3, Appli
  169     173    9.6   3774  2  US-08-341-843B-1         Sequence 1, Appli
  170     173    9.6   3774  2  US-08-427-497E-1         Sequence 1, Appli
  171     173    9.6   3774  2  US-08-427-497E-2         Sequence 2, Appli
  172     173    9.6   3888  3  US-08-506-296B-13        Sequence 13, Appl
  173     172    9.5   1630  3  US-08-468-856B-2         Sequence 2, Appli
  174     172    9.5   1630  3  US-08-468-859A-2         Sequence 2, Appli
  175     172    9.5   2116  4  US-09-023-655-1256       Sequence 1256, Ap
  176     172    9.5   3461  3  US-08-468-856B-6         Sequence 6, Appli
  177     172    9.5   3461  3  US-08-468-859A-6         Sequence 6, Appli
  178   171.5    9.5   2352  1  US-08-232-538-17         Sequence 17, Appl
  179   171.5    9.5   2352  2  US-08-786-164-17         Sequence 17, Appl
  180   171.5    9.5   4014  4  US-09-119-014D-5         Sequence 5, Appli
  181   171.5    9.5   7680  4  US-09-953-318-3          Sequence 3, Appli
  182     171    9.5   1473  2  US-08-602-725-31         Sequence 31, Appl
  183     171    9.5   1473  4  US-09-949-016-245        Sequence 245, App
  184     171    9.5   1475  4  US-09-949-016-1654       Sequence 1654, Ap
  185     170    9.4    862  3  US-08-468-856B-4         Sequence 4, Appli
  186     170    9.4    862  3  US-08-468-859A-4         Sequence 4, Appli
  187     169    9.4   1339  3  US-08-468-856B-3         Sequence 3, Appli
  188     169    9.4   1339  3  US-08-468-859A-3         Sequence 3, Appli
  189     168    9.3   2383  1  US-08-232-538-18         Sequence 18, Appl
  190     168    9.3   2383  2  US-08-786-164-18         Sequence 18, Appl
c 191   167.5    9.3    842  4  US-09-270-767-11483      Sequence 11483, A
  192     167    9.2   2264  1  US-08-232-538-16         Sequence 16, Appl
  193     167    9.2   2264  2  US-08-786-164-16         Sequence 16, Appl
  194     167    9.2   2292  3  US-09-142-956B-1         Sequence 1, Appli
  195     167    9.2   4071  3  US-09-098-707A-1         Sequence 1, Appli
  196     167    9.2   4071  3  US-09-483-539-1          Sequence 1, Appli
  197     167    9.2   4236  1  US-08-810-116-7          Sequence 7, Appli
  198     167    9.2   4236  2  US-07-930-548A-7         Sequence 7, Appli
  199     167    9.2   5830  4  US-09-967-655-3          Sequence 3, Appli
  200     167    9.2   5830  4  US-09-949-016-327        Sequence 327, App
  201     167    9.2   5831  4  US-09-949-016-3982       Sequence 3982, Ap
  202   166.5    9.2    909  3  US-09-877-730-13         Sequence 13, Appl
  203   166.5    9.2   1143  3  US-09-877-730-3          Sequence 3, Appli
  204   166.5    9.2   1405  4  US-08-755-235-3          Sequence 3, Appli
  205     166    9.2   2523  3  US-09-051-363-1          Sequence 1, Appli
  206   165.5    9.2   1960  4  US-09-653-961-3          Sequence 3, Appli
  207   165.5    9.2   1962  4  US-09-653-961-5          Sequence 5, Appli
  208   165.5    9.2   2487  1  US-08-261-304-1          Sequence 1, Appli
  209   165.5    9.2   2539  2  US-08-432-016-1          Sequence 1, Appli
  210   165.5    9.2   2539  2  US-08-684-594-1          Sequence 1, Appli
  211   165.5    9.2   2580  4  US-09-774-528-327        Sequence 327, App
  212   165.5    9.2   3306  4  US-09-023-655-1434       Sequence 1434, Ap
  213   165.5    9.2   3583  4  US-09-949-016-857        Sequence 857, App
  214   165.5    9.2   4854  4  US-09-784-358-15         Sequence 15, Appl
  215   165.5    9.2   5076  4  US-09-784-358-1          Sequence 1, Appli
  216   165.5    9.2   7718  4  US-09-976-594-244        Sequence 244, App
  217   165.5    9.2   8578  4  US-09-784-358-17         Sequence 17, Appl
  218     165    9.1   2166  2  US-08-408-095-30         Sequence 30, Appl
  219   164.5    9.1   2539  4  US-09-023-655-1496       Sequence 1496, Ap
  220   164.5    9.1   2565  1  US-08-597-495B-29        Sequence 29, Appl
  221   164.5    9.1   2565  3  US-09-068-051A-31        Sequence 31, Appl
  222   164.5    9.1   2793  3  US-09-336-536-68         Sequence 68, Appl
  223   164.5    9.1   2803  3  US-09-068-051A-33        Sequence 33, Appl
  224     164    9.1   1378  4  US-09-419-788-3          Sequence 3, Appli
  225     164    9.1   1742  3  US-09-383-586-23         Sequence 23, Appl
  226     164    9.1   1742  4  US-09-823-038A-23        Sequence 23, Appl
  227     164    9.1   1983  3  US-09-057-860A-8         Sequence 8, Appli
  228     164    9.1   2418  4  US-09-949-016-1694       Sequence 1694, Ap
  229   163.5    9.1   1950  4  US-09-653-961-1          Sequence 1, Appli
  230   163.5    9.1   2539  4  US-09-949-016-3677       Sequence 3677, Ap
  231   163.5    9.1   2697  4  US-09-949-016-5335       Sequence 5335, Ap
  232   163.5    9.1   4235  4  US-09-702-705-317          Sequence 317, App
  233   163.5    9.1   4235  4  US-09-736-457-317          Sequence 317, App
  234   163.5    9.1   4235  4  US-09-614-124B-317         Sequence 317, App
  235   163.5    9.1   4235  4  US-09-671-325-317          Sequence 317, App
  236   163.5    9.1   4235  4  US-09-589-184-317          Sequence 317, App
  237   163.5    9.1   4235  4  US-09-658-824-317          Sequence 317, App
  238   163.5    9.1   5720  4  US-09-800-729-18           Sequence 18, Appl
  239     163    9.0   2775  1  US-08-481-130-25           Sequence 25, Appl
  240     163    9.0   2775  1  US-08-656-984A-25          Sequence 25, Appl
  241     163    9.0   2775  1  US-08-485-604-25           Sequence 25, Appl
  242     163    9.0   2775  2  US-08-487-595-25           Sequence 25, Appl
  243     163    9.0   2927  1  US-08-481-130-27           Sequence 27, Appl
  244     163    9.0   2927  1  US-08-656-984A-27          Sequence 27, Appl
  245     163    9.0   2927  1  US-08-485-604-27           Sequence 27, Appl
  246     163    9.0   2927  2  US-08-487-595-27           Sequence 27, Appl
  247     162    9.0   1024  6  5169835-16                Patent No. 5169835
  248     162    9.0   1024  6  5169835-16                Patent No. 5169835
  249     162    9.0   3503  1  US-07-631-717A-1           Sequence 1, Appli
  250     162    9.0   3503  1  US-08-166-717D-1           Sequence 1, Appli
  251     161    8.9   1869  4  US-09-499-846-1            Sequence 1, Appli
  252     161    8.9   3554  4  US-09-907-794A-422         Sequence 422, App
  253     161    8.9   3554  4  US-09-905-125A-422         Sequence 422, App
  254     161    8.9   3554  4  US-09-902-775A-422         Sequence 422, App
  255     161    8.9   3554  4  US-09-906-700-422          Sequence 422, App
  256     161    8.9   3554  4  US-09-903-603A-422         Sequence 422, App
  257     161    8.9   3554  4  US-09-904-920A-422         Sequence 422, App
  258     161    8.9   3554  4  US-09-909-064-422          Sequence 422, App
  259     161    8.9   3554  4  US-09-905-381A-422         Sequence 422, App
  260     161    8.9   3554  4  US-09-906-618-422          Sequence 422, App
  261     161    8.9   5470  2  US-08-443-861-1            Sequence 1, Appli
  262     161    8.9   5470  3  US-08-193-829B-1           Sequence 1, Appli
  263     161    8.9   5470  4  US-09-967-655-10           Sequence 10, Appl
  264   160.5    8.9   3159  3  US-08-986-485-3            Sequence 3, Appli
  265   160.5    8.9   4111  4  US-09-375-248-1            Sequence 1, Appli
  266   160.5    8.9   4195  1  US-08-340-011-1            Sequence 1, Appli
  267   160.5    8.9   4195  3  US-08-901-710-1            Sequence 1, Appli
  268   160.5    8.9   4195  4  US-09-169-079-1            Sequence 1, Appli
  269   160.5    8.9   4416  3  US-08-795-430-1            Sequence 1, Appli
  270   160.5    8.9   4416  3  US-09-355-700-1            Sequence 1, Appli
  271   160.5    8.9   4416  3  US-08-601-132-36           Sequence 36, Appl
  272   160.5    8.9   4416  4  US-08-671-573B-36          Sequence 36, Appl
  273   160.5    8.9   4416  4  US-09-631-092B-36          Sequence 36, Appl
  274   160.5    8.9   4416  4  US-09-534-376A-1           Sequence 1, Appli
  275   160.5    8.9   4425  1  US-08-222-616-31           Sequence 31, Appl
  276   160.5    8.9   4425  3  US-08-446-648-31           Sequence 31, Appl
  277   160.5    8.9   4425  4  US-09-023-655-889          Sequence 889, App
  278   160.5    8.9   4425  4  US-09-982-610-31           Sequence 31, Appl
  279   160.5    8.9   4425  5  PCT-US95-04228-31          Sequence 31, Appl
  280   160.5    8.9   4795  1  US-08-340-011-3            Sequence 3, Appli
  281   160.5    8.9   4795  3  US-08-901-710-3            Sequence 3, Appli
  282   160.5    8.9   4795  4  US-09-169-079-3            Sequence 3, Appli
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  290     160    8.9   2469  5  US-07-997-133-2            Sequence 2, Appli
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  298     160    8.9   3944  4  US-09-949-016-1879         Sequence 1879, Ap
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c 303     159    8.8    462  4  US-09-270-767-2319         Sequence 2319, Ap
c 304     159    8.8    462  4  US-09-270-767-17601        Sequence 17601, A
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  312     157    8.7   1421  3  US-09-188-930-254          Sequence 254, App
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  314     157    8.7   1822  4  US-09-397-243D-1           Sequence 1, Appli
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  334   155.5    8.6   3785  3  US-08-447-314-9            Sequence 9, Appli
  335   155.5    8.6   3785  3  US-08-445-461-9            Sequence 9, Appli
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391     150   8.3  2676  1  US-08-471-570-7           Sequence 7, Appli
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396   148.5   8.2  6000  2  US-08-800-825A-6          Sequence 6, Appli
397   148.5   8.2  6000  3  US-09-158-657-6           Sequence 6, Appli
398   148.5   8.2  6000  5  PCT-US94-10166-6          Sequence 6, Appli
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406     144   8.0  3992  4  US-09-944-807-9           Sequence 9, Appli
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  554   138.5    7.7   1193  3  US-08-470-335-134          Sequence 134, App
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  556   138.5    7.7   1193  3  US-08-734-664A-134         Sequence 134, App
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  1277     107    5.9   1149  4  US-09-766-995-5             Sequence 5, Appli
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                              ALIGNMENTS

RESULT 1
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; Patent No. 6664383
; GENERAL INFORMATION:
;  APPLICANT:  Ono Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION:   No. 6664383el Polypeptides, cDNA encoding the same, and use of
;  FILE REFERENCE:   Q61459
;  CURRENT APPLICATION NUMBER: US/09/700,397
;  CURRENT FILING DATE:  2001-01-05
;  PRIOR APPLICATION NUMBER:    JP 10-131815
;  PRIOR FILING DATE:   1998-05-14
;  PRIOR APPLICATION NUMBER:   PCT/JP99/02485
;  PRIOR FILING DATE:   1999-05-13
;  NUMBER OF SEQ ID NOS:   19
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1032
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-700-397-1

Alignment Scores:
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Score:                    1806.00        Matches:       344
Percent Similarity:       100.00%        Conservative:  0
Best Local Similarity:    100.00%        Mismatches:    0
Query Match:              100.00%        Indels:        0
DB:                       4              Gaps:          0

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 420

Qy          141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480

Qy          161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 540

Qy          181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600

Qy          201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 660

Qy          221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 720

Qy          241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 780

Qy          261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 840

Qy          281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 900

Qy          301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 960

Qy          321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1020

Qy          341 LeuLeuLysPhe 344
                ||||||||||||
Db         1021 CTTCTCAAATTT 1032
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```
RESULT 2
US-09-700-397-2
; Sequence 2, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
;  APPLICANT:  Ono Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION:   No. 6664383el Polypeptides, cDNA encoding the same, and use of
;  FILE REFERENCE:   Q61459
;  CURRENT APPLICATION NUMBER: US/09/700,397
;  CURRENT FILING DATE:  2001-01-05
;  PRIOR APPLICATION NUMBER:   JP 10-131815
;  PRIOR FILING DATE:   1998-05-14
;  PRIOR APPLICATION NUMBER:   PCT/JP99/02485
;  PRIOR FILING DATE:   1999-05-13
;  NUMBER OF SEQ ID NOS:   19
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 1693
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Clone OC001 derived from human brain
;   NAME/KEY: CDS
;   LOCATION: (130)..(1161)
;   NAME/KEY: sig_peptide
;   LOCATION: (130)..(213)
;   NAME/KEY: mat_peptide
;   LOCATION: (214)..()
US-09-700-397-2

Alignment Scores:
Pred. No.:                3.35e-221       Length:          1693
Score:                    1806.00         Matches:         344
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       4               Gaps:            0

US-10-017-084A-523 (1-344) x US-09-700-397-2 (1-1693)

Qy            1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          130 ATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGGGCTG 189

Qy           21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          190 GCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 249

Qy           41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          250 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 309

Qy           61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          310 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGAC 369

Qy           81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          370 AAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATC 429

Qy          101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          430 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 489

Qy          121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          490 AACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAG 549

Qy          141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          550 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 609

Qy          161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          610 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTG 669

Qy          181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          670 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 729

Qy          201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAAC 789

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 TATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACA 849

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 CTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAA 909

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAAACTC 969

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAG 1029

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1089

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 AACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTG 1149

Qy        341 LeuLeuLysPhe 344
              ||||||||||||
Db       1150 CTTCTCAAATTT 1161

RESULT 3
US-09-700-397-5
; Sequence 5, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
;  APPLICANT:  Ono Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION:   No. 6664383el Polypeptides, cDNA encoding the same, and use of
;  FILE REFERENCE:   Q61459
;  CURRENT APPLICATION NUMBER: US/09/700,397
;  CURRENT FILING DATE:  2001-01-05
;  PRIOR APPLICATION NUMBER:   JP 10-131815
;  PRIOR FILING DATE:   1998-05-14
;  PRIOR APPLICATION NUMBER:   PCT/JP99/02485
;  PRIOR FILING DATE:   1999-05-13
;  NUMBER OF SEQ ID NOS:   19
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 939
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-700-397-5

Alignment Scores:
Pred. No.:                1.41e-200      Length:        939
Score:                    1642.00        Matches:       313
Percent Similarity:       100.00%        Conservative:  0
Best Local Similarity:    100.00%        Mismatches:    0
Query Match:              90.92%         Indels:        0
DB:                       4              Gaps:          0

US-10-017-084A-523 (1-344) x US-09-700-397-5 (1-939)

Qy         32 ArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGlyGlu 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAG 60

Qy         52 SerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArg 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGC 120

Qy         72 SerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeu 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTG 180

Qy         92 SerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGly 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGC 240

Qy        112 ProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeuIle 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATT 300

Qy        132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC 360

Qy        152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACAC 420

Qy        172 IleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIle 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATC 480

Qy        192 ThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTG 540

Qy        212 ValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThr 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACA 600

Qy        232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCA 660

Qy        252 GluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLysVal 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTG 720

Qy        272 GluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGly 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGG 780

Qy        292 AsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPhe 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTT 840

Qy        312 GlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrp 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGG 900

Qy        332 LeuLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
              |||||||||||||||||||||||||||||||||||||||
Db        901 CTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 939

RESULT 4
US-09-976-594-403
; Sequence 403, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 403
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
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;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 1640555CB1
US-09-976-594-403

Alignment Scores:
Pred. No.:              3.83e-109      Length:        1195
Score:                  931.50         Matches:       180
Percent Similarity:     73.85%         Conservative:  60
Best Local Similarity:  55.38%         Mismatches:    80
Query Match:            51.58%         Indels:        5
DB:                     4              Gaps:          4

US-10-017-084A-523 (1-344) x US-09-976-594-403 (1-1195)

Qy            20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
                 |||      |||||||||         |||:::||||||||||||   |||      |||
Db            49 CTGAGATTGCTCTGCCTTCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTT 102

Qy            39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                    :::      ||||||:::|||||||||||||||::::::|||   |||||||||
Db           103 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGACACAGCCATCCTCAGGTGCGTT 162

Qy            59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
                 ::::::::::::   ::::::|||||||||||||||||||||   |||::::::||||||
Db           163 CTAGAAGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGA 222

Qy            79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
                 :::|||||||||   |||||||||||||||   |||                  :::|||
Db           223 CATGACAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATAC 282

Qy            99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
                 |||:::   ||||||   |||||||||||||||||||||   ||||||||||||||||||
Db           283 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAG 342

Qy           119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
                 |||   :::   ||||||||||||:::|||:::|||||||||||||||   |||||||||
Db           343 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATC 402

Qy           139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
                       ||||||||||||:::::::::|||||||||:::|||::::::|||   |||:::
Db           403 TCCAATATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATG 462

Qy           159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
                 |||   |||||||||||||||   :::||||||||||||::::::|||
Db           463 GCCAATGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAA 522

Qy           179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
                 |||      |||:::|||||||||||||||   ||||||||||||||||||||||||
Db           523 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAA 582

Qy           199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
                 |||||||||   |||:::|||:::|||::::::      |||::::::||||||||||||
Db           583 TATGAGTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACT 642

Qy           219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
                 |||||||||||||||   |||:::|||:::|||                  |||::::::
Db           643 GTGAACTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAA 702

Qy           239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
                    :::|||:::|||||||||||||||||||||:::   :::|||:::||||||:::|||
Db           703 GCTTCACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 762

Qy           259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
                 |||   |||   |||            |||:::::::::::::::            |||
Db           763 GACACTAGG---ATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCT 819

Qy           279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                    |||         ||||||:::|||      ||||||||||||||||||||||||:::
Db           820 TCCCTGACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCC 879

Qy           299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
                 ||||||||||||   ||||||||||||::::::||||||   ||||||:::|||
Db           880 AACAAGCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAGGA 939
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Qy           319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
                 :::   ||||||:::         |||      :::|||||||||         :::|||
Db           940 ATA---AATGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCATCTCTGCTC 996

Qy           339 HisLeuLeuLeuLys 343
                    ||||||   |||
Db           997 TGCCTTCTCAGCAAA 1011

RESULT 5
US-08-414-657D-5
; Sequence 5, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1014 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1014
;      OTHER INFORMATION:
US-08-414-657D-5

Alignment Scores:
Pred. No.:              1.27e-108      Length:        1014
Score:                  926.50         Matches:       179
Percent Similarity:     73.54%         Conservative:  60
Best Local Similarity:  55.08%         Mismatches:    81
Query Match:            51.30%         Indels:        5
DB:                     2              Gaps:          4

US-10-017-084A-523 (1-344) x US-08-414-657D-5 (1-1014)

Qy            20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
                 |||      |||||||||         |||:::||||||||||||   |||      |||
Db            49 CTGAGACTGCTCTGCCTTCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTT 102
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Qy            39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                    :::      ||||||:::|||||||||||||||::::::|||   |||||||||
Db           103 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGACACGGCCATCCTCAGGTGTGTG 162

Qy            59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
                 ::::::::::::   ::::::|||||||||||||||||||||   |||::::::||||||
Db           163 GTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGA 222

Qy            79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
                 :::|||||||||   |||||||||||||||   |||                  :::|||
Db           223 CACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 282

Qy            99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
                 |||:::   ||||||   |||||||||||||||||||||   ||||||||||||||||||
Db           283 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAG 342

Qy           119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
                 |||   :::   |||||||||||||||:::|||:::||||||||||||   |||||||||
Db           343 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATC 402

Qy           139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
                       ||||||||||||:::::::::|||||||||:::|||::::::|||   |||:::
Db           403 TCCAACATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATG 462

Qy           159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
                 |||   |||||||||||||||   :::||||||||||||::::::|||
Db           463 GCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAA 522

Qy           179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
                 |||      |||:::|||||||||||||||   ||||||||||||||||||||||||
Db           523 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAA 582

Qy           199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
                 |||||||||   |||:::|||:::|||::::::      |||::::::||||||||||||
Db           583 TATGAGTGCAAGGCTGCCAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACT 642

Qy           219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
                 |||||||||||||||   |||:::|||:::|||                  |||::::::
Db           643 GTGAACTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAA 702

Qy           239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
                    :::|||:::|||||||||||||||||||||:::   :::|||:::||||||:::|||
Db           703 GCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 762

Qy           259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
                 |||   |||   |||               |||:::::::::::::::            |||
Db           763 GACACCAGG---ATAAACAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCC 819

Qy           279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                    |||         ||||||:::|||      ||||||||||||||||||||||||:::
Db           820 TCCCTGACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCC 879

Qy           299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
                 ||||||||||||   ||||||||||||::::::||||||   ||||||:::|||
Db           880 AACAAGCTCGGCGTCACCAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAGGA 939

Qy           319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
                 :::   ||||||:::         |||      :::|||||||||         :::
Db           940 ATC---AACGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTC 996

Qy           339 HisLeuLeuLeuLys 343
                    ||||||   |||
Db           997 TGCCTTCTCAGCAAA 1011

RESULT 6
US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1014 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1014
;      OTHER INFORMATION:
US-09-135-080-7

Alignment Scores:
Pred. No.:              1.27e-108      Length:         1014
Score:                  926.50         Matches:        179
Percent Similarity:     73.54%         Conservative:   60
Best Local Similarity:  55.08%         Mismatches:     81
Query Match:            51.30%         Indels:         5
DB:                     3              Gaps:           4

US-10-017-084A-523 (1-344) x US-09-135-080-7 (1-1014)

Qy            20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
                 |||      |||||||||         |||:::||||||||||||   |||      |||
Db            49 CTGAGACTGCTCTGCCTTCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTT 102

Qy            39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                    :::      ||||||:::|||||||||||||||::::::|||   |||||||||
Db           103 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGACACGGCCATCCTCAGGTGTGTG 162

Qy            59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
                 ::::::::::::   ::::::|||||||||||||||||||||   |||::::::||||||
Db           163 GTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGA 222

Qy            79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
                 :::|||||||||   |||||||||||||||   |||                  :::|||
Db           223 CACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 282

Qy            99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
                 |||:::   ||||||   |||||||||||||||||||||   ||||||||||||||||||
Db           283 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAG 342
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Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
              |||   :::   ||||||||||||:::|||:::|||||||||||||||   |||||||||
Db        343 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATC 402

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
                    ||||||||||||:::::::::|||||||||:::|||::::::|||   |||:::
Db        403 TCCAACATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATG 462

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
              |||   |||||||||||||||   :::||||||||||||::::::|||
Db        463 GCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAA 522

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
              |||      |||:::|||||||||||||||   ||||||||||||||||||||||||
Db        523 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAA 582

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
              |||||||||   |||:::|||:::|||::::::      |||::::::||||||||||||
Db        583 TATGAGTGCAAGGCTGCCAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACT 642

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
              |||||||||||||||   |||:::|||:::|||                  |||::::::
Db        643 GTGAACTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAA 702

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
                 :::|||:::|||||||||||||||||||||:::   :::|||:::||||||:::|||
Db        703 GCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 762

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
              |||   |||   |||            |||:::::::::::::::            |||
Db        763 GACACCAGG---ATAAACAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCC 819

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                 |||         ||||||:::|||      ||||||||||||||||||||||||:::
Db        820 TCCCTGACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCC 879

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
              ||||||||||||   ||||||||||||::::::||||||   ||||||:::|||
Db        880 AACAAGCTCGGCGTCACCAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAGGA 939

Qy        319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
              :::   ||||||:::         |||      :::|||||||||         :::
Db        940 ATC---AACGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTC 996

Qy        339 HisLeuLeuLeuLys 343
                 ||||||   |||
Db        997 TGCCTTCTCAGCAAA 1011

RESULT 7
US-08-414-657D-3
; Sequence 3, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1238 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  56...1069
;      OTHER INFORMATION:
US-08-414-657D-3

Alignment Scores:
Pred. No.:              1.78e-108      Length:         1238
Score:                  926.50         Matches:        179
Percent Similarity:     73.54%         Conservative:   60
Best Local Similarity:  55.08%         Mismatches:     81
Query Match:            51.30%         Indels:         5
DB:                     2              Gaps:           4

US-10-017-084A-523 (1-344) x US-08-414-657D-3 (1-1238)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
              |||      |||||||||         |||:::||||||||||||   |||      |||
Db        104 CTGAGACTGCTCTGCCTTCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTT 157

Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                 :::      ||||||:::|||||||||||||||::::::|||   |||||||||
Db        158 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTG 217

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
              ::::::::::::   ::::::|||||||||||||||||||||   |||::::::||||||
Db        218 GTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGA 277

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
              :::|||||||||   |||||||||||||||   |||                  :::|||
Db        278 CACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 337

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
              |||:::   ||||||   |||||||||||||||||||||   ||||||||||||||||||
Db        338 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAG 397

Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
              |||   :::   ||||||||||||:::|||:::|||||||||||||||   |||||||||
Db        398 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATC 457

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
                    ||||||||||||:::::::::|||||||||:::|||::::::|||   |||:::
Db        458 TCCAACATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATG 517

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
              |||   |||||||||||||||   :::||||||||||||::::::|||
Db        518 GCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAA 577

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
              |||      |||:::|||||||||||||||   ||||||||||||||||||||||||
Db        578 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAA 637

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
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              |||||||||   |||:::|||:::|||::::::      |||::::::||||||||||||
Db        638 TATGAGTGCAAGGCTGCCAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACT 697

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
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Db        698 GTGAACTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAA 757

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
                 :::|||:::|||||||||||||||||||||:::   :::|||:::||||||:::|||
Db        758 GCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 817

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
              |||   |||   |||            |||:::::::::::::::            |||
Db        818 GACACCAGG---ATAAACAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCC 874

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                 |||         ||||||:::|||      ||||||||||||||||||||||||:::
Db        875 TCCCTGACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCC 934

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
              ||||||||||||   ||||||||||||::::::||||||   ||||||:::|||
Db        935 AACAAGCTCGGCGTCACCAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAGGA 994

Qy        319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
              :::   ||||||:::         |||      :::|||||||||         :::
Db        995 ATC---AACGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTC 1051

Qy        339 HisLeuLeuLeuLys 343
                 ||||||   |||
Db       1052 TGCCTTCTCAGCAAA 1066

RESULT 8
US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1238 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  56...1069
;      OTHER INFORMATION:
US-09-135-080-3

Alignment Scores:
Pred. No.:                  1.78e-108      Length:        1238
Score:                      926.50         Matches:       179
Percent Similarity:         73.54%         Conservative:  60
Best Local Similarity:      55.08%         Mismatches:    81
Query Match:                51.30%         Indels:        5
DB:                         3              Gaps:          4

US-10-017-084A-523 (1-344) x US-09-135-080-3 (1-1238)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
              |||      |||||||||         |||:::||||||||||||   |||      |||
Db        104 CTGAGACTGCTCTGCCTTCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTT 157

Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                 :::      ||||||:::|||||||||||||||::::::|||   |||||||||
Db        158 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTG 217

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
              ::::::::::::   ::::::|||||||||||||||||||||   |||::::::||||||
Db        218 GTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGA 277

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
              :::|||||||||   |||||||||||||||   |||                  :::|||
Db        278 CACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 337

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
              |||:::   ||||||   |||||||||||||||||||||   ||||||||||||||||||
Db        338 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAG 397

Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
              |||   :::   ||||||||||||:::|||:::|||||||||||||||   |||||||||
Db        398 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATC 457

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
                    ||||||||||||:::::::::|||||||||:::|||::::::|||   |||:::
Db        458 TCCAACATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATG 517

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
              |||   |||||||||||||||   :::||||||||||||::::::|||
Db        518 GCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAA 577

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
              |||      |||:::|||||||||||||||   ||||||||||||||||||||||||
Db        578 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAA 637

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
              |||||||||   |||:::|||:::|||::::::      |||::::::||||||||||||
Db        638 TATGAGTGCAAGGCTGCCAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACT 697

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
              |||||||||||||||   |||:::|||:::|||                  |||::::::
Db        698 GTGAACTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAA 757

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
                 :::|||:::|||||||||||||||||||||:::   :::|||:::||||||:::|||
Db        758 GCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 817

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
              |||   |||   |||            |||:::::::::::::::            |||
Db        818 GACACCAGG---ATAAACAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCC 874

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                 |||         ||||||:::|||      ||||||||||||||||||||||||:::
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Db        875 TCCCTGACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCC 934

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
              ||||||||||||   ||||||||||||::::::||||||   ||||||:::|||
Db        935 AACAAGCTCGGCGTCACCAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAGGA 994

Qy        319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
              :::   ||||||:::         |||      :::|||||||||         :::
Db        995 ATC---AACGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCGTCCCTGTTC 1051

Qy        339 HisLeuLeuLeuLys 343
                 ||||||   |||
Db       1052 TGCCTTCTCAGCAAA 1066

RESULT 9
US-08-414-657D-1
; Sequence 1, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  2...976
;      OTHER INFORMATION:
US-08-414-657D-1

Alignment Scores:
Pred. No.:               2.89e-108      Length:        977
Score:                   923.50         Matches:       177
Percent Similarity:      74.06%         Conservative:  60
Best Local Similarity:   55.31%         Mismatches:    78
Query Match:             51.14%         Indels:        5
DB:                      2              Gaps:          4
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US-10-017-084A-523 (1-344) x US-08-414-657D-1 (1-977)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
              |||      |||||||||         |||:::||||||||||||   |||      |||
Db         29 CTGAGATTGCTCTGCCTTCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTT 82

Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                 :::      ||||||:::|||||||||||||||::::::|||   |||||||||
Db         83 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTT 142

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
              ::::::::::::   ::::::|||||||||||||||||||||   |||::::::||||||
Db        143 CTAGAAGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGA 202

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
              :::|||||||||   |||||||||||||||   |||                  :::|||
Db        203 CATGACAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATAC 262

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
              |||:::   ||||||   |||||||||||||||||||||   ||||||||||||||||||
Db        263 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAG 322

Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
              |||   :::   ||||||||||||:::|||:::|||||||||||||||   |||||||||
Db        323 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATC 382

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
                    ||||||||||||:::::::::|||||||||:::|||::::::|||   |||:::
Db        383 TCCAATATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATG 442

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
              |||   |||||||||||||||   :::||||||||||||::::::|||
Db        443 GCCAATGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAA 502

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
              |||      |||:::|||||||||||||||   ||||||||||||||||||||||||
Db        503 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAA 562

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
              |||||||||   |||:::|||:::|||::::::      |||::::::||||||||||||
Db        563 TATGAGTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACT 622

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
              |||||||||||||||   |||:::|||:::|||                  |||::::::
Db        623 GTGAACTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAA 682

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
                 :::|||:::|||||||||||||||||||||:::   :::|||:::||||||:::|||
Db        683 GCTTCACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 742

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
              |||   |||   |||            |||:::::::::::::::            |||
Db        743 GACACTAGG---ATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCT 799

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                 |||         ||||||:::|||      ||||||||||||||||||||||||:::
Db        800 TCCCTGACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCC 859

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
              ||||||||||||   ||||||||||||::::::||||||   ||||||:::|||
Db        860 AACAAGCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAGGA 919

Qy        319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
              :::   ||||||:::         |||      :::|||||||||         :::|||
Db        920 ATA---AATGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCATCTCTGCTC 976

RESULT 10
US-09-135-080-1
; Sequence 1, Application US/09135080
; Patent No. 6423827
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat R.
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/135,080
;      FILING DATE:  17-AUG-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/414,657
;      FILING DATE:  31-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-620-3214
;      TELEFAX:  609-620-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  2...976
;      OTHER INFORMATION:
US-09-135-080-1

Alignment Scores:
Pred. No.:              2.89e-108      Length:         977
Score:                  923.50         Matches:        177
Percent Similarity:     74.06%         Conservative:   60
Best Local Similarity:  55.31%         Mismatches:     78
Query Match:            51.14%         Indels:         5
DB:                     3              Gaps:           4

US-10-017-084A-523 (1-344) x US-09-135-080-1 (1-977)

Qy         20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
              |||      |||||||||         |||:::||||||||||||   |||      |||
Db         29 CTGAGATTGCTCTGCCTTCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTT 82

Qy         39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                 :::      ||||||:::|||||||||||||||::::::|||   |||||||||
Db         83 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTT 142

Qy         59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
              ::::::::::::   ::::::|||||||||||||||||||||   |||::::::||||||
Db        143 CTAGAAGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTTGCTGGA 202

Qy         79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
              :::|||||||||   |||||||||||||||   |||                  :::|||
Db        203 CATGACAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATAC 262

Qy         99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
              |||:::   ||||||   |||||||||||||||||||||   ||||||||||||||||||
Db        263 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAG 322
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Qy        119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
              |||   :::   ||||||||||||:::|||:::|||||||||||||||   |||||||||
Db        323 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATC 382

Qy        139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
                    ||||||||||||:::::::::|||||||||:::|||::::::|||   |||:::
Db        383 TCCAATATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATG 442

Qy        159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
              |||   |||||||||||||||   :::||||||||||||::::::|||
Db        443 GCCAATGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAA 502

Qy        179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
              |||      |||:::|||||||||||||||   ||||||||||||||||||||||||
Db        503 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAA 562

Qy        199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
              |||||||||   |||:::|||:::|||::::::      |||::::::||||||||||||
Db        563 TATGAGTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACT 622

Qy        219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
              |||||||||||||||   |||:::|||:::|||                  |||::::::
Db        623 GTGAACTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAA 682

Qy        239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
                 :::|||:::|||||||||||||||||||||:::   :::|||:::||||||:::|||
Db        683 GCTTCACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 742

Qy        259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
              |||   |||   |||            |||:::::::::::::::            |||
Db        743 GACACTAGG---ATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCT 799

Qy        279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                 |||         ||||||:::|||      ||||||||||||||||||||||||:::
Db        800 TCCCTGACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCC 859

Qy        299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
              ||||||||||||   ||||||||||||::::::||||||   ||||||:::|||
Db        860 AACAAGCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAGGA 919

Qy        319 ValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
              :::   ||||||:::         |||      :::|||||||||         :::|||
Db        920 ATA---AATGGATCCATCAGTCTGGCCGTACCACTGTGGCTGCTGGCAGCATCTCTGCTC 976

RESULT 11
US-08-414-657D-7
; Sequence 7, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  924 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...924
;      OTHER INFORMATION:
US-08-414-657D-7

Alignment Scores:
Pred. No.:              2.57e-106      Length:         924
Score:                  908.00         Matches:        170
Percent Similarity:     75.50%         Conservative:   58
Best Local Similarity:  56.29%         Mismatches:     70
Query Match:            50.28%         Indels:         4
DB:                     2              Gaps:           3

US-10-017-084A-523 (1-344) x US-08-414-657D-7 (1-924)

Qy            20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
                 |||      |||||||||         |||:::||||||||||||   |||      |||
Db            28 CTGAGATTGCTCTGCCTTCTTCCCACAGGACTGCCTGTTCGCAGCGTGGAT------TTT 81

Qy            39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                    :::      ||||||:::|||||||||||||||::::::|||   |||||||||
Db            82 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACAGCCATCCTCAGGTGCGTT 141

Qy            59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
                 ::::::::::::   ::::::|||||||||||||||||||||   |||::::::||||||
Db           142 CTAGAAGACAAGAACTCAAAGGTGGCCTGGTTGAACCGTTCTGGCATCATTTTGCTGGA 201

Qy            79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
                 :::|||||||||   |||||||||||||||   |||                  :::|||
Db           202 CATGACAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATAC 261

Qy            99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
                 |||:::   ||||||   |||||||||||||||||||||   ||||||||||||||||||
Db           262 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAGGGTTCCTACACTTGCTCAGTTCAG 321

Qy           119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
                 |||   :::   ||||||||||||:::|||:::|||||||||||||||   |||||||||
Db           322 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGATCGTACAAGTCCCACCAAAGATC 381

Qy           139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
                       ||||||||||||:::::::::|||||||||:::|||::::::|||   |||:::
Db           382 TCCAATATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAACGTGACTCTGGTCTGCATG 441

Qy           159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
                 |||   |||||||||||||||   :::||||||||||||::::::|||
Db           442 GCCAATGGCCGTCCTGAACCTGTTATCACCTGGAGACACCTTACACCAACTGGAAGGGAA 501

Qy           179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
                 |||      |||:::|||||||||||||||   ||||||||||||||||||||||||
Db           502 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTTGGCATCACCAGGGAGCAGTCAGGCAAA 561

Qy           199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
                 |||||||||   |||:::|||:::|||::::::      |||::::::||||||||||||
Db           562 TATGAGTGCAAAGCTGCCAACGAGGTCTCCTCGGCGGATGTCAAACAAGTCAAGGTCACT 621

Qy           219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
                 |||||||||||||||   |||:::|||:::|||                  |||::::::
Db           622 GTGAACTATCCTCCCACTATCACAGAATCCAAGAGCAATGAAGCCACCACAGGACGACAA 681

Qy           239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
                    :::|||:::|||||||||||||||||||||:::   :::|||:::||||||:::|||
Db           682 GCTTCACTCAAATGTGAGGCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 741

Qy           259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
                 |||   |||   |||            |||:::::::::::::::            |||
Db           742 GACACTAGG---ATAAATAGTGCCAATGGCCTTGAGATTAAGAGCACGGAGGGCCAGTCT 798

Qy           279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                    |||         ||||||:::|||      ||||||||||||||||||||||||:::
Db           799 TCCCTGACGGTGACCAACGTCACTGAGGAGCACTACGGCAACTACACCTGTGTGGCTGCC 858

Qy           299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
                 ||||||||||||   ||||||||||||::::::||||||   ||||||:::|||
Db           859 AACAAGCTGGGGGTCACCAATGCCAGCCTAGTCCTTTTCAGACCTGGGTCGGTGAGAGGA 918

Qy           319 ValSer 320
                 ::::::
Db           919 ATAAAT 924

RESULT 12
US-08-414-657D-8
; Sequence 8, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  945 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...945
;      OTHER INFORMATION:
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US-08-414-657D-8

Alignment Scores:
Pred. No.:              3.59e-106      Length:        945
Score:                  907.00         Matches:       170
Percent Similarity:     75.50%         Conservative:  58
Best Local Similarity:  56.29%         Mismatches:    70
Query Match:            50.22%         Indels:        4
DB:                     2              Gaps:          3

US-10-017-084A-523 (1-344) x US-08-414-657D-8 (1-945)

Qy           20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
                |||      |||||||||         |||:::||||||||||||   |||      |||
Db           49 CTGAGACTGCTCTGCCTTCTTCCCACAGGACTGCCCGTTCGCAGCGTGGAT------TTT 102

Qy           39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
                   :::      ||||||:::|||||||||||||||::::::|||   |||||||||
Db          103 AACCGAGGCACGGACAACATCACCGTGAGGCAGGGGGACACGGCCATCCTCAGGTGTGTG 162

Qy           59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
                ::::::::::::   ::::::|||||||||||||||||||||   |||::::::||||||
Db          163 GTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGA 222

Qy           79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
                :::|||||||||   |||||||||||||||   |||                  :::|||
Db          223 CACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 282

Qy           99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
                |||:::   ||||||   |||||||||||||||||||||   ||||||||||||||||||
Db          283 AGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAAGGATCCTACACATGCTCAGTTCAG 342

Qy          119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
                |||   :::   ||||||||||||:::|||:::|||||||||||||||   |||||||||
Db          343 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGATTGTACAAGTTCCACCAAAGATC 402

Qy          139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
                      ||||||||||||:::::::::|||||||||:::|||::::::|||   |||:::
Db          403 TCCAACATCTCCTCGGATGTCACTGTGAATGAGGGCAGCAATGTAACCCTGGTCTGCATG 462

Qy          159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
                |||   |||||||||||||||   :::||||||||||||::::::|||
Db          463 GCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACTTGGAAGAGAA 522

Qy          179 PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
                |||      |||:::|||||||||||||||   ||||||||||||||||||||||||
Db          523 TTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGCATCACCAGGGAACAGTCAGGCAAA 582

Qy          199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
                |||||||||   |||:::|||:::|||::::::      |||::::::||||||||||||
Db          583 TATGAGTGCAAGGCTGCCAACGAGGTCTCCTCCGCGGATGTCAAACAAGTCAAGGTCACT 642

Qy          219 ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
                |||||||||||||||   |||:::|||:::|||                  |||::::::
Db          643 GTGAACTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACCACAGGACGACAA 702

Qy          239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
                   :::|||:::|||||||||||||||||||||:::   :::|||:::||||||:::|||
Db          703 GCTTCCCTCAAATGTGAAGCCTCAGCGGTGCCTGCACCTGACTTTGAGTGGTACCGGGAT 762

Qy          259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
                |||   |||   |||            |||:::::::::::::::            |||
Db          763 GACACCAGG---ATAAACAGTGCAAACGGCCTTGAGATTAAGAGCACTGAGGGCCAGTCC 819

Qy          279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
                   |||         ||||||:::|||      ||||||||||||||||||||||||:::
Db          820 TCCCTGACGGTGACCAACGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCC 879

Qy          299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
                ||||||||||||   ||||||||||||::::::||||||   ||||||:::|||
Db          880 AACAAGCTCGGCGTCACCAATGCCAGCCTAGTCCTTTTCAGACCCGGGTCGGTGAGAGGA 939

Qy          319 ValSer 320
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                ::::::
Db          940 ATCAAC 945

RESULT 13
US-08-414-657D-6
; Sequence 6, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  912 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...912
;      OTHER INFORMATION:
US-08-414-657D-6

Alignment Scores:
Pred. No.:              1.48e-105      Length:        912
Score:                  902.00         Matches:       171
Percent Similarity:     74.68%         Conservative:  59
Best Local Similarity:  55.52%         Mismatches:    74
Query Match:            49.94%         Indels:        4
DB:                     2              Gaps:          3

US-10-017-084A-523 (1-344) x US-08-414-657D-6 (1-912)

Qy           31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
                |||||||||   |||      |||   :::      ||||||:::|||||||||||||||
Db            1 GTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAACATCACCGTGAGGCAGGGG 54

Qy           51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
                ::::::|||   |||||||||   ::::::::::::   ::::::|||||||||||||||
Db           55 GACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTCAAAGGTGGCCTGGTTGAAC 114

Qy           71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
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                ||||||   |||::::::||||||:::|||||||||   |||||||||||||||   |||
Db         115 CGTTCTGGCATCATTTTGCTGGACATGACAAGTGGTCTCTGGACCCACGGGTTGAGCTG 174

Qy          91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
                                  :::||||||:::   ||||||   ||||||||||||||||||
Db         175 GAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAG 234

Qy         111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
                |||   |||||||||||||||||||||   :::   ||||||||||||:::|||:::|||
Db         235 GGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTG 294

Qy         131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
                ||||||||||||   |||||||||      ||||||||||||:::::::::|||||||||
Db         295 ATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGATGTCACTGTGAATGAGGGC 354

Qy         151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
                :::|||::::::|||   |||:::|||   |||||||||||||||   :::|||||||||
Db         355 AGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGAACCTGTTATCACCTGGAGA 414

Qy         171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
                |||::::::|||            |||      |||:::|||||||||||||||   |||
Db         415 CACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGAATATCTGGAGATCCTTGGC 474

Qy         191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
                |||||||||||||||||||||   |||||||||   |||:::|||:::|||::::::
Db         475 ATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGCCAACGAGGTCTCCTCGGCG 534

Qy         211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
                   |||::::::|||||||||||||||||||||||||||   |||:::|||:::|||
Db         535 GATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCACTATCACAGAATCCAAGAGC 594

Qy         231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
                               |||::::::   :::|||:::|||||||||||||||||||||:::
Db         595 AATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGAGGCCTCGGCAGTGCCTGCA 654

Qy         251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
                   :::|||:::||||||:::||||||   |||   |||            |||::::::
Db         655 CCTGACTTTGAGTGGTACCGGGATGACACTAGG---ATAAATAGTGCCAATGGCCTTGAG 711

Qy         271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
                :::::::::            |||   |||         ||||||:::|||      |||
Db         712 ATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAACGTCACTGAGGAGCACTAC 771

Qy         291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
                |||||||||||||||||||||:::||||||||||||   ||||||||||||::::::|||
Db         772 GGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCACCAATGCCAGCCTAGTCCTT 831

Qy         311 PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVal 330
                |||   ||||||:::|||      :::   ||||||:::         |||      :::
Db         832 TTCAGACCTGGGTCGGTGAGAGGAATA---AATGGATCCATCAGTCTGGCCGTACCACTG 888

Qy         331 TrpLeuLeuProLeuLeuValLeu 338
                |||||||||         :::|||
Db         889 TGGCTGCTGGCAGCATCTCTGCTC 912

RESULT 14
US-08-414-657D-9
; Sequence 9, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  861 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...861
;      OTHER INFORMATION:
US-08-414-657D-9

Alignment Scores:
Pred. No.:              1.31e-103     Length:        861
Score:                  886.50        Matches:       164
Percent Similarity:     76.21%        Conservative:  57
Best Local Similarity:  56.55%        Mismatches:    66
Query Match:            49.09%        Indels:        3
DB:                     2             Gaps:          2

US-10-017-084A-523 (1-344) x US-08-414-657D-9 (1-861)

Qy          31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
                |||||||||   |||      |||   :::      ||||||:::|||||||||||||||
Db           1 GTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAACATCACCGTGAGGCAGGGG 54

Qy          51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
                ::::::|||   |||||||||   ::::::::::::   ::::::|||||||||||||||
Db          55 GACACAGCCATCCTCAGGTGCGTTCTAGAAGACAAGAACTCAAAGGTGGCCTGGTTGAAC 114

Qy          71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
                ||||||   |||::::::||||||:::|||||||||   |||||||||||||||   |||
Db         115 CGTTCTGGCATCATTTTGCTGGACATGACAAGTGGTCTCTGGACCCACGGGTTGAGCTG 174

Qy          91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
                                  :::||||||:::   ||||||   ||||||||||||||||||
Db         175 GAGAAACGCCATTCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAG 234

Qy         111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
                |||   |||||||||||||||||||||   :::   ||||||||||||:::|||:::|||
Db         235 GGTTCCTACACTTGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTG 294

Qy         131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
                ||||||||||||   |||||||||      ||||||||||||:::::::::|||||||||
Db         295 ATCGTACAAGTCCCACCAAAGATCTCCAATATCTCCTCGGATGTCACTGTGAATGAGGGC 354

Qy         151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
                :::|||::::::|||   |||:::|||   |||||||||||||||   :::|||||||||
Db         355 AGCAACGTGACTCTGGTCTGCATGGCCAATGGCCGTCCTGAACCTGTTATCACCTGGAGA 414

Qy         171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
                |||::::::|||            |||      |||:::|||||||||||||||   |||
Db       415 CACCTTACACCAACTGGAAGGGAATTTGAAGGAGAAGAAGAATATCTGGAGATCCTTGGC 474

Qy       191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
             |||||||||||||||||||||   |||||||||   |||:::|||:::|||::::::   
Db       475 ATCACCAGGGAGCAGTCAGGCAAATATGAGTGCAAAGCTGCCAACGAGGTCTCCTCGGCG 534

Qy       211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
                |||::::::|||||||||||||||||||||||||||   |||:::|||:::|||   
Db       535 GATGTCAAACAAGTCAAGGTCACTGTGAACTATCCTCCCACTATCACAGAATCCAAGAGC 594

Qy       231 ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer 250
                            ||||||::::::   :::|||:::|||||||||||||||||||||:::
Db       595 AATGAAGCCACCACAGGACGACAAGCTTCACTCAAATGTGAGGCCTCGGCAGTGCCTGCA 654

Qy       251 AlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLys 270
                :::|||:::||||||:::||||||   |||   |||            |||::::::
Db       655 CCTGACTTTGAGTGGTACCGGGATGACACTAGG---ATAAATAGTGCCAATGGCCTTGAG 711

Qy       271 ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr 290
             :::::::::            |||   |||         ||||||:::|||      |||
Db       712 ATTAAGAGCACGGAGGGCCAGTCTTCCCTGACGGTGACCAACGTCACTGAGGAGCACTAC 771

Qy       291 GlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu 310
             |||||||||||||||||||||:::||||||||||||   ||||||||||||::::::|||
Db       772 GGCAACTACACCTGTGTGGCTGCCAACAAGCTGGGGGTCACCAATGCCAGCCTAGTCCTT 831

Qy       311 PheGlyProGlyAlaValSerGluValSer 320
             |||   ||||||:::|||      ::::::
Db       832 TTCAGACCTGGGTCGGTGAGAGGAATAAAT 861

RESULT 15
US-08-414-657D-10
; Sequence 10, Application US/08414657D
; Patent No. 5861283
;  GENERAL INFORMATION:
;    APPLICANT:  Levitt, Pat
;    APPLICANT:  Pimenta, Aurea
;    APPLICANT:  Fischer, Itzhak
;    APPLICANT:  Zhukareva, Victoria
;    TITLE OF INVENTION:  Limbic System-Associated Membrane
;    TITLE OF INVENTION:  Protein and DNA
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dechert Price & Rhoads
;      STREET:  997 Lenox Drive, Building 3, Suite 210
;      CITY:  Lawrenceville
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08543
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,657D
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bloom, Allen
;      REGISTRATION NUMBER:  29,135
;      REFERENCE/DOCKET NUMBER:  317743-102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-520-3214
;      TELEFAX:  609-520-3259
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  861 base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...861
;      OTHER INFORMATION:
US-08-414-657D-10

Alignment Scores:
Pred. No.:              1.77e-103      Length:        861
Score:                  885.50         Matches:       164
Percent Similarity:     76.21%         Conservative:  57
Best Local Similarity:  56.55%         Mismatches:    66
Query Match:            49.03%         Indels:        3
DB:                     2              Gaps:          2

US-10-017-084A-523 (1-344) x US-08-414-657D-10 (1-861)

Qy        31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
             |||||||||   |||      |||   :::      ||||||:::|||||||||||||||
Db         1 GTTCGCAGCGTGGAT------TTTAACCGAGGCACGGACAACATCACCGTGAGGCAGGGG 54

Qy        51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
             ::::::|||   |||||||||   ::::::::::::   ::::::|||||||||||||||
Db        55 GACACGGCCATCCTCAGGTGTGTGGTAGAAGACAAGAACTCGAAAGTGGCCTGGTTGAAC 114

Qy        71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
             ||||||   |||::::::||||||:::|||||||||   |||||||||||||||   |||
Db       115 CGCTCTGGCATCATCTTCGCTGGACACGACAAGTGGTCTCTGGACCCTCGGGTTGAGCTG 174

Qy        91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
                               :::||||||:::   ||||||   ||||||||||||||||||
Db       175 GAGAAACGCCATGCTCTGGAATACAGCCTCCGAATCCAGAAGGTGGATGTCTATGATGAA 234

Qy       111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
             |||   |||||||||||||||||||||   :::   ||||||||||||:::|||:::|||
Db       235 GGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTG 294

Qy       131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
             ||||||||||||   |||||||||      ||||||||||||:::::::::|||||||||
Db       295 ATTGTACAAGTTCCACCAAAGATCTCCAACATCTCCTCGGATGTCACTGTGAATGAGGGC 354

Qy       151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
             :::|||::::::|||   |||:::|||   |||||||||||||||   :::|||||||||
Db       355 AGCAATGTAACCCTGGTCTGCATGGCCAATGGGCGCCCTGAACCTGTTATCACCTGGAGA 414

Qy       171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
             |||::::::|||            |||      |||:::|||||||||||||||   |||
Db       415 CACCTTACACCACTTGGAAGAGAATTTGAAGGAGAAGAAGAATATCTGGAGATCCTAGGC 474

Qy       191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
             |||||||||||||||||||||   |||||||||   |||:::|||:::|||::::::   
Db       475 ATCACCAGGGAACAGTCAGGCAAATATGAGTGCAAGGCTGCCAACGAGGTCTCCTCCGCG 534

Qy       211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
                |||::::::|||||||||||||||||||||||||||   |||:::|||:::|||   
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Job time : 253 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on:         June 16, 2005, 06:58:07 ; Search time 2109 Seconds
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Searched:       6054689 seqs, 3103772919 residues

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 1127    231  12.8  14194  21  US-10-741-600-274         Sequence 274, App
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Job time : 2173 secs
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                    GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:         June 16, 2005, 10:29:07 ; Search time 3857 Seconds
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Searched:       34239544 seqs, 19032134700 residues

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Post-processing: Minimum Match 0%
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      Pred. No. is the number of results predicted by chance to have a
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                    %
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    3     1506     83.4    874  9  AY406347                     AY406347 Homo sapi
    4     1488     82.4    874  9  AY406349                     AY406349 Mus muscu
    5     1324     73.3    773  9  AY406348                     AY406348 Pan trogl
    6     1321     73.1   1450  7  CO635648                     CO635648 Contig266
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   76      705     39.0    934  7  CN015939                     CN015939 AGENCOURT
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    91    666  36.9   764  4  BI752729         BI752729 603028343
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   150    510  28.2   579  2  BB644523         BB644523 BB644523
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   157    498  27.6   914  5  BX843874         BX843874 BX843874
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   166    483  26.7   755  5  BX913106         BX913106 BX913106
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   168    480  26.6   795  1  AU080106         AU080106 AU080106
   169    478  26.5   566  7  CF977262         CF977262 2-84-B04.
   170    477  26.4   478  5  BY245406         BY245406 BY245406
   171    476  26.4   661  6  CA452139         CA452139 UI-M-FZ0-
   172  475.5  26.3   392  2  BE651010         BE651010 UI-M-BH3-
   173    475  26.3   646  6  CA334396         CA334396 NISC_ls08
   174  474.5  26.3   953  5  BU116264         BU116264 603139651
   175    473  26.2   284  7  CR543721         CR543721 DKFZp459H
   176  468.5  25.9   703  7  CF530869         CF530869 UI-M-GH0-
c  177  468.5  25.9   772  7  CK776016         CK776016 967158 MA
   178    468  25.9   936  5  BQ227365         BQ227365 AGENCOURT
   179  467.5  25.9   617  6  BY730405         BY730405 BY730405
   180    467  25.9   390  4  BM719375         BM719375 UI-E-EJ1-
   181    467  25.9   390  4  BM719757         BM719757 UI-E-EJ1-
   182    467  25.9   390  5  BM931279         BM931279 UI-E-EJ1-
c  183    467  25.9   394  4  BM684112         BM684112 UI-E-EJ1-
c  184    467  25.9   394  4  BM684852         BM684852 UI-E-EJ1-
c  185    467  25.9   394  5  BQ184395         BQ184395 UI-E-EJ1-
c  186    467  25.9   394  5  BQ184512         BQ184512 UI-E-EJ1-
c  187    467  25.9   394  7  CK300895         CK300895 UI-E-EJ1-
c  188    467  25.9   403  4  BM684212         BM684212 UI-E-EJ1-
   189    467  25.9   608  5  BQ188988         BQ188988 UI-E-EJ1-
   190    467  25.9   700  5  BQ189788         BQ189788 UI-E-EJ1-
   191    467  25.9   734  5  BQ187606         BQ187606 UI-E-EJ1-
   192  466.5  25.8   884  5  BU323269         BU323269 603405983
c  193  463.5  25.7   564  7  CO602836         CO602836 DG8-249i1
   194    463  25.6   666  5  BM951674         BM951674 UI-M-EG0-
   195    461  25.5   795  7  CO395735         CO395735 AGENCOURT
c  196    460  25.5   572  2  BF407747         BF407747 UI-R-BJ2-
   197    459  25.4   282  7  R75391           R75391 MDB0556R Mo
   198    459  25.4   858  2  BF676478         BF676478 602086277
   199  457.5  25.3   718  6  CB460692         CB460692 720592 MA
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   201  453.5  25.1   651  6  BY726997         BY726997 BY726997
   202    448  24.8   257  2  AW327110         AW327110 20640 MAR
   203    448  24.8   909  5  BU132565         BU132565 603120307
c  204  445.5  24.7   637  6  CB528708         CB528708 UI-H-FT2-
   205    444  24.6   894  6  CB199088         CB199088 AGENCOURT
   206  443.5  24.6   791  7  CK308721         CK308721 SB02047A2
   207  441.5  24.4   497  7  CV036959         CV036959 4134532 B
   208    441  24.4   801  5  BU357013         BU357013 603475462
   209  440.5  24.4   700  7  CN458398         CN458398 UI-M-HN0-
   210    440  24.4   445  5  BY269882         BY269882 BY269882
   211  433.5  24.0   584  5  BP257486         BP257486 BP257486
   212  432.5  23.9   892  5  BP462753         BP462753 BP462753
   213    432  23.9   457  5  BY249728         BY249728 BY249728
c  214  427.5  23.7   580  7  CN089827         CN089827 EC2BBA32B
c  215    426  23.6   541  5  BU735309         BU735309 UI-E-DW0-
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   217    423  23.4   481  5  BY256150         BY256150 BY256150
   218  416.5  23.1   496  7  CK693129         CK693129 ZF101-P00
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   220  411.5  22.8   617  4  BJ622933         BJ622933 BJ622933
   221  407.5  22.6   778  7  CK315507         CK315507 SB02026A1
   222  407.5  22.6   788  4  BI767217         BI767217 603057906
   223    402  22.3   277  4  BI011319         BI011319 QV2-EN009
   224  401.5  22.2   600  6  CA526928         CA526928 8023-83 M
   225  396.5  22.0   862  5  BP462754         BP462754 BP462754
c  226    394  21.8   598  1  AI815935         AI815935 au43g02.x
   227  390.5  21.6   771  7  CN528825         CN528825 UI-M-HQ0-
c  228    390  21.6   465  1  AI934791         AI934791 wp89e04.x
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  229   389.5   21.6    878  5  BP165624                BP165624 BP165624
  230     389   21.5    450  5  BY263302                BY263302 BY263302
c 231     388   21.5    294  7  W15256                  W15256 zc16h07.s1
  232     388   21.5    357  5  BY303236                BY303236 BY303236
  233     385   21.3    673  7  CR736885                CR736885 CR736885
  234   384.5   21.3    444  1  AA682970                AA682970 ae89a04.s
  235   380.5   21.1    775  4  BI199955                BI199955 602761121
  236   379.5   21.0    660  5  BW337636                BW337636 BW337636
  237   377.5   20.9    853  5  BP164129                BP164129 BP164129
  238   376.5   20.8    535  9  AY409768                AY409768 Pan trogl
c 239     376   20.8    470  1  AI580850                AI580850 ta33e06.x
  240   373.5   20.7    478  6  CA885050                CA885050 B0115E08-
c 241     372   20.6    511  1  AI415689                AI415689 mc70a03.x
c 242   371.5   20.6    723  9  AG035406                AG035406 Pan trogl
  243     370   20.5    863  6  CA475514                CA475514 AGENCOURT
  244   365.5   20.2    809  2  BF304194                BF304194 601887043
  245     364   20.2    268  1  AA296886                AA296886 EST112650
  246   363.5   20.1    801  5  BX852740                BX852740 BX852740
c 247     363   20.1    519  1  AA826266                AA826266 od03e04.s
  248     362   20.0    229  1  AA450172                AA450172 zx42d09.r
  249     358   19.8    855  5  BP158085                BP158085 BP158085
  250   357.5   19.8    483  7  CR536826                CR536826 DKFZp459J
c 251   355.5   19.7    368  2  BF350775                BF350775 QV0-HT036
  252     355   19.7    348  7  R55964                  R55964 yg89e11.r1
  253     355   19.7    431  5  BY276402                BY276402 BY276402
  254     353   19.5    711  5  BU363662                BU363662 603790080
  255   352.5   19.5    729  2  BB585976                BB585976 BB585976
  256     351   19.4    429  5  BY272572                BY272572 BY272572
  257     350   19.4    504  5  BX281785                BX281785 BX281785
  258   348.5   19.3    868  5  BQ672092                BQ672092 AGENCOURT
  259   342.5   19.0    960  5  BQ933325                BQ933325 AGENCOURT
c 260     341   18.9    525  1  AL919221                AL919221 AL919221
  261   339.5   18.8    825  5  BP464677                BP464677 BP464677
  262   338.5   18.7    514  4  BG814603                BG814603 daf69d01.
  263   338.5   18.7    807  5  BP168056                BP168056 BP168056
  264   331.5   18.4    801  7  CK303983                CK303983 SB02022A1
  265     331   18.3    594  5  BU400899                BU400899 603481850
  266     330   18.3    410  5  BY276506                BY276506 BY276506
  267     329   18.2    651  6  CB557691                CB557691 AMGNNUC:N
c 268   327.5   18.1    458  7  CO667956                CO667956 DG33-31f8
  269   323.5   17.9    562  5  BU381982                BU381982 603582664
  270   320.5   17.7    470  5  BX954423                BX954423 DKFZp781K
  271   320.5   17.7    613  7  CF892168                CF892168 A0106B07-
  272     320   17.7    579  7  CN089828                CN089828 EC2BBA32B
c 273   318.5   17.6    446  7  CO352257                CO352257 DR_AOV_SU
c 274     315   17.4    422  1  AI288864                AI288864 qn24f12.x
c 275     314   17.4    845  4  BM042630                BM042630 603615963
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c 282   310.5   17.2    789  7  CR531801                CR531801 CR531801
c 283     310   17.2    359  2  BE156390                BE156390 QV0-HT036
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  287   307.5   17.0    705  7  CN108877                CN108877 EC2CAA32D
  288     307   17.0    178  6  CB118055                CB118055 K-EST0164
  289   306.5   17.0    730  5  BX610460                BX610460 BX610460
c 290   306.5   17.0    770  7  CR526028                CR526028 CR526028
c 291     304   16.8    528  2  AW490008                AW490008 UI-M-BH3-
  292   303.5   16.8    790  5  BP141505                BP141505 BP141505
  293   302.5   16.7    394  9  AY400233                AY400233 Homo sapi
  294   302.5   16.7    394  9  AY400234                AY400234 Pan trogl
  295   300.5   16.6    481  5  BY247646                BY247646 BY247646
  296     300   16.6    377  7  CF977263                CF977263 2-98-A10.
  297     300   16.6    646  5  BW346790                BW346790 BW346790
  298     298   16.5    372  6  BY768835                BY768835 BY768835
  299     298   16.5    386  5  BY263646                BY263646 BY263646
c 300     297   16.4    708  7  CK661144                CK661144 LP20336.5
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  302   296.5   16.4    417  6  CA884109                CA884109 B0107H12-
  303     295   16.3    994  6  CD325921                CD325921 AGENCOURT
c 304   294.5   16.3    451  1  AA933871                AA933871 o191d04.s
  305     293   16.2    220  7  H16176                  H16176 ym21g09.r1
  306     293   16.2    665  9  BX243020                BX243020 Danio rer
  307     293   16.2    761  6  CD755145                CD755145 AGENCOURT
  308   291.5   16.1    899  5  BU134624                BU134624 603119839
  309     291   16.1    402  5  BY289266                BY289266 BY289266
c 310   290.5   16.1    733  7  CO619752                CO619752 DG9-1d13
c 311     290   16.1    585  7  CO628980                CO628980 DG9-3m14
  312   289.5   16.0    726  5  BU395513                BU395513 603404749
  313   288.5   16.0    411  5  BY288341                BY288341 BY288341
  314     288   15.9    422  4  BI390270                BI390270 pgp1c.pk0
c 315     285   15.8    691  7  CK661190                CK661190 LP20417.5
c 316     285   15.8    693  7  CK657729                CK657729 LP24251.5
  317     283   15.7    386  6  CB806970                CB806970 AMGNNUC:N
  318     283   15.7    488  5  BX477962                BX477962 DKFZp686N
  319   282.5   15.6   2193  9  AY418859                AY418859 Mus muscu
  320   282.5   15.6   2709  3  AK082621                AK082621 Mus muscu
  321   282.5   15.6   2713  3  AK051197                AK051197 Mus muscu
  322   278.5   15.4    473  5  BY261511                BY261511 BY261511
  323     278   15.4   2190  9  AY418858                AY418858 Pan trogl
  324     276   15.3   2190  9  AY418857                AY418857 Homo sapi
  325     275   15.2    583  6  CA353359                CA353359 624860 NC
c 326   273.5   15.1    314  7  CN075611                CN075611 EC2BBA10C
c 327   271.5   15.0    316  1  AI884993                AI884993 wl88c02.x
c 328   269.5   14.9    452  1  AI262821                AI262821 qk35h10.x
  329   269.5   14.9    656  2  BB617916                BB617916 BB617916
c 330     268   14.8    402  2  AW522667                AW522667 UI-R-BO0-
  331     268   14.8   3089  3  BC062942                BC062942 Mus muscu
  332   267.5   14.8    392  5  BY267956                BY267956 BY267956
  333   265.5   14.7    421  5  BY275639                BY275639 BY275639
  334     263   14.6   2397  3  AK033973                AK033973 Mus muscu
  335     263   14.6   2509  3  AK046800                AK046800 Mus muscu
  336     263   14.6   3880  3  AK043760                AK043760 Mus muscu
  337     263   14.6   3892  3  AK038842                AK038842 Mus muscu
  338     260   14.4    412  5  BY274659                BY274659 BY274659
  339   257.5   14.3    401  5  BY266910                BY266910 BY266910
  340   257.5   14.3   3315  3  HSM805302               AL834270 Homo sapi
  341     257   14.2   1080  5  BM916998                BM916998 AGENCOURT
  342     256   14.2    336  5  BY134531                BY134531 BY134531
  343   254.5   14.1    763  1  AI427225                AI427225 mc70a03.y
  344     253   14.0    456  5  BY249027                BY249027 BY249027
  345     253   14.0    760  6  CD636199                CD636199 56030958J
  346     253   14.0    929  5  BX409828                BX409828 BX409828
  347   251.5   13.9    700  6  CD636207                CD636207 56031034J
  348   251.5   13.9    815  1  AU079716                AU079716 AU079716
c 349     251   13.9    332  2  BE826737                BE826737 QV1-EN004
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  355   248.5   13.8    783  6  CD636239                CD636239 56038369J
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  357   246.5   13.6   5626  3  CR749495                CR749495 Homo sapi
  358     246   13.6    385  5  BY275013                BY275013 BY275013
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  361     246   13.6   3198  9  AY416712                AY416712 Homo sapi
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  365   243.5   13.5    649  6  CD636211                CD636211 56031058J
  366   243.5   13.5    690  6  CD636247                CD636247 56038477J
  367   243.5   13.5   1946  3  BC028193                BC028193 Homo sapi
c 368   242.5   13.4    354  2  BE826697                BE826697 QV1-EN004
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  370   241.5   13.4    632  6  CD636203                CD636203 56030974J
c 371     241   13.3    733  9  BX190380                BX190380 Danio rer
  372   240.5   13.3    629  6  CD636245                CD636245 56038469J
  373   239.5   13.3    656  2  BB645027                BB645027 BB645027
  374   238.5   13.2    374  5  BY294857                BY294857 BY294857
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  378   237.5   13.2   3179  3  AK028527          AK028527 Mus muscu
  379   237.5   13.2   3948  3  AK036116          AK036116 Mus muscu
  380   236.5   13.1    646  4  BI393264          BI393264 pgp1n.pk0
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  383     235   13.0    711  7  CO669353          CO669353 DG33-50b1
c 384     233   12.9    582  7  CO626674          CO626674 DG9-278a2
  385     232   12.8    747  7  CF743366          CF743366 UI-M-GV0-
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  387   231.5   12.8   3057  9  AY417678          AY417678 Homo sapi
  388   231.5   12.8   4327  3  BC039255          BC039255 Homo sapi
  389     231   12.8   3392  3  BC036338          BC036338 Homo sapi
  390     231   12.8   3480  9  AY418997          AY418997 Mus muscu
  391     230   12.7    339  2  BE826667          BE826667 QV1-EN004
  392     230   12.7    872  5  BU411493          BU411493 602954338
  393   229.5   12.7    705  6  CD636208          CD636208 56031050H
c 394     229   12.7    782  8  AZ731274          AZ731274 RPCI-24-1
  395   228.5   12.7    442  7  CN081576          CN081576 EC2BBA19C
  396   228.5   12.7    897  7  CN161781          CN161781 951102 MA
  397   228.5   12.7   2530  3  AK018522          AK018522 Mus muscu
  398     228   12.6    194  4  BI337742          BI337742 361263 MA
  399     228   12.6    816  5  BU385923          BU385923 603858616
  400     228   12.6   3468  3  AK052972          AK052972 Mus muscu
  401     227   12.6   3988  3  BC034594          BC034594 Mus muscu
  402     227   12.6   4131  3  AK078536          AK078536 Mus muscu
  403   226.5   12.5    550  2  BE012499          BE012499 121990 MA
  404   226.5   12.5    763  4  BG519515          BG519515 602577790
c 405     226   12.5    368  7  CN086072          CN086072 EC2BBA26C
  406   224.5   12.4   3050  9  AY417680          AY417680 Mus muscu
  407     224   12.4    652  7  CV462964          CV462964 CS_hyp_49
  408     224   12.4   4187  3  AK053044          AK053044 Mus muscu
  409     223   12.3    336  4  BG199531          BG199531 RST18822
c 410     223   12.3    433  1  AL921475          AL921475 AL921475
  411     223   12.3    494  4  BI515616          BI515616 BB160019B
  412     223   12.3    544  4  BI515545          BI515545 BB160019B
  413     223   12.3   3540  9  AY418995          AY418995 Homo sapi
  414     222   12.3    723  5  BU704037          BU704037 UI-M-FO0-
  415     222   12.3    932  5  BX409829          BX409829 BX409829
  416   221.5   12.3   1118  3  AK013775          AK013775 Mus muscu
  417   220.5   12.2   1372  3  AK053839          AK053839 Mus muscu
  418   220.5   12.2   2126  3  AK013911          AK013911 Mus muscu
c 419     220   12.2    754  6  CA448116          CA448116 UI-H-ED1-
c 420     220   12.2    770  2  AW117456          AW117456 xd92a06.x
  421     220   12.2   2664  3  AK043379          AK043379 Mus muscu
  422   219.5   12.2   3345  9  AY403614          AY403614 Homo sapi
  423     219   12.1    821  5  BU389844          BU389844 603511165
  424   218.5   12.1    916  5  BQ672140          BQ672140 AGENCOURT
  425     218   12.1    712  5  BU212380          BU212380 603952444
  426     218   12.1   2874  3  AK036262          AK036262 Mus muscu
  427   217.5   12.0    586  4  BM696801          BM696801 UI-E-DW0-
  428   217.5   12.0    866  5  BQ923836          BQ923836 AGENCOURT
c 429     217   12.0    780  5  BX917601          BX917601 BX917601
  430   216.5   12.0    375  5  BY292584          BY292584 BY292584
  431   216.5   12.0    473  7  CO280999          CO280999 EK155707.
  432   215.5   11.9    657  2  BB618284          BB618284 BB618284
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  434   214.5   11.9    734  6  CB448011          CB448011 702065 MA
  435   214.5   11.9    742  7  CO395507          CO395507 AGENCOURT
  436     214   11.8    711  1  AU004083          AU004083 AU004083
  437     214   11.8    724  7  CO561566          CO561566 AGENCOURT
  438     214   11.8    813  4  BI651587          BI651587 603298063
  439     214   11.8   1280  3  CR648110          CR648110 Tetraodon
  440     214   11.8   2464  3  AK043507          AK043507 Mus muscu
  441     214   11.8   2535  3  BC012380          BC012380 Homo sapi
  442     214   11.8   2553  3  BC046975          BC046975 Mus muscu
  443   213.5   11.8    701  5  BW223428          BW223428 BW223428
  444   213.5   11.8   1306  3  CR605082          CR605082 full-leng
  445   213.5   11.8   1315  3  CR733537          CR733537 Tetraodon
  446     213   11.8    558  7  CK875240          CK875240 SGP136467
  447     213   11.8    593  5  BX499713          BX499713 DKFZp779M

  448     213   11.8    669  6  CB246171          CB246171 UI-M-FO0-
c 449     213   11.8    737  5  BX915880          BX915880 BX915880
  450     213   11.8    761  5  BU355132          BU355132 603475958
  451     213   11.8   1288  3  CR728377          CR728377 Tetraodon
  452     213   11.8   1304  3  CR644432          CR644432 Tetraodon
  453     213   11.8   3219  3  AK041230          AK041230 Mus muscu
  454     213   11.8   3518  3  BC036088          BC036088 Homo sapi
  455     212   11.7   1253  3  CR636279          CR636279 Tetraodon
  456     212   11.7   1270  3  CR637013          CR637013 Tetraodon
  457   211.5   11.7    710  6  CA349374          CA349374 619770 NC
  458   211.5   11.7    768  6  CD636212          CD636212 56031066H
  459   211.5   11.7   3342  9  AY403616          AY403616 Mus muscu
  460   211.5   11.7   4015  3  AK028770          AK028770 Mus muscu
  461   211.5   11.7   4429  3  AK028889          AK028889 Mus muscu
  462     211   11.7    687  4  BI827613          BI827613 603073581
c 463     211   11.7    723  5  BX923781          BX923781 BX923781
  464     211   11.7   1623  3  AK038917          AK038917 Mus muscu
  465     211   11.7   4113  3  AK053077          AK053077 Mus muscu
  466     210   11.6    640  9  CC573801          CC573801 CH240_450
  467   209.5   11.6    588  6  CD636204          CD636204 56030983H
  468     209   11.6    870  4  BI913885          BI913885 603183295
  469     209   11.6   3037  3  AK052440          AK052440 Mus muscu
  470   208.5   11.5    492  4  BI359722          BI359722 384371 MA
  471   208.5   11.5    562  5  BX952176          BX952176 DKFZp781K
  472   208.5   11.5    694  7  CF125589          CF125589 UI-HF-EL0
  473     208   11.5    700  2  BB652926          BB652926 BB652926
c 474     208   11.5    712  6  CD620699          CD620699 56100889J
  475     208   11.5    990  9  AY418721          AY418721 Mus muscu
  476   207.5   11.5   1290  3  CR649578          CR649578 Tetraodon
  477   207.5   11.5   2104  3  AK033487          AK033487 Mus muscu
  478   207.5   11.5   4441  3  AK081990          AK081990 Mus muscu
  479     207   11.5    842  6  CA317300          CA317300 UI-M-FW0-
  480   206.5   11.4    685  4  BJ000543          BJ000543 BJ000543
  481   206.5   11.4    779  6  CA511514          CA511514 UI-R-FJ0-
c 482   206.5   11.4    904  6  CB756103          CB756103 AGENCOURT
c 483     206   11.4    778  6  CD620690          CD620690 56100765H
  484     206   11.4   1516  3  CR727897          CR727897 Tetraodon
  485   205.5   11.4    783  7  CF540537          CF540537 UI-M-GV0-
  486   205.5   11.4   2017  3  AK042488          AK042488 Mus muscu
  487     205   11.4    729  7  CN533735          CN533735 UI-M-HO0-
  488     205   11.4    990  9  AY418719          AY418719 Homo sapi
  489     205   11.4   1228  3  CR648907          CR648907 Tetraodon
c 490   204.5   11.3    701  5  BX669319          BX669319 BX669319
  491   204.5   11.3    893  5  BU523040          BU523040 AGENCOURT
  492   204.5   11.3   1237  3  CR641398          CR641398 Tetraodon
  493     204   11.3    843  5  BX854499          BX854499 BX854499
c 494   203.5   11.3    613  6  CD636184          CD636184 56020447H
  495   203.5   11.3   3642  3  AK084609          AK084609 Mus muscu
c 496     203   11.2    334  1  AI422503          AI422503 tf11e04.x
  497   202.5   11.2    651  7  CK831552          CK831552 4055165 B
  498   202.5   11.2    687  5  BP461989          BP461989 BP461989
  499     202   11.2    810  5  BU338342          BU338342 603514255
  500     202   11.2    846  5  BQ423040          BQ423040 AGENCOURT
c 501     202   11.2    867  7  CN163166          CN163166 952638 MA
  502     202   11.2   3123  3  AK049284          AK049284 Mus muscu
c 503   201.5   11.2    467  4  BI134406          BI134406 UI-M-BH3-
  504   201.5   11.2    701  7  CO422929          CO422929 GGEZHT102
  505   201.5   11.2   1304  3  CR639237          CR639237 Tetraodon
  506   201.5   11.2   1548  3  CR728005          CR728005 Tetraodon
  507     201   11.1    865  7  CK401822          CK401822 AUF_IfInt
  508     201   11.1   1788  9  AY411536          AY411536 Mus muscu
  509   200.5   11.1    525  6  CB720159          CB720159 AMGNNUC:N
  510   200.5   11.1    541  6  CD803660          CD803660 UI-M-GV0-
  511   200.5   11.1    935  5  BQ893857          BQ893857 AGENCOURT
  512     200   11.1    550  6  CD636197          CD636197 56030950J
  513     200   11.1    703  7  CV434528          CV434528 CS_hyp_36
c 514     200   11.1   1062  5  BX343871          BX343871 BX343871
  515   199.5   11.0    783  7  CN055172          CN055172 Salamande
c 516   199.5   11.0   1025  7  CR754135          CR754135 CR754135
c 517   199.5   11.0   1074  7  CR754275          CR754275 CR754275
  518   199.5   11.0   1267  3  CR634286          CR634286 Tetraodon
  519     199   11.0    816  1  AU117395          AU117395 AU117395
  520     199   11.0    954  1  AL551492          AL551492 AL551492
  521     199   11.0   2236  3  BC030834                BC030834 Homo sapi
  522     199   11.0   2705  3  AK090377                AK090377 Mus muscu
  523     199   11.0   4068  9  AY406427                AY406427 Mus muscu
  524   198.5   11.0    618  6  CD636200                CD636200 56030966H
c 525   198.5   11.0    732  7  CN358175                CN358175 170005328
c 526   198.5   11.0    796  6  CD620697                CD620697 56100881J
  527   198.5   11.0   4919  3  BC040674                BC040674 Homo sapi
  528     198   11.0    625  4  BJ032692                BJ032692 BJ032692
  529     198   11.0    728  7  CF728819                CF728819 UI-M-HE0-
  530     198   11.0    838  7  CK028945                CK028945 AGENCOURT
  531     198   11.0   1104  7  CR755975                CR755975 CR755975
  532   197.5   10.9    534  7  CN950627                CN950627 Ha_mx0_36
  533   197.5   10.9    766  6  CA326802                CA326802 UI-M-FY0-
  534   197.5   10.9    795  7  CN532710                CN532710 UI-M-HO0-
c 535   197.5   10.9   1145  7  CR754709                CR754709 CR754709
  536     197   10.9    433  4  BG515406                BG515406 dae04h10.
  537     197   10.9    474  2  BB682022                BB682022 BB682022
  538     197   10.9    631  4  BM426245                BM426245 pgf2n.pk0
c 539     197   10.9    781  6  CD620693                CD620693 56100781J
  540   196.5   10.9    582  5  BP355301                BP355301 BP355301
  541   196.5   10.9    686  6  CA372777                CA372777 646750 NC
  542   196.5   10.9    812  5  BQ180027                BQ180027 UI-M-EW0-
  543   196.5   10.9    923  5  BU140452                BU140452 603135370
  544   196.5   10.9   1272  3  CR731454                CR731454 Tetraodon
  545   196.5   10.9   3647  3  BC046957                BC046957 Mus muscu
  546     196   10.9    895  7  CN761982                CN761982 ID0AAA3BG
  547     196   10.9    925  4  BG419088                BG419088 602446318
  548     196   10.9    987  6  CD507156                CD507156 CDA83-C12
  549     196   10.9   4068  9  AY406425                AY406425 Homo sapi
  550   195.5   10.8    576  1  AL699151                AL699151 DKFZp686E
  551   195.5   10.8    632  7  CO432230                CO432230 UI-M-HX0-
  552   195.5   10.8    675  7  CN060015                CN060015 Salamande
  553   195.5   10.8    787  6  CD802924                CD802924 UI-M-GV0-
  554   195.5   10.8    857  6  CB520168                CB520168 UI-M-GI0-
  555   195.5   10.8   1261  3  CR640626                CR640626 Tetraodon
  556   195.5   10.8   1263  3  CR647139                CR647139 Tetraodon
  557     195   10.8    617  5  BQ555199                BQ555199 H4032G01-
  558     195   10.8    666  7  CN832582                CN832582 AGENCOURT
  559   194.5   10.8    455  7  CO337067                CO337067 EN13754.5
  560   194.5   10.8    652  7  CK689464                CK689464 ZF101-P00
  561   194.5   10.8    730  6  CA357629                CA357629 630022 NC
  562   194.5   10.8    763  6  CB519682                CB519682 UI-M-GH0-
  563   194.5   10.8    852  7  CR422792                CR422792 CR422792
  564     194   10.7    523  4  BI512632                BI512632 BB160009B
  565     194   10.7    896  6  CD514588                CD514588 AGENCOURT
  566     194   10.7   3424  3  AK044694                AK044694 Mus muscu
  567   193.5   10.7    837  6  CD352315                CD352315 UI-M-GI0-
  568   193.5   10.7   4178  3  AK087693                AK087693 Mus muscu
  569     193   10.7    226  1  AA776056                AA776056 ae79a07.s
  570     193   10.7    710  7  CN225540                CN225540 WLA073F11
  571     193   10.7    808  5  BU746846                BU746846 CH3#007_D
  572   192.5   10.7    614  6  CD636183                CD636183 56020347J
  573   192.5   10.7    944  5  BQ681009                BQ681009 AGENCOURT
c 574   192.5   10.7    945  9  CNS04AD2                AL281711 Tetraodon
  575   192.5   10.7   1259  3  CR636055                CR636055 Tetraodon
  576   192.5   10.7   2283  9  AY418472                AY418472 Mus muscu
  577   192.5   10.7   4329  3  AK040765                AK040765 Mus muscu
  578     192   10.6    534  7  CR556169                CR556169 DKFZp459D
  579     192   10.6    730  7  CO505029                CO505029 GGEZEB103
  580     192   10.6    839  6  CD578410                CD578410 UI-M-FY0-
  581     192   10.6    877  5  BU322077                BU322077 603850177
  582     192   10.6   2132  3  BC045734                BC045734 Homo sapi
  583     192   10.6   4068  9  AY406426                AY406426 Pan trogl
c 584   191.5   10.6    581  8  BH269028                BH269028 CH230-66P
  585   191.5   10.6    702  7  CN359049                CN359049 170004245
c 586   191.5   10.6    779  8  BH292378                BH292378 CH230-44D
  587   191.5   10.6   1291  3  CR641448                CR641448 Tetraodon
  588   191.5   10.6   3157  9  AY403615                AY403615 Pan trogl
  589     191   10.6    613  4  BM487940                BM487940 pgm2n.pk0
  590     191   10.6    754  7  CF530715                CF530715 UI-M-FY0-
  591     191   10.6   1055  4  BM551034                BM551034 AGENCOURT
  592   190.5   10.5    643  6  CA385573                CA385573 666709 NC
  593   190.5   10.5    649  7  CO505951                CO505951 GGEZEB103

  594   190.5   10.5    779  5  BU419715                BU419715 603953627
  595   190.5   10.5    797  7  CK311806                CK311806 SB02010A1
  596   190.5   10.5    924  5  BQ882851                BQ882851 AGENCOURT
  597   190.5   10.5   1499  3  CR636336                CR636336 Tetraodon
  598     190   10.5    514  5  BX111689                BX111689 BX111689
  599     190   10.5    769  5  BX857871                BX857871 BX857871
c 600     190   10.5   1463  8  CC288776                CC288776 CH261-170
  601   189.5   10.5    714  7  CN460823                CN460823 UI-M-HB0-
  602   189.5   10.5    748  5  BU058289                BU058289 UI-M-FO0-
  603   189.5   10.5    946  4  BI549835                BI549835 603194572
  604   189.5   10.5   2211  9  AY418471                AY418471 Pan trogl
  605   189.5   10.5   3057  9  AY417679                AY417679 Pan trogl
  606     189   10.5    609  6  CA381472                CA381472 660987 NC
  607     189   10.5    683  2  BB318882                BB318882 BB318882
  608     189   10.5    706  6  CA324144                CA324144 UI-M-FY0-
  609     189   10.5    710  7  CK638303                CK638303 UI-M-HO0-
  610     189   10.5    938  5  BX708988                BX708988 BX708988
  611   188.5   10.4    603  1  AL679324                AL679324 AL679324
  612   188.5   10.4    663  5  BU708530                BU708530 UI-M-FI0-
  613   188.5   10.4    720  3  CR644200                CR644200 Tetraodon
  614   188.5   10.4    773  6  CD348004                CD348004 UI-M-FY0-
  615   188.5   10.4    839  4  BI851286                BI851286 603377864
  616   188.5   10.4    922  4  BM802337                BM802337 AGENCOURT
  617   188.5   10.4   4185  3  AK083540                AK083540 Mus muscu
  618     188   10.4    313  2  AW430704                AW430704 70599 MAR
  619     188   10.4    558  6  CB448500                CB448500 702638 MA
  620     188   10.4    722  7  CN530508                CN530508 UI-M-HO0-
c 621     188   10.4    833  6  CD636250                CD636250 56038493H
  622     188   10.4   1121  7  CR755403                CR755403 CR755403
  623   187.5   10.4    582  5  BP355339                BP355339 BP355339
c 624   187.5   10.4    652  8  BH269030                BH269030 CH230-66P
  625   187.5   10.4    655  1  AI980307                AI980307 pat.pk002
  626   187.5   10.4    759  7  CN430206                CN430206 170005315
  627   187.5   10.4    784  7  CK478969                CK478969 AGENCOURT
  628     187   10.4    497  5  BX515241                BX515241 BX515241
  629     187   10.4    616  7  CN532902                CN532902 UI-M-HO0-
  630     187   10.4    766  2  BE213159                BE213159 IpBrn0200
c 631     187   10.4    837  7  CF345598                CF345598 AGENCOURT
  632     187   10.4   3531  3  AK035110                AK035110 Mus muscu
  633     187   10.4   3821  3  AK085461                AK085461 Mus muscu
  634   186.5   10.3    664  4  BJ732469                BJ732469 BJ732469
  635   186.5   10.3    835  7  CK847657                CK847657 970316 MA
  636   186.5   10.3    923  5  BU326524                BU326524 603489483
  637   186.5   10.3   1230  3  CR641410                CR641410 Tetraodon
  638     186   10.3    644  6  CB518611                CB518611 UI-M-GH0-
  639     186   10.3    648  5  BM935487                BM935487 UI-M-BH3-
  640     186   10.3    727  7  CO431177                CO431177 UI-M-HX0-
  641     186   10.3    752  7  CF741342                CF741342 UI-M-GH0-
  642     186   10.3    788  7  CF737289                CF737289 UI-M-HD0-
  643     186   10.3    791  7  CO557024                CO557024 AGENCOURT
  644     186   10.3    883  7  CN985580                CN985580 58560_126
  645     186   10.3   1146  7  CR755551                CR755551 CR755551
  646     186   10.3   1791  9  AY411534                AY411534 Homo sapi
  647   185.5   10.3    636  5  BU363294                BU363294 603585969
  648   185.5   10.3    761  6  CA384559                CA384559 665213 NC
  649   185.5   10.3    987  2  BF579256                BF579256 602093426
  650   185.5   10.3   1215  9  AY421473                AY421473 Homo sapi
  651   185.5   10.3   2299  9  AY418470                AY418470 Homo sapi
  652     185   10.2    736  1  AA439246                AA439246 LD13756.5
  653     185   10.2    951  5  BQ680360                BQ680360 AGENCOURT
  654     185   10.2    990  9  AY418720                AY418720 Pan trogl
  655     185   10.2   3638  3  AK045373                AK045373 Mus muscu
  656   184.5   10.2    644  5  BQ561052                BQ561052 H4068A05-
  657   184.5   10.2    700  4  BM623297                BM623297 170006874
  658   184.5   10.2   1497  3  AK053039                AK053039 Mus muscu
  659     184   10.2    565  4  BG732685                BG732685 333483 MA
  660     184   10.2    662  4  BM624477                BM624477 170006874
  661     184   10.2    669  7  CF745309                CF745309 UI-M-GV0-
  662     184   10.2    670  4  BM171749                BM171749 imageqc_5
  663     184   10.2    791  7  CO572836                CO572836 AGENCOURT
c 664     184   10.2    838  6  CD636246                CD636246 56038477H
  665     184   10.2    865  5  BX725298                BX725298 BX725298
  666     184   10.2    940  7  CK871065                CK871065 AGENCOURT
  667    184   10.2    970  5  BU107306             BU107306 602954168
  668  183.5   10.2    558  4  BI067163             BI067163 pgf1n.pk0
  669  183.5   10.2    774  6  CB247631             CB247631 UI-M-FI0-
  670  183.5   10.2    863  6  CD514529             CD514529 AGENCOURT
  671  183.5   10.2    904  5  BU144883             BU144883 603229681
  672  183.5   10.2    974  5  BU559792             BU559792 AGENCOURT
  673  183.5   10.2   1064  5  BX343872             BX343872 BX343872
  674    183   10.1    550  2  AW653843             AW653843 102720 MA
  675    183   10.1    609  1  AL673319             AL673319 AL673319
  676    183   10.1    671  5  BU344752             BU344752 603407056
  677    183   10.1    865  6  CA327194             CA327194 UI-M-FY0-
  678    183   10.1    914  5  BU184213             BU184213 AGENCOURT
  679    183   10.1   1064  5  BQ055710             BQ055710 AGENCOURT
  680  182.5   10.1    627  7  CF534081             CF534081 UI-M-GH0-
  681  182.5   10.1    717  7  CF534534             CF534534 UI-M-GI0-
  682  182.5   10.1    743  6  CD636180             CD636180 56005276H
c 683  182.5   10.1    799  6  CD620695             CD620695 56100873J
  684  182.5   10.1    862  1  AA698836             AA698836 HL05774.5
  685  182.5   10.1   1086  5  BQ071438             BQ071438 AGENCOURT
c 686    182   10.1    496  4  BF995884             BF995884 QV1-GN020
  687    182   10.1    867  6  CB519811             CB519811 UI-M-GH0-
c 688    182   10.1    900  5  BX350637             BX350637 BX350637
  689    182   10.1    922  5  BQ948697             BQ948697 AGENCOURT
  690    182   10.1   2197  3  CR614873             CR614873 full-leng
  691  181.5   10.0    563  6  CA370225             CA370225 650349 NC
  692  181.5   10.0    629  7  CF723085             CF723085 UI-M-GV0-
  693  181.5   10.0    676  2  BE731113             BE731113 601566330
  694  181.5   10.0    731  4  BJ712564             BJ712564 BJ712564
  695  181.5   10.0    740  7  CO881919             CO881919 BovGen_10
  696  181.5   10.0   2906  3  AK051027             AK051027 Mus muscu
c 697    181   10.0    400  7  CO339200             CO339200 EP01053.3
  698    181   10.0    580  7  CK889202             CK889202 SGP161216
  699    181   10.0    624  2  AV988998             AV988998 AV988998
  700    181   10.0    975  5  BX335437             BX335437 BX335437
  701    181   10.0   4168  3  BC060216             BC060216 Mus muscu
  702    181   10.0   4962  3  HSM804543            AL833232 Homo sapi
  703  180.5   10.0    588  4  BJ031875             BJ031875 BJ031875
  704  180.5   10.0    713  5  BU311407             BU311407 603543724
  705  180.5   10.0    802  1  AU124625             AU124625 AU124625
  706    180   10.0    290  2  BF362977             BF362977 CM4-NN008
  707    180   10.0    364  1  AI940007             AI940007 QV0-CT001
  708    180   10.0    434  1  AI279142             AI279142 qm18e02.x
c 709    180   10.0    442  5  BX112198             BX112198 BX112198
  710    180   10.0    468  2  BF110673             BF110673 7n55h10.x
  711    180   10.0    502  1  AI796834             AI796834 we22h06.x
  712    180   10.0    523  2  BE550993             BE550993 7b67a03.x
  713    180   10.0    583  6  CB586460             CB586460 AMGNNUC:N
  714    180   10.0    585  2  AV959095             AV959095 AV959095
c 715    180   10.0    671  7  CF366096             CF366096 836780 MA
  716    180   10.0    713  7  CN442065             CN442065 BE04028A1
  717    180   10.0    776  7  CK780892             CK780892 UI-M-HE0-
  718    180   10.0    796  5  BX348968             BX348968 BX348968
  719    180   10.0    858  6  CB196421             CB196421 AGENCOURT
  720    180   10.0    866  7  CK872817             CK872817 AGENCOURT
  721    180   10.0   1135  7  CK027809             CK027809 AGENCOURT
c 722  179.5    9.9    452  7  CO289807             CO289807 EK072116.
  723  179.5    9.9    747  7  CF948722             CF948722 UI-M-HJ0-
  724    179    9.9    594  4  BJ489405             BJ489405 BJ489405
  725    179    9.9    645  4  BM488779             BM488779 pgm2n.pk0
  726    179    9.9    794  7  CF533313             CF533313 UI-M-FY0-
c 727    179    9.9    811  6  CD636248             CD636248 56038485H
  728    179    9.9    939  7  CK865923             CK865923 AGENCOURT
  729    179    9.9   2453  3  AK033574             AK033574 Mus muscu
  730    179    9.9   3939  3  AK036698             AK036698 Mus muscu
  731  178.5    9.9    710  6  CA378084             CA378084 656807 NC
  732  178.5    9.9    772  7  CO430864             CO430864 UI-M-HX0-
c 733  178.5    9.9    825  6  CD636240             CD636240 56038385H
  734  178.5    9.9    883  5  BQ955157             BQ955157 AGENCOURT
  735  178.5    9.9    894  5  BQ642447             BQ642447 AGENCOURT
  736  178.5    9.9    910  5  BQ895192             BQ895192 AGENCOURT
  737  178.5    9.9    912  5  BU154175             BU154175 AGENCOURT
  738  178.5    9.9    967  1  AL538691             AL538691 AL538691
  739    178    9.9    208  1  AU281844             AU281844 AU281844
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c 740    178    9.9    653  7  CF180026             CF180026 815076 MA
  741    178    9.9    738  5  BU448181             BU448181 603764825
  742    178    9.9    871  7  CF551909             CF551909 AGENCOURT
  743    178    9.9    883  2  BF792657             BF792657 602253836
  744    178    9.9    893  9  CNS02MVY             AL204631 Tetraodon
  745    178    9.9   1285  3  AK010350             AK010350 Mus muscu
  746    178    9.9   3903  3  AK076423             AK076423 Mus muscu
  747    178    9.9   4544  3  AK052489             AK052489 Mus muscu
  748  177.5    9.8    548  5  BQ636532             BQ636532 hd11a05.y
c 749  177.5    9.8    593  5  BX676568             BX676568 BX676568
  750  177.5    9.8    714  2  BF575974             BF575974 602132952
  751  177.5    9.8    726  4  BJ708729             BJ708729 BJ708729
  752  177.5    9.8    734  2  BF529510             BF529510 602043274
  753  177.5    9.8    814  7  CV121409             CV121409 AGENCOURT
  754  177.5    9.8    951  5  BQ919823             BQ919823 AGENCOURT
  755  177.5    9.8   1088  5  BQ062993             BQ062993 AGENCOURT
  756  177.5    9.8   1516  9  AY408377             AY408377 Mus muscu
  757    177    9.8    371  7  CO196400             CO196400 EK004112.
  758    177    9.8    757  6  CB953709             CB953709 AGENCOURT
  759    177    9.8    760  4  BI559288             BI559288 603241144
  760    177    9.8    908  6  CD796854             CD796854 EST668215
  761    177    9.8    909  5  BQ435144             BQ435144 AGENCOURT
  762    177    9.8   2942  3  AK031495             AK031495 Mus muscu
  763    177    9.8   3865  3  AF077041             AF077041 Homo sapi
c 764  176.5    9.8    587  4  BM153637             BM153637 TCBAP2E11
  765  176.5    9.8    607  5  BU948358             BU948358 io50a10.y
  766  176.5    9.8    652  6  CA376364             CA376364 654703 NC
  767  176.5    9.8    671  7  CK003726             CK003726 AGENCOURT
  768  176.5    9.8    674  4  BG722412             BG722412 602693645
  769  176.5    9.8    679  7  CR538523             CR538523 DKFZp459F
  770  176.5    9.8    706  4  BI914768             BI914768 603184148
c 771  176.5    9.8    787  6  CD636242             CD636242 56038393H
  772  176.5    9.8    801  4  BI553374             BI553374 603193319
  773  176.5    9.8    816  5  BQ881760             BQ881760 AGENCOURT
  774  176.5    9.8    898  5  BQ951309             BQ951309 AGENCOURT
  775  176.5    9.8   1163  9  AY421474             AY421474 Pan trogl
  776  176.5    9.8   2334  9  AY408375             AY408375 Homo sapi
  777    176    9.7    524  7  CN304965             CN304965 170005325
  778    176    9.7    702  5  BX299781             BX299781 BX299781
  779    176    9.7    727  6  CA346240             CA346240 677090 NC
  780    176    9.7    744  7  CK693733             CK693733 ZF101-P00
  781    176    9.7    820  6  CD758447             CD758447 AGENCOURT
  782    176    9.7    857  7  CK192396             CK192396 EST781711
  783    176    9.7   2178  3  AK018613             AK018613 Mus muscu
  784    176    9.7   2369  3  BC034042             BC034042 Homo sapi
c 785    176    9.7   2894  3  AK033581             AK033581 Mus muscu
  786  175.5    9.7    608  5  BQ582107             BQ582107 il12h03.y
  787  175.5    9.7    631  5  BX709958             BX709958 BX709958
  788  175.5    9.7    675  6  CB722950             CB722950 UI-M-GH0-
  789  175.5    9.7    675  6  CD625574             CD625574 55147942H
  790  175.5    9.7    702  7  CK781415             CK781415 UI-M-GV0-
  791  175.5    9.7    758  7  CK475728             CK475728 AGENCOURT
c 792  175.5    9.7    831  6  CD636244             CD636244 56038469H
  793  175.5    9.7    847  7  CK475175             CK475175 AGENCOURT
  794  175.5    9.7    952  5  BU556507             BU556507 AGENCOURT
  795  175.5    9.7   2271  9  AY418467             AY418467 Homo sapi
  796  175.5    9.7   2334  9  AY408376             AY408376 Pan trogl
  797    175    9.7    234  1  AV349585             AV349585 AV349585
c 798    175    9.7    303  1  AI422504             AI422504 tf11e05.x
c 799    175    9.7    526  4  BI045435             BI045435 MR3-FN020
  800    175    9.7    606  6  CB273099             CB273099 mai66h01.
  801    175    9.7    631  4  BI553967             BI553967 603193844
  802    175    9.7    651  7  CK679637             CK679637 ZF101-P00
  803    175    9.7    660  5  BM986302             BM986302 EST531210
  804    175    9.7    714  6  CB527370             CB527370 UI-M-FY0-
  805    175    9.7    752  5  BU203628             BU203628 603103394
  806    175    9.7    770  7  CK780689             CK780689 UI-M-HD0-
c 807    175    9.7    888  7  CN075890             CN075890 EC2BBA11A
  808  174.5    9.7    550  7  CR544600             CR544600 DKFZp459F
  809  174.5    9.7    582  5  BP316461             BP316461 BP316461
  810  174.5    9.7    752  5  BU707206             BU707206 UI-M-FR0-
  811  174.5    9.7    775  1  AU006387             AU006387 AU006387
  812  174.5    9.7    836  2  BE747501             BE747501 601573016
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    813    174.5    9.7     847  7  CF374272          CF374272 AGENCOURT
    814    174.5    9.7     875  5  BX403262          BX403262 BX403262
    815      174    9.6     285  7  CN209637          CN209637 4115576 B
    816      174    9.6     581  5  BP217876          BP217876 BP217876
    817      174    9.6     625  1  AU134398          AU134398 AU134398
    818      174    9.6     669  5  BX670963          BX670963 BX670963
c   819      174    9.6     736  8  AZ989621          AZ989621 2M0273I04
    820      174    9.6     940  7  CK865164          CK865164 AGENCOURT
    821      174    9.6    2756  3  AK038385          AK038385 Mus muscu
    822      174    9.6    3075  3  AK034142          AK034142 Mus muscu
    823      174    9.6    4152  3  AK079332          AK079332 Mus muscu
    824    173.5    9.6     569  6  CB616002          CB616002 AMGNNUC:N
    825    173.5    9.6     629  7  CF364674          CF364674 834668 MA
    826    173.5    9.6     634  6  CB577096          CB577096 AMGNNUC:N
    827    173.5    9.6     888  7  CK424119          CK424119 AUF_IpSto
    828    173.5    9.6    2240  9  AY418469          AY418469 Mus_muscu
c   829      173    9.6     527  1  AA741334          AA741334 ob30f08.s
c   830      173    9.6     619  6  CD636182          CD636182 56020347H
    831      173    9.6     642  4  BM310781          BM310781 ig48d12.y
    832      173    9.6     765  7  CN535749          CN535749 UI-M-HS0-
    833      173    9.6     812  7  CO426708          CO426708 UI-M-HU0-
    834      173    9.6     935  7  CK870930          CK870930 AGENCOURT
    835      173    9.6    1088  7  CK030075          CK030075 AGENCOURT
    836      173    9.6    2976  3  HSM801624         AL136654 Homo sapi
    837    172.5    9.6     452  7  CN359001          CN359001 170005322
    838    172.5    9.6     643  7  CF895017          CF895017 A0142H05-
    839    172.5    9.6     646  4  BM576695          BM576695 170006871
    840    172.5    9.6     685  7  CR790517          CR790517 DKFZp459K
c   841    172.5    9.6     761  6  CD636201          CD636201 56030966J
    842    172.5    9.6     782  7  CK807818          CK807818 AGENCOURT
c   843    172.5    9.6     808  5  BX771524          BX771524 BX771524
    844    172.5    9.6     814  6  CD758575          CD758575 AGENCOURT
    845    172.5    9.6     842  7  CK597432          CK597432 AGENCOURT
    846    172.5    9.6     889  7  CF375649          CF375649 AGENCOURT
    847    172.5    9.6     892  1  AU079295          AU079295 AU079295
    848    172.5    9.6     930  5  BQ950644          BQ950644 AGENCOURT
    849    172.5    9.6     933  7  CK867774          CK867774 AGENCOURT
    850    172.5    9.6    2784  3  AK052040          AK052040 Mus muscu
c   851      172    9.5     616  1  AI924653          AI924653 wn57h07.x
    852      172    9.5     728  7  CN530285          CN530285 UI-M-HQ0-
    853      172    9.5     800  4  BG293215          BG293215 602390177
c   854      172    9.5     802  7  CK777862          CK777862 965008 MA
c   855      172    9.5     811  5  BX761240          BX761240 BX761240
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    857      172    9.5     840  1  AL524519          AL524519 AL524519
    858    171.5    9.5     567  5  BP370399          BP370399 BP370399
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    861    171.5    9.5     580  5  BP210849          BP210849 BP210849
    862    171.5    9.5     582  5  BP194652          BP194652 BP194652
    863    171.5    9.5     583  5  BP359006          BP359006 BP359006
    864    171.5    9.5     583  7  CN359285          CN359285 170005326
    865    171.5    9.5     587  5  BQ270237          BQ270237 ik08a10.y
    866    171.5    9.5     590  5  BP309421          BP309421 BP309421
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    868    171.5    9.5     603  5  BX316915          BX316915 BX316915
    869    171.5    9.5     668  6  CD296956          CD296956 StrPu691.
    870    171.5    9.5     685  7  CK544312          CK544312 rswhb0_01
    871    171.5    9.5     686  7  CO505010          CO505010 GGEZEB103
c   872    171.5    9.5     726  6  CD636205          CD636205 56030983J
    873    171.5    9.5     757  4  BG819912          BG819912 602782004
    874    171.5    9.5     786  2  BE306404          BE306404 601103309
c   875    171.5    9.5     801  6  CD636213          CD636213 56031066J
c   876    171.5    9.5     806  6  CD636192          CD636192 56030942H
c   877    171.5    9.5     816  6  CD636238          CD636238 56038369H
    878    171.5    9.5    1749  3  CR643698          CR643698 Tetraodon
    879      171    9.5     583  5  BP219778          BP219778 BP219778
c   880      171    9.5     684  5  BU625289          BU625289 UI-H-FG1-
    881      171    9.5     816  7  CF220776          CF220776 AGENCOURT
    882      171    9.5    1386  3  CR608576          CR608576 full-leng
    883      171    9.5    1653  3  BC024164          BC024164 Homo sapi
c   884    170.5    9.4     484  5  BX099260          BX099260 BX099260
    885    170.5    9.4     526  7  CN677790          CN677790 E0102B04-
    886    170.5    9.4     585  5  BP377151          BP377151 BP377151
    887    170.5    9.4     588  6  CB585172          CB585172 AMGNNUC:N
    888    170.5    9.4     600  4  BG806560          BG806560 2032-50 M
    889    170.5    9.4     600  5  BU920372          BU920372 .6053-62
    890    170.5    9.4     614  6  CD351134          CD351134 UI-M-FY0-
c   891    170.5    9.4     746  6  CD636196          CD636196 56030950H
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    893    170.5    9.4     816  7  CF220046          CF220046 AGENCOURT
    894    170.5    9.4     892  5  BU135652          BU135652 603124302
    895    170.5    9.4     893  7  CN507252          CN507252 AGENCOURT
    896    170.5    9.4     999  4  BM561628          BM561628 AGENCOURT
    897      170    9.4     561  7  CN991327          CN991327 67958_125
    898      170    9.4     723  9  CG784243          CG784243 FHCRC-GT-
    899      170    9.4     748  6  CD620698          CD620698 56100889H
    900      170    9.4     776  7  CN171251          CN171251 AGENCOURT
    901      170    9.4     825  7  CF222141          CF222141 AGENCOURT
    902      170    9.4     827  7  CR445411          CR445411 CR445411
    903      170    9.4     836  7  CF147692          CF147692 AGENCOURT
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    905    169.5    9.4     499  2  BF151777          BF151777 uz20c07.y
    906    169.5    9.4     563  7  CF534807          CF534807 UI-M-GH0-
    907    169.5    9.4     581  5  BP195803          BP195803 BP195803
    908    169.5    9.4     662  2  BB665541          BB665541 BB665541
    909    169.5    9.4     708  6  CB423451          CB423451 596888 MA
    910    169.5    9.4     752  7  CF729863          CF729863 UI-M-HE0-
c   911    169.5    9.4     755  4  BJ723979          BJ723979 BJ723979
    912    169.5    9.4     759  7  CK871118          CK871118 AGENCOURT
    913    169.5    9.4     760  6  CA513275          CA513275 UI-R-FJ0-
    914    169.5    9.4     803  1  AU131954          AU131954 AU131954
    915    169.5    9.4     804  7  CK869114          CK869114 AGENCOURT
c   916    169.5    9.4     832  9  BX238729          BX238729 Danio rer
    917    169.5    9.4     843  7  CN157026          CN157026 944474 MA
    918    169.5    9.4    1097  7  CK232248          CK232248 ILLUMIGEN
c   919    169.5    9.4    1106  1  AL561703          AL561703 AL561703
    920    169.5    9.4    3230  3  AK011916          AK011916 Mus muscu
    921      169    9.4     547  7  CK656925          CK656925 3017HFEX2
    922      169    9.4     582  5  BP194396          BP194396 BP194396
    923      169    9.4     595  1  AI722009          AI722009 fd18c09.y
c   924      169    9.4     604  2  AW025115          AW025115 wu71h04.x
    925      169    9.4     658  4  BJ011427          BJ011427 BJ011427
c   926      169    9.4     702  5  BW098413          BW098413 BW098413
    927      169    9.4     740  7  CF744590          CF744590 UI-M-GV0-
    928      169    9.4     767  6  CA345552          CA345552 676226 NC
    929      169    9.4     799  7  CR409324          CR409324 CR409324
    930      169    9.4     805  5  BQ745652          BQ745652 UI-M-EW0-
    931      169    9.4     886  6  CD172256          CD172256 AGENCOURT
    932      169    9.4     888  7  CK409633          CK409633 AUF_IfLvr
    933      169    9.4    1143  6  CD503634          CD503634 CDA63-E09
    934      169    9.4    1735  2  AW888221          AW888221 MXRA5 Hum
    935      169    9.4    3553  3  AK081793          AK081793 Mus muscu
    936    168.5    9.3     528  6  CB719651          CB719651 AMGNNUC:N
c   937    168.5    9.3     539  1  AL918370          AL918370 AL918370
    938    168.5    9.3     543  1  AU207958          AU207958 AU207958
    939    168.5    9.3     579  6  CB607385          CB607385 AMGNNUC:N
    940    168.5    9.3     606  7  CV040428          CV040428 4137944 B
    941    168.5    9.3     671  7  CO389127          CO389127 AGENCOURT
    942    168.5    9.3     673  6  CB248224          CB248224 UI-M-FI0-
    943    168.5    9.3    2645  3  BC038036          BC038036 Mus muscu
    944    168.5    9.3    4199  3  AK030591          AK030591 Mus muscu
    945      168    9.3     535  2  AW786664          AW786664 120025 MA
    946      168    9.3     571  4  BM272758          BM272758 ig99a06.y
    947      168    9.3     581  5  BP194328          BP194328 BP194328
    948      168    9.3     639  6  CA328483          CA328483 UI-M-FY0-
    949      168    9.3     762  7  CO245579          CO245579 AGENCOURT
    950      168    9.3     774  5  BU205766          BU205766 603102289
    951      168    9.3     804  7  CR414090          CR414090 CR414090
    952      168    9.3     873  7  CF251316          CF251316 esa023_e1
    953      168    9.3     921  5  BU520481          BU520481 AGENCOURT
c   954    167.5    9.3     573  1  AI685262          AI685262 wa75e11.x
    955    167.5    9.3     725  7  CK691938          CK691938 ZF101-P00
    956    167.5    9.3     736  7  CK367468          CK367468 AGENCOURT
    957    167.5    9.3     786  5  BU382983          BU382983 603582371
    958    167.5    9.3     798  7  CK481268          CK481268 AGENCOURT
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  959   167.5    9.3    817  4  BG912522                    BG912522 602806620
  960   167.5    9.3    831  5  BU491858                    BU491858 604131047
  961   167.5    9.3    930  7  CK407450                    CK407450 AUF_IfLvr
  962   167.5    9.3    981  5  BQ964910                    BQ964910 AGENCOURT
  963   167.5    9.3   1469  3  AK044527                    AK044527 Mus muscu
  964     167    9.2    514  6  CB716703                    CB716703 AMGNNUC:N
  965     167    9.2    608  6  CD636186                    CD636186 56020455H
  966     167    9.2    616  7  CN164688                    CN164688 995050 MA
  967     167    9.2    696  1  AI542894                    AI542894 SD09407.5
  968     167    9.2    707  7  CK869511                    CK869511 AGENCOURT
  969     167    9.2    726  5  BU446195                    BU446195 603766375
  970     167    9.2    912  7  CK870512                    CK870512 AGENCOURT
  971     167    9.2   1289  3  CR729255                    CR729255 Tetraodon
  972     167    9.2   3628  3  AK031696                    AK031696 Mus muscu
  973   166.5    9.2    583  5  BP321297                    BP321297 BP321297
  974   166.5    9.2    775  7  CF348727                    CF348727 AGENCOURT
  975   166.5    9.2    779  1  AU125657                    AU125657 AU125657
  976   166.5    9.2    812  6  CB723208                    CB723208 UI-M-GH0-
  977   166.5    9.2    822  6  CA510738                    CA510738 UI-R-FJ0-
  978   166.5    9.2    928  5  BQ891778                    BQ891778 AGENCOURT
  979     166    9.2    583  4  BG223754                    BG223754 1M00018F0
  980     166    9.2    647  7  CK781448                    CK781448 UI-M-GV0-
  981     166    9.2    656  7  CK659672                    CK659672 LP17591.5
  982     166    9.2    680  7  CF899461                    CF899461 A0303E02-
c 983     166    9.2    740  4  BJ720179                    BJ720179 BJ720179
  984     166    9.2    796  6  CD653854                    CD653854 AGENCOURT
  985     166    9.2    805  4  BG117787                    BG117787 602350472
  986     166    9.2    805  7  CF785901                    CF785901 AGENCOURT
  987     166    9.2    910  5  BX324896                    BX324896 BX324896
  988   165.5    9.2    420  6  CB798880                    CB798880 AMGNNUC:N
c 989   165.5    9.2    517  6  CD290273                    CD290273 StrPu538.
c 990   165.5    9.2    589  1  AA606149                    AA606149 fa16d03.s
  991   165.5    9.2    634  6  CD803622                    CD803622 UI-M-GV0-
  992   165.5    9.2    654  7  CF744226                    CF744226 UI-M-GV0-
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 1013     165    9.1   1137  6  CD507144                    CD507144 CDA83-C06
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 1035     164    9.1   1930  3  AK003326                    AK003326 Mus muscu
 1036     164    9.1   2814  3  CR593108                    CR593108 full-leng
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 1052   163.5    9.1    923  7  CN322132                    CN322132 AGENCOURT
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 1056   163.5    9.1   3248  3  AK004821                    AK004821 Mus muscu
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 1261   157.5    8.7    987  5  BX375028              BX375028 BX375028
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 1263   157.5    8.7   1046  4  BM552640              BM552640 AGENCOURT
 1264   157.5    8.7   1072  7  CN642560              CN642560 ILLUMIGEN
 1265   157.5    8.7   1488  3  CR608619              CR608619 full-leng
 1266   157.5    8.7   1594  3  CR617107              CR617107 full-leng
 1267   157.5    8.7   1742  9  AY413879              AY413879 Mus muscu
 1268   157.5    8.7   2090  3  AK003152              AK003152 Mus muscu
 1269   157.5    8.7   2209  3  AK017447              AK017447 Mus muscu
 1270   157.5    8.7   2735  3  AK029024              AK029024 Mus muscu
 1271   157.5    8.7   3652  3  AK030851              AK030851 Mus muscu
 1272   157.5    8.7   4118  3  AK031391              AK031391 Mus muscu
 1273     157    8.7    578  5  BP368062              BP368062 BP368062
c1274     157    8.7    608  5  BX917921              BX917921 BX917921
 1275     157    8.7    612  4  BM795050              BM795050 K-EST0076
 1276     157    8.7    641  2  BB664453              BB664453 BB664453
 1277     157    8.7    690  6  CD636219              CD636219 56031467J
 1278     157    8.7    695  7  CK949734              CK949734 4074697 B
 1279     157    8.7    722  6  CD805128              CD805128 UI-M-GW0-
 1280     157    8.7    727  7  CK961924              CK961924 4076329 B
 1281     157    8.7    737  4  BI915307              BI915307 603184382
 1282     157    8.7    757  6  CB519019              CB519019 UI-M-GH0-
 1283     157    8.7    781  6  CD348686              CD348686 UI-M-FY0-
 1284     157    8.7    805  1  AU131165              AU131165 AU131165
c1285     157    8.7    826  6  CB165550              CB165550 BEQ603160
 1286     157    8.7    848  7  CN020324              CN020324 AGENCOURT
 1287     157    8.7    850  5  BX739790              BX739790 BX739790
 1288     157    8.7    876  7  CK948326              CK948326 4073246 B
 1289     157    8.7    886  5  BQ945091              BQ945091 AGENCOURT
 1290     157    8.7    896  5  BX379273              BX379273 BX379273
 1291     157    8.7    910  5  BU192138              BU192138 AGENCOURT
 1292     157    8.7    930  7  CN315936              CN315936 AGENCOURT
 1293     157    8.7    933  9  AY417086              AY417086 Mus muscu
 1294     157    8.7   1020  4  BM548873              BM548873 AGENCOURT
 1295     157    8.7   1034  1  AL553289              AL553289 AL553289
 1296     157    8.7   1071  5  BU503048              BU503048 AGENCOURT
 1297     157    8.7   1127  1  AL549623              AL549623 AL549623
 1298     157    8.7   1514  3  CR617300              CR617300 full-leng
 1299     157    8.7   1867  3  AK087272              AK087272 Mus muscu
 1300     157    8.7   1892  3  CR622259              CR622259 full-leng
 1301     157    8.7   2791  3  BC013698              BC013698 Homo sapi
 1302   156.5    8.7    568  1  AI629069              AI629069 fc09b12.y
 1303   156.5    8.7    618  4  BI065290              BI065290 pgf1n.pk0
 1304   156.5    8.7    627  4  BJ112590              BJ112590 BJ112590
 1305   156.5    8.7    630  1  AI295266              AI295266 LP08849.5
 1306   156.5    8.7    630  5  BQ390372              BQ390372 NISC_mq12
 1307   156.5    8.7    684  6  CA354756              CA354756 626528 NC
 1308   156.5    8.7    725  4  BI736575              BI736575 603361039
 1309   156.5    8.7    740  5  BU058190              BU058190 UI-M-FO0-
 1310   156.5    8.7    751  5  BP673676              BP673676 BP673676
 1311   156.5    8.7    768  7  CN172200              CN172200 AGENCOURT
 1312 - 156.5    8.7    776  5  BQ442214              BQ442214 UI-M-EX0-
 1313   156.5    8.7    858  5  BU470108              BU470108 603365843
 1314   156.5    8.7    914  7  CF594392              CF594392 AGENCOURT
 1315   156.5    8.7    928  5  BQ733716              BQ733716 AGENCOURT
 1316   156.5    8.7    937  7  CO248697              CO248697 AGENCOURT
 1317   156.5    8.7   1004  5  BU134013              BU134013 603121573
 1318   156.5    8.7   1014  6  CB206098              CB206098 AGENCOURT
 1319   156.5    8.7   1028  7  CN642108              CN642108 ILLUMIGEN
 1320   156.5    8.7   1319  7  CV182470              CV182470 tai87g02.
 1321   156.5    8.7   3465  9  AY418996              AY418996 Pan trogl
 1322   156.5    8.7   3689  3  AK004723              AK004723 Mus muscu
 1323   156.5    8.7   3865  3  AK087355              AK087355 Mus muscu
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 1324     156    8.6    477  7  CN359280              CN359280 170005319
 1325     156    8.6    596  1  AL599774              AL599774 DKFZp313M
c1326     156    8.6    628  4  BJ685150              BJ685150 BJ685150
 1327     156    8.6    653  7  CK003476              CK003476 AGENCOURT
 1328     156    8.6    691  1  AV384111              AV384111 AV384111
 1329     156    8.6    729  4  BM621283              BM621283 170006874
 1330     156    8.6    740  7  CN531505              CN531505 UI-M-HQ0-
 1331     156    8.6    760  7  CN531514              CN531514 UI-M-HQ0-
 1332     156    8.6    767  2  AW175139              AW175139 fi32f09.y
 1333     156    8.6    775  6  CD080814              CD080814 MA3-9999U
 1334     156    8.6    780  5  BX444240              BX444240 BX444240
 1335     156    8.6    784  6  CA350777              CA350777 621665 NC
 1336     156    8.6    795  7  CO248560              CO248560 AGENCOURT
 1337     156    8.6    810  7  CO799885              CO799885 AGENCOURT
 1338     156    8.6   1096  7  CN642525              CN642525 ILLUMIGEN
 1339     156    8.6   2036  3  AK089498              AK089498 Mus muscu
 1340     156    8.6   2850  3  AK047868              AK047868 Mus muscu
 1341     156    8.6   3312  3  AK004947              AK004947 Mus muscu
 1342     156    8.6   3449  3  AK041299              AK041299 Mus muscu
 1343     156    8.6   3559  9  AY404032              AY404032 Pan trogl
 1344     156    8.6   3687  3  AK079247              AK079247 Mus muscu
 1345   155.5    8.6    409  2  BE226893              BE226893 us74a09.y
 1346   155.5    8.6    581  5  BP193219              BP193219 BP193219
 1347   155.5    8.6    581  5  BP195771              BP195771 BP195771
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 1349   155.5    8.6    617  5  BW305475              BW305475 BW305475
 1350   155.5    8.6    638  6  CD629100              CD629100 56059934H
 1351   155.5    8.6    649  1  AL864304              AL864304 AL864304
c1352   155.5    8.6    702  9  CNS02PTU              AL208443 Tetraodon
c1353   155.5    8.6    718  6  CD636336              CD636336 56048995J
 1354   155.5    8.6    727  4  BM290618              BM290618 EST577152
 1355   155.5    8.6    769  7  CN505057              CN505057 AGENCOURT
 1356   155.5    8.6    786  7  CN302526              CN302526 170006001
c1357   155.5    8.6    796  5  BX923150              BX923150 BX923150
c1358   155.5    8.6    796  5  BX926278              BX926278 BX926278
 1359   155.5    8.6    797  6  CD642524              CD642524 AGENCOURT
 1360   155.5    8.6    850  5  BP264898              BP264898 BP264898
 1361   155.5    8.6    850  7  CO557070              CO557070 AGENCOURT
c1362   155.5    8.6    861  6  CD636209              CD636209 56031050J
 1363   155.5    8.6    880  5  BU542115              BU542115 AGENCOURT
 1364   155.5    8.6    979  7  CN642097              CN642097 ILLUMIGEN
 1365   155.5    8.6   1039  5  BQ057979              BQ057979 AGENCOURT
 1366   155.5    8.6   1091  7  CK232190              CK232190 ILLUMIGEN
 1367   155.5    8.6   1376  3  CR635265              CR635265 Tetraodon
 1368   155.5    8.6   4017  3  AK028983              AK028983 Mus muscu
 1369   155.5    8.6   5635  9  AY412619              AY412619 Mus muscu
 1370     155    8.6    427  7  CO436236              CO436236 ddPCR2_17
 1371     155    8.6    545  4  BM440456              BM440456 pgr1n.pk0
 1372     155    8.6    571  4  BJ124803              BJ124803 BJ124803
 1373     155    8.6    602  6  CA317092              CA317092 UI-M-FW0-
c1374     155    8.6    617  6  CD636187              CD636187 56020455J
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 1376     155    8.6    694  6  CD349249              CD349249 UI-M-FY0-
c1377     155    8.6    705  7  CR753907              CR753907 CR753907
 1378     155    8.6    710  7  CN053418              CN053418 Salamande
 1379     155    8.6    726  7  CN302510              CN302510 170005318
 1380     155    8.6    739  7  CN302524              CN302524 170004710
 1381     155    8.6    755  7  CN302501              CN302501 170005322
 1382     155    8.6    778  7  CK634628              CK634628 UI-M-HN0-
 1383     155    8.6    781  5  BU383797              BU383797 603581533
 1384     155    8.6    792  4  BI772811              BI772811 603054461
 1385     155    8.6    793  7  CF288820              CF288820 AGENCOURT
 1386     155    8.6    833  1  AA941031              AA941031 LD23480.5
 1387     155    8.6    836  4  BI824985              BI824985 603033468
 1388     155    8.6    891  6  CD384890              CD384890 AGENCOURT
 1389     155    8.6    907  5  BQ928239              BQ928239 AGENCOURT
 1390     155    8.6    913  2  BE912082              BE912082 601663261
 1391     155    8.6    922  5  BU518914              BU518914 AGENCOURT
 1392     155    8.6    933  9  AY417084              AY417084 Homo sapi
 1393     155    8.6    941  5  BQ928243              BQ928243 AGENCOURT
 1394     155    8.6    993  1  AL560725              AL560725 AL560725
 1395     155    8.6   1047  7  CK230378              CK230378 ILLUMIGEN
 1396     155    8.6   1971  3  AK076123              AK076123 Mus muscu
 1397     155     8.6   1992  3  AK034125              AK034125 Mus muscu
 1398     155     8.6   3133  3  AK085723              AK085723.Mus muscu
c1399   154.5     8.6    247  7  CR474371              CR474371 CR474371
 1400   154.5     8.6    450  1  AA168307              AA168307 ms54b12.r
 1401   154.5     8.6    498  6  CB070225              CB070225 is27f12.y
 1402   154.5     8.6    506  7  CO328919              CO328919 EK291651.
 1403   154.5     8.6    598  1  AL856990              AL856990 AL856990
c1404   154.5     8.6    648  8  AZ379719              AZ379719 1M0135K02
 1405   154.5     8.6    670  5  BX622375              BX622375 BX622375
 1406   154.5     8.6    677  5  BU204691              BU204691 604159805
 1407   154.5     8.6    689  7  CF533968              CF533968 UI-M-GH0-
c1408   154.5     8.6    702  6  CD620688              CD620688 56087531H
 1409   154.5     8.6    715  4  BJ487033              BJ487033 BJ487033
 1410   154.5     8.6    732  4  BM292745              BM292745 EST575287
 1411   154.5     8.6    778  5  BQ745865              BQ745865 UI-M-EX0-
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 1413   154.5     8.6    808  4  BI523511              BI523511 603175329
 1414   154.5     8.6    811  7  CF539481              CF539481 UI-M-GH0-
 1415   154.5     8.6    840  5  BX729243              BX729243 BX729243
 1416   154.5     8.6   1002  4  BM472841              BM472841 AGENCOURT
 1417   154.5     8.6   1029  7  CN642582              CN642582 ILLUMIGEN
 1418   154.5     8.6   1311  5  BP938160              BP938160 BP938160
 1419   154.5     8.6   5724  9  AY412617              AY412617 Homo sapi
c1420     154     8.5    513  4  BM152259              BM152259 TCBAP1E85
 1421     154     8.5    525  5  BX317406              BX317406 BX317406
 1422     154     8.5    563  5  BQ637244              BQ637244 he07e09.y
c1423     154     8.5    588  2  AW977089              AW977089 EST389198
 1424     154     8.5    595  4  BJ071900              BJ071900 BJ071900
 1425     154     8.5    620  1  AL876779              AL876779 AL876779
 1426     154     8.5    620  1  AL892876              AL892876 AL892876
 1427     154     8.5    659  7  CK639629              CK639629 UI-M-HN0-
 1428     154     8.5    677  7  CV027585              CV027585 5879 Full
c1429     154     8.5    684  6  CA307499              CA307499 UI-H-FT1-
 1430     154     8.5    692  7  CN302521              CN302521 170005325
 1431     154     8.5    723  6  CD217761              CD217761 pgr1n.pk0
 1432     154     8.5    735  4  BG468165              BG468165 602509740
 1433     154     8.5    814  7  CK871988              CK871988 AGENCOURT
 1434     154     8.5   2151  3  AK011949              AK011949 Mus muscu
 1435     154     8.5   3754  9  AY404033              AY404033 Mus muscu
 1436   153.5     8.5    529  7  CO302094              CO302094 EK183041.
 1437   153.5     8.5    553  7  CV067547              CV067547 Le_mx0_30
 1438   153.5     8.5    569  7  CK554083              CK554083 rswla0_01
 1439   153.5     8.5    657  5  BQ078813              BQ078813 fy81c06.y
 1440   153.5     8.5    692  5  BW437745              BW437745 BW437745
 1441   153.5     8.5    745  6  CD802869              CD802869 UI-M-GV0-
 1442   153.5     8.5    765  7  CN080626              CN080626 EC2BBA18B
 1443   153.5     8.5    772  5  BP686752              BP686752 BP686752
 1444   153.5     8.5    806  7  CO248525              CO248525 AGENCOURT
 1445   153.5     8.5    866  7  CR414240              CR414240 CR414240
 1446   153.5     8.5    915  5  BU914386              BU914386 AGENCOURT
 1447   153.5     8.5    916  5  BQ682463              BQ682463 AGENCOURT
 1448   153.5     8.5    933  6  CA979380              CA979380 AGENCOURT
 1449   153.5     8.5   1090  7  CK232196              CK232196 ILLUMIGEN
 1450   153.5     8.5   2265  9  AY418468              AY418468 Pan trogl
 1451   153.5     8.5   2931  3  AK033723              AK033723 Mus muscu
c1452     153     8.5    457  2  AW487927              AW487927 UI-M-BH3-
 1453     153     8.5    560  7  CO315167              CO315167 EK239550.
 1454     153     8.5    573  7  CF977921              CF977921 FAR17G1.R
 1455     153     8.5    579  5  BP253163              BP253163 BP253163
 1456     153     8.5    609  1  AV611538              AV611538 AV611538
c1457     153     8.5    629  4  BG638272              BG638272 LD21470.3
 1458     153     8.5    644  5  BX299780              BX299780 BX299780
 1459     153     8.5    646  6  CA969841              CA969841 CcLX06a24
 1460     153     8.5    707  7  CN853558              CN853558 Ha_mx0_14
c1461     153     8.5    708  4  BJ508410              BJ508410 BJ508410
 1462     153     8.5    717  6  CD625578              CD625578 55147850H
 1463     153     8.5    752  7  CN302505              CN302505 170004245
 1464     153     8.5    817  7  CO431094              CO431094 UI-M-HX0-
 1465     153     8.5    826  7  CN988932              CN988932 64879_125
 1466     153     8.5    844  7  CN987704              CN987704 63433_125
 1467     153     8.5    866  7  CN978018              CN978018 28737_125
 1468     153     8.5    941  5  BQ917338              BQ917338 AGENCOURT
 1469     153     8.5   2802  9  AY416713              AY416713 Pan trogl
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 1470   152.5     8.4    430  5  BU947992              BU947992 io56e11.y
 1471   152.5     8.4    548  5  BX271825              BX271825 BX271825
 1472   152.5     8.4    594  5  BW221728              BW221728 BW221728
 1473   152.5     8.4    668  4  BI394312              BI394312 pgp1n.pk0
 1474   152.5     8.4    709  5  BU316030              BU316030 603488360
 1475   152.5     8.4    710  9  AG286398              AG286398 Mus muscu
 1476   152.5     8.4    723  6  CB526860              CB526860 UI-M-FY0-
 1477   152.5     8.4    745  4  BI080347              BI080347 602876784
c1478   152.5     8.4    768  5  BX918182              BX918182 BX918182
c1479   152.5     8.4    769  5  BX856025              BX856025 BX856025
 1480   152.5     8.4    822  6  CB245137              CB245137 UI-M-FY0-
 1481   152.5     8.4    833  7  CN837756              CN837756 AGENCOURT
 1482   152.5     8.4    867  6  CA788252              CA788252 AGENCOURT
 1483   152.5     8.4    912  6  CD515059              CD515059 AGENCOURT
 1484   152.5     8.4    950  1  AL523470              AL523470 AL523470
 1485   152.5     8.4   1004  7  CN642068              CN642068 ILLUMIGEN
 1486   152.5     8.4   1028  9  CNS007QA              AL067489 Drosophil
 1487   152.5     8.4   2338  3  AK032604              AK032604 Mus muscu
 1488   152.5     8.4   4050  3  AK049704              AK049704 Mus muscu
 1489   152.5     8.4   5655  9  AY412618              AY412618 Pan trogl
 1490     152     8.4    530  7  CK580486              CK580486 IST_WI5_2
c1491     152     8.4    602  5  BU741589              BU741589 UI-E-EO1-
c1492     152     8.4    622  8  BH374792              BH374792 AG-ND-138
 1493     152     8.4    717  4  BM622248              BM622248 170006874
 1494     152     8.4    731  6  CA750190              CA750190 UI-M-FD0-
 1495     152     8.4    808  7  CF744297              CF744297 UI-M-GV0-
 1496     152     8.4    878  7  CN643444              CN643444 ILLUMIGEN
 1497     152     8.4    888  5  BQ945830              BQ945830 AGENCOURT
 1498     152     8.4    919  7  CN646263              CN646263 ILLUMIGEN
 1499     152     8.4    925  6  CA982594              CA982594 AGENCOURT
 1500     152     8.4    979  7  CN642895              CN642895 ILLUMIGEN


                                 ALIGNMENTS


RESULT 1
AK045973
LOCUS       AK045973                1808 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male corpora quadrigemina cDNA, RIKEN
            full-length enriched library, clone:B230328N06 product:NEUROTRIMIN
            PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
ACCESSION   AK045973
VERSION     AK045973.1  GI:26337738
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE  99279253
    PUBMED  10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE  20499374
    PUBMED  11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1808)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:               6.59e-198     Length:        1808
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Score:                  1780.00        Matches:       337
Percent Similarity:     99.42%         Conservative:  5
Best Local Similarity:  97.97%         Mismatches:    2
Query Match:            98.56%         Indels:        0
DB:                     3              Gaps:          0

US-10-017-084A-523 (1-344) x AK045973 (1-1808)

Qy          1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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Qy         21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db        264 GCGGCTCTGTGCCTCTTCCAAGGAGTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAA 323

Qy         41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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Qy         61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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Db        384 AACCGAGTCACCCGGGTGGCCTGGCTAAACCGCAGTACCATCCTCTATGCTGGAAATGAC 443

Qy         81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
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Qy        181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Qy           341 LeuLeuLysPhe 344
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RESULT 2
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LOCUS       AK046377                1808 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male corpora quadrigemina cDNA, RIKEN
            full-length enriched library, clone:B230377K17 product:NEUROTRIMIN
            PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
ACCESSION   AK046377
VERSION     AK046377.1  GI:26338018
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1808)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
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                     LLVLHLLLKF"
ORIGIN

Alignment Scores:
Pred. No.:              6.59e-198       Length:         1808
Score:                  1780.00         Matches:        337
Percent Similarity:     99.42%          Conservative:   5
Best Local Similarity:  97.97%          Mismatches:     2
Query Match:            98.56%          Indels:         0
DB:                     3               Gaps:           0

US-10-017-084A-523 (1-344) x AK046377 (1-1808)

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Qy          141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Qy          161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Qy          261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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RESULT 3
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DEFINITION  Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY406347
VERSION     AY406347.1  GI:39762321
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
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ORIGIN

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Query Match:            83.39%         Indels:          2
DB:                     9              Gaps:            1

US-10-017-084A-523 (1-344) x AY406347 (1-874)

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Db           62 GCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACG 121

Qy           97 GlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSer 116
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          122 CAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCG 181

Qy          117 ValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerPro 136
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          182 GTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCC 241

Qy          137 LysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThr 156
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          242 AAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACC 301

Qy          157 CysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLys--- 175
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          302 TGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAACCC 361

Qy          176 ---AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlu 194
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          362 GCAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAG 421

Qy          195 GlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArg 214
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          422 CAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGA 481

Qy          215 ValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValPro 234
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          482 GTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCC 541

Qy          235 ValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGln 254
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          542 GTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAG 601

Qy          255 TrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArg 274
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          602 TGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGA 661
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Qy        275 ProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThr 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACT 721

Qy        295 CysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGly 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 TGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGC 781

Qy        315 AlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuPro 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCT 841

Qy        335 LeuLeuValLeuHisLeuLeuLeuLysPhe 344
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Db        842 CTTCTGGTCTTGCACCTGCTTCTCAAATTT 871

RESULT 4
AY406349
LOCUS       AY406349                 874 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406349
VERSION     AY406349.1  GI:39762323
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 874)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..874
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1..>874
                     /locus_tag="HCM2527"
ORIGIN

Alignment Scores:
Pred. No.:              5.29e-164       Length:         874
Score:                  1488.00         Matches:        282
Percent Similarity:     98.97%          Conservative:   5
Best Local Similarity:  97.24%          Mismatches:     1
Query Match:            82.39%          Indels:         2
DB:                     9               Gaps:           1

US-10-017-084A-523 (1-344) x AY406349 (1-874)

Qy         57 CysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyr 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TGCACAATTGACAACCGAGTCACCCGGGTGGCCTGGCTAAACCGCAGTACCATCCTCTAT 61

Qy         77 AlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GCTGGAAATGACAAGTGGTGCCTAGATCCTCGTGTGGTCCTCCTGAGTAACACCCAGACC 121

Qy         97 GlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSer 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CAGTACAGCATTGAGATCCAGAATGTGGATGTGTACGATGAGGGCCCTTATACCTGCTCG 181

Qy        117 ValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerPro 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GTACAGACAGACAACCACCCTAAGACCTCCAGGGTCCACCTCATTGTACAAGTATCTCCC 241

Qy        137 LysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThr 156
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAACATCAGCCTCACT 301

Qy        157 CysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLys--- 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   
Db        302 TGCATAGCCACAGGTAGACCGGAGCCTACAGTAACCTGGAGACATATTTCTCCCAAGCCC 361

Qy        176 ---AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlu 194
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GCAGCCGTTGGCTTTGTGAGTGAGGATGAGTACCTGGAGATCCAGGGCATCACTCGGGAA 421

Qy        195 GlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArg 214
              |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 CAGTCAGGCGAGTACGAGTGCAGCGCCTCCAACGACGTGGCGGCACCAGTGGTACGAAGA 481

Qy        215 ValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValPro 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GTGAAGGTCACCGTGAACTATCCACCATACATCTCAGAAGCTAAGGGCACAGGTGTCCCC 541

Qy        235 ValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGln 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GTGGGGCAGAAGGGGACTCTGCAGTGTGAAGCTTCCGCAGTCCCTTCAGCAGAATTTCAA 601

Qy        255 TrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArg 274
              |||:::||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        602 TGGTTCAAGGATGACAAAAGACTGGTCGAAGGAAAGAAGGGAGTCAAAGTGGAAAACAGA 661

Qy        275 ProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThr 294
              ||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db        662 CCTTTCCTTTCAAAACTCACCTTTTTCAACGTCTCTGAACATGACTATGGGAACTACACA 721

Qy        295 CysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGly 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 TGTGTGGCCTCCAACAAGCTGGGTCACACCAACGCCAGCATCATGCTATTTGGTCCCGGT 781

Qy        315 AlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuPro 334
              |||||||||||||||:::|||||||||||||||||||||||||||:::||||||||||||
Db        782 GCTGTCAGTGAGGTCAACAATGGACATCAAGGAGGGCAGGCTGCATTTGGCTCCTCCCT 841

Qy        335 LeuLeuValLeuHisLeuLeuLeuLysPhe 344
              ||||||||||||||||||||||||||||||
Db        842 CTTCTGGTCTTACACCTGCTCCTCAAATTT 871

RESULT 5
AY406348
LOCUS       AY406348                 773 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Pan troglodytes HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406348
VERSION     AY406348.1  GI:39762322
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 773)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE   2  (bases 1 to 773)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .773
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>773
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ORIGIN

Alignment Scores:
Pred. No.:              8.99e-145       Length:         773
Score:                  1324.00         Matches:        253
Percent Similarity:     98.44%          Conservative:   0
Best Local Similarity:  98.44%          Mismatches:     2
Query Match:            73.31%          Indels:         2
DB:                     9               Gaps:           1

US-10-017-084A-523 (1-344) x AY406348 (1-773)

Qy          57 CysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyr 76
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 TGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTAT 61

Qy          77 AlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr 96
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 GCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACG 121

Qy          97 GlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSer 116
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 CAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCG 181

Qy         117 ValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerPro 136
               ||||||||||||||||||||||||||||||||||||||||||||||||      ||||||
Db         182 GTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCNNNTATCTCCC 241

Qy         137 LysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThr 156
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         242 AAAATTGTAGAGATTTCTTCAGATATCTCCATTAACGAAGGGAACAATATCAGCCTCACC 301

Qy         157 CysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLys--- 175
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         302 TGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCCCCCAAACCC 361

Qy         176 ---AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlu 194
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         362 GCAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAG 421

Qy         195 GlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArg 214
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         422 CAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGA 481

Qy         215 ValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValPro 234
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Db         482 GTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCC 541

Qy         235 ValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGln 254
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Db         542 GTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAG 601

Qy         255 TrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArg 274
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         602 TGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGA 661
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Qy         275 ProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThr 294
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Db         662 CCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACT 721

Qy         295 CysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPhe 311
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Db         722 TGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTT 772

RESULT 6
CO635648
LOCUS       CO635648                1450 bp    mRNA    linear   EST 22-JUL-2004
DEFINITION  Contig2663 WL/RJ Phraped ESTs Gallus gallus cDNA 5', mRNA sequence.
ACCESSION   CO635648
VERSION     CO635648.1  GI:50538871
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1450)
  AUTHORS   Fitzsimmons,C.J., Savolainen,P., Amini,B., Hjalm,G., Lundeberg,J.
            and Andersson,L.
  TITLE     Detection of sequence polymorphisms in red junglefowl and White
            Leghorn ESTs
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Carolyn Fitzsimmons
            Leif Andersson IMBIM/Dept. Animal Breeding and Genetics
            Uppsala University/Swedish University of Agricultural Sciences
            Box 597, SE-751 24 Uppsala, SWEDEN
            Tel: 00 46 (0)18 471 4593
            Fax: 00 46 (0)18 471 4833
            Email: Carolyn.Fitzsimmons@bmc.uu.se
            This EST is a consensus sequence obtained from a Phrap assembly of
            4 cDNA libraries. The consensus sequence is submitted because SNP
            data in the publication 'Detection of sequence polymorphisms in red
            junglefowl and White Leghorn ESTs', is reported with reference to
            positions in the Phrap consensus sequence.
            Seq primer: (5'-end) M13 reverse.
FEATURES             Location/Qualifiers
     source          1. .1450
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Red junglefowl/White Leghorn"
                     /db_xref="taxon:9031"
                     /sex="female/male"
                     /lab_host="ElectroMAX DH10B (Invitrogen)"
                     /clone_lib="WL/RJ Phraped ESTs"
                     /note="Organ: brain/testis; Vector: pSPORT-1; Site_1: Hind
                     III; Site_2: EcoRI; The cDNA libraries were created with
                     the Superscript Plasmid System (Invitrogen)."
ORIGIN

Alignment Scores:
Pred. No.:              5.27e-144       Length:         1450
Score:                  1321.00         Matches:        255
Percent Similarity:     87.58%          Conservative:   27
Best Local Similarity:  79.19%          Mismatches:     34
Query Match:            73.15%          Indels:         6
DB:                     7               Gaps:           2

US-10-017-084A-523 (1-344) x CO635648 (1-1450)

Qy          27 GlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThr 46
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Db         308 CAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACT 367

Qy          47 ValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgVal 66
               |||||||||||||||||||||||||||||||||::::::|||||||||||||||||||||
Db         368 GTGCGGCAAGGGGAGAGTGCCACGCTCAGGTGCTCCGTGGACAACCGCGTCACCCGCGTG 427

Qy          67 AlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspPro 86
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               ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db         428 GCCTGGCTGAACCGCAGCAGCATCCTCTATGCCGGCAATGACAAGTGGTGCTTGGACCCG 487

Qy          87 ArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAsp 106
               |||||||||||||||:::||||||:::|||||||||||||||:::|||   :::||||||
Db         488 AGGGTGGTGCTCCTGGCCAACACCAAAACCCAGTACAGCATCCAGATCCACGACGTGGAC 547

Qy         107 ValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSer 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         548 GTGTACGATGAAGGGCCCTACACCTGCTCCGTGCAGACAGACAATCACCCCAAGACATCT 607

Qy         127 ArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSer 146
               ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db         608 CGCGTGCACCTCATTGTGCAAGTGTCGCCGAAAATTACCGAGATCTCTTCTGACATCTCC 667

Qy         147 IleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThr 166
               ||||||||||||   |||:::||||||||||||||||||||||||||||||:::||||||
Db         668 ATCAATGAAGGTGGCAACGTCAGCCTCACCTGCATAGCCACGGGCAGGCCAGACCCCACA 727

Qy         167 ValThrTrpArgHisIleSerProLysAlaValGly-PheValSerGluAspGluTyrLe 186
               :::|||||||||||||||||||||||||||||||||  |||:::||||||||||||||||
Db         728 ATCACCTGGAGACACATCTCGCCCAAAGCTGTGGGCCTTCATCAGCGAGGATGAGTACCT 787

Qy         186 uGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAs 206
               |||||||   ||||||||||||||||||||||||:::|||||||||||||||   |||||
Db         788 GGAGATCACGGGCATCACACGGGAGCAGTCGGGCGAGTATGAGTGCAGTGCTGTCAATGA 847

Qy         206 pValAlaAlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSe 226
               |||||||   |||   ||||||:::|||||||||||||||||||||||||||||||||||
Db         848 TGTGGCTGTCCCAGATGTCCGGAAAGTCAAAGTCACTGTCAACTACCCGCCGTACATCTC 907

Qy         226 rGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSe 246
               |   ||||||   ||||||      |||||||||||||||   |||||||||||||||||
Db         908 CAATGCCAAGAACACAGGCGCCTCAGTGGGCCAGAAGGGCATCCTGCAGTGCGAGGCCTC 967

Qy         246 rAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLy 266
               ||||||||||   |||||||||||||||:::|||:::|||   ||||||      |||
Db         968 GGCTGTTCCCGTGGCAGAGTTTCAGTGGTTCAAGGAGGACACCAGGTTAGCAAATGGGCT 1027

Qy         266 sLysGlyValLysValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSe 286
                :::||||||::::::|||::::::      ||||||   |||   ||||||||||||||
Db        1028 GGAGGGCGTGCGGATCGAGAGCAAGGGCCGCCTCTCGACGCTGACCTTCTTCAATGTGTC 1087

Qy         286 rGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAl 306
               ||||   |||||||||||||||||||||||||||:::||||||||||||:::||||||||
Db        1088 GGAGAAGGACTATGGCAACTACACGTGTGTGGCCACAAACAAGTTGGGCAACACCAATGC 1147

Qy         306 aSerIleMetLeuPhe-GlyProGlyAlaValSerGluValSerAsnGlyThrSerArgA 326
               |||||||:::|||::: |||||||||||||||   :::      |||      ||||||
Db        1148 CAGCATCATCCTGTACGGGCCCCGGAGCGGTGCACGACAGTGGCAATGCAGCCTCCCGGG 1207

Qy         326 rgAlaGly------CysValTrpLeuLeuProLeuLeuValLeuHisLeuLeuLeuLysP 344
                 |||         |||:::|||            |||:::      |||||||||   |
Db        1208 CAGCCGCTGGCCTCTGCCTCTGG------GCCACCCTCCTCGCTCGCCTCCTCCTCGACT 1261

Qy         344 he 344
               ||
Db        1262 TT 1263

RESULT 7
CD354474
LOCUS       CD354474                 765 bp    mRNA    linear   EST 15-JUL-2003
DEFINITION  UI-M-GM0-cgd-g-16-0-UI.r1 NIH_BMAP_GM0 Mus musculus cDNA clone
            IMAGE:30361215 5', mRNA sequence.
ACCESSION   CD354474
VERSION     CD354474.1  GI:31146975
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 765)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .765
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30361215"
                     /tissue_type="whole brain"
                     /dev_stage="1, 5 and 15 days newborn"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_GM0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel.First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site.Double strand cDNA was size
                     selected according to mRNA size fraction,ligated with EcoR
                     I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is CGAACTGAAT. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
ORIGIN

Alignment Scores:
Pred. No.:              1.55e-136      Length:         765
Score:                  1254.00        Matches:        246
Percent Similarity:     97.24%         Conservative:   1
Best Local Similarity:  96.85%         Mismatches:     6
Query Match:            69.44%         Indels:         2
DB:                     6              Gaps:           1

US-10-017-084A-523 (1-344) x CD354474 (1-765)

Qy           7 LysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe 26
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           5 AAAATGCACAATTCTATCTCGTGGGCAATCTTCACGGGGCTGGCGGCTCTGTGCCTCTTC 64

Qy          27 GlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThr 46
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          65 CAAGGAGTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAACGTGACG 124

Qy          47 ValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgVal 66
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         125 GTCAGGCAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCGGGTG 184

Qy          67 AlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspPro 86
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         185 GCCTGGCTAAACCGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGATCCT 244

Qy          87 ArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAsp 106
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         245 CGTGTGGTCCTCCTGAGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGTGGAT 304

Qy         107 ValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSer 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GTGTACGATGAGGGCCCTTATACCTGCTCGGTACAGACAGACAACCACCCTAAGACCTCC 364

Qy        127 ArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSer 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 AGGGTCCACCTCATTGTACAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCC 424

Qy        147 IleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThr 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 ATTAATGAAGGGAACAACATCAGCCTCACTTGCATAGCCACAGGTAGACCGGAGCCTACA 484

Qy        167 ValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeu 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 GTAACCTGGAGACATATTTCTCCCAAGGCCGTTGGCTTTGTGAGTGAGGATGAGTACCTG 544

Qy        187 GluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAsp 206
              |||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db        545 GAGATCCAGGGCATCACTCGGAACAGTCAGGCGAGTACGAGTGCAGCGCCTCCAACGAC 604

Qy        207 ValAlaAlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSer 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 GTGGCGGCACCAGTGGTACGAAGAGTGAAGGTCACCGTGAACTATCCACCATACATCTCA 664

Qy        227 GluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSer 246
              |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        665 GAAGCTAAGGGCACANGTGTCCCCGTGGGCAGAAGGGGACTCTGCAGTGTGAAGCTTCG 724

Qy        247 AlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
                    |||||||||||||||            |||||||||
Db        725 CAGT--CCTTCAGCAGAATTTCATGGT---CNGGATGACAAA 761

RESULT 8
BU155617
LOCUS       BU155617                 856 bp    mRNA    linear   EST 03-SEP-2002
DEFINITION  AGENCOURT_7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839
            5', mRNA sequence.
ACCESSION   BU155617
VERSION     BU155617.1  GI:22669149
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 856)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13527  row: m  column: 16
            High quality sequence stop: 593.
FEATURES             Location/Qualifiers
     source          1..856
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6166839"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
ORIGIN

Alignment Scores:
```

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Pred. No.:                4.8e-130       Length:          856
Score:                    1199.50        Matches:         243
Percent Similarity:       92.99%         Conservative:    9
Best Local Similarity:    89.67%         Mismatches:      13
Query Match:              66.42%         Indels:          7
DB:                       5              Gaps:            3

US-10-017-084A-523 (1-344) x BU155617 (1-856)

Qy         11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
              |||   ||||||:::      :::|||      :::|||            |||||||||
Db         48 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 103

Qy         31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 163

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 GAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAAC 223

Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 283

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 343

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 403

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 463

Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 523

Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 583

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 ATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 643

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 703

Qy        231 ThrGlyVal-ProValGlyGlnLysGlyThrLeuGln-CysGluAlaSerAlaValProS 250
              ||||||||| ||||||||||||||||||||||||||| ||||||   |||||||||||||
Db        704 ACAGGTGTCCCCCGTGGGACAAAAGGGGACACTGCAGTTGTGAAACCTCAGCAGTCCCCT 763

Qy        250 erAlaGlu-PheGlnTrpTyrLysAspAsp---LysArgLeuIleGluGlyLysLysGly 268
              |||||||| ||||||||||||:::|||:::   |||      ::::::||||||||||||
Db        764 CAGCAGAAATTCCAGTGGTACAGGGATGAACCAAAGACTGATTTGAAGGGAAAAAAAGGG 823

Qy        269 Val---LysValGluAsnArgProPhe 276
              |||   :::   :::|||   ||||||
Db        824 GTGGAAAGGGGGAAAAACGAACCTTTC 850

RESULT 9
BE798585
LOCUS       BE798585                1039 bp    mRNA    linear   EST 20-SEP-2000
DEFINITION  601581610F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935955 5',
            mRNA sequence.
ACCESSION   BE798585
VERSION     BE798585.1  GI:10219783
KEYWORDS    EST.
```

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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1039)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM779  row: d  column: 04
            High quality sequence stop: 849.
FEATURES             Location/Qualifiers
     source          1. .1039
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3935955"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

Alignment Scores:
Pred. No.:              4.33e-126       Length:         1039
Score:                  1167.00         Matches:        243
Percent Similarity:     80.71%          Conservative:   8
Best Local Similarity:  78.14%          Mismatches:     24
Query Match:            64.62%          Indels:         37
DB:                     2               Gaps:           7

US-10-017-084A-523 (1-344) x BE798585 (1-1039)

Qy           56 ArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeu 75
                ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db           66 AGGTGCACTATTGACAACCGGGTCGCCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTC 125

Qy           76 TyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGln 95
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          126 TATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAA 185

Qy           96 ThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCys 115
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          186 ACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGC 245

Qy          116 SerValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSer 135
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          246 TCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCT 305

Qy          136 ProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeu 155
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          306 CCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTC 365

Qy          156 ThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLys 175
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          366 ACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAA 425

Qy          176 AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGln 195
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          426 GCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAG 485

Qy          196 SerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgVal 215
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          486 TCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTA 545

Qy          216 LysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProVal 235
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          546 AAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCCGTG 605

Qy          236 GlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrp 255
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          606 GGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCCAGTGG 665

Qy          256 TyrLysAspAspLysArgLeuIleGluGly---LysLysGlyValLysValGluAsnArg 274
                ||||||||||||||||||||||||||||||      :::|||   ::::::|||||||||
Db          666 TACAAGGATGACAAAAGACTGATTGAAGGAACAGACAGGGGTGAACAGTTGGAAAACAGA 725

Qy          275 ProPheLeuSerLysLeuIlePhe------PheAsnValSer---GluHisAspTyr-Gl 291
                ||||||   |||      :::         |||||||||            |||||| ||
Db          726 CCTTTTTCCTCCTCAAAAGTCATTCCTTCTTTCAATGTCCTCTGANCCATGGACTATGGG 785

Qy          291 yAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAla-------------- 306
                |||||||||||||   |||      |||   |||||||||||||||
Db          786 GAACTACACTTGCGGGGCTCCCA--AAAGCTGGGCACACCAATGCCAGATCATGCTATTG 843

Qy          307 ----------------------------------------------------------Se 307

Db          844 ACGTAAATAGAGAGCAGTAGAAAAGTTGGTACCAGTGGAGAGCCACAATGCCGGATAGGA 903

Qy          307 rIleMetLeuPheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArg----- 325
                       ::::::   |||   :::|||||||||                  |||
Db          904 CAGTCCAGTCTACAGCCCC---AGTGTGAGCGAGCCAAAGAAGAGCAGGGGCCGCGAGTG 960

Qy          326 ----------ArgAlaGly---CysValTrp 331
                          |||||||||   |||:::|||
Db          961 AGCAAGCTAGAGGGCGGGTTGGTGCCTCTGG 991

RESULT 10
CN362539
LOCUS       CN362539                 748 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000470517655 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN362539
VERSION     CN362539.1  GI:47362473
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 748)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 748   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .748
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, embryoid bodies
                     derived from H1, H7 and H9 cells"
                     /clone_lib="GRN_EB"
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                    /note="oligo dT primed, full-length enriched cDNA library
                    from embryoid body outgrowths derived from hES cell lines
                    H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                    conditions."
ORIGIN

Alignment Scores:
Pred. No.:              1.77e-120     Length:         748
Score:                  1117.50       Matches:        218
Percent Similarity:     96.09%        Conservative:   3
Best Local Similarity:  94.78%        Mismatches:     8
Query Match:            61.88%        Indels:         2
DB:                     7             Gaps:           1

US-10-017-084A-523 (1-344) x CN362539 (1-748)

Qy         11 SerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGlnGlyValPro 30
              |||   ||||||:::      :::|||      :::|||            |||||||||
Db         63 AGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTGTTCCTTG---TACCC-ACAGGAGTGCCC 118

Qy         31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 GTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGG 178

Qy         51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 GAGAGCGCCACCCTCAGGTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAAC 238

Qy         71 ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CGCAGCACCATCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCCTT 298

Qy         91 LeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAspGlu 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 CTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG 358

Qy        111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTC 418

Qy        131 IleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGly 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 ATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGG 478

Qy        151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 AACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGA 538

Qy        171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 CACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC 598

Qy        191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCC 658

Qy        211 ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GTGGTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGT 718

Qy        231 ThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||||||||||||||
Db        719 ACAGGTGTCCCCGTGGGACAAAAGGGGACA 748

RESULT 11
CD327172
LOCUS       CD327172                 890 bp    mRNA    linear   EST 28-MAY-2003
DEFINITION  AGENCOURT_14148239 NICHD_XGC_Eye1 Xenopus laevis cDNA clone
            IMAGE:6949575 5', mRNA sequence.
ACCESSION   CD327172
VERSION     CD327172.1  GI:31091503
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 890)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement:
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14565  row: k  column: 14
            High quality sequence stop: 757.
FEATURES             Location/Qualifiers
     source          1..890
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:6949575"
                     /dev_stage="adult"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_XGC_Eye1"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: This is a Xenopus Gene Collection
                     (XGC) library."
ORIGIN

Alignment Scores:
Pred. No.:              1.02e-119     Length:         890
Score:                  1112.00       Matches:        209
Percent Similarity:     88.93%        Conservative:   32
Best Local Similarity:  77.12%        Mismatches:     28
Query Match:            61.57%        Indels:         2
DB:                     6             Gaps:           0

US-10-017-084A-523 (1-344) x CD327172 (1-890)

Qy          4 IleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeu 23
              :::|||   :::|||   :::|||:::   |||   ||||||:::|||||||||   |||
Db         69 CTGCAGGCAAGGATGCTGCACTCGGTTCCTTGGGTTATCTTCAGTGGGCTGGCTGTTCTT 128

Qy         24 CysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAsp 43
              ||||||   ||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        129 TGCCTCCTGCAAGGAGTGCCGGTGCGCAGCGGGGATGCCGGCTTCCCTAAAGCCATGGAC 188

Qy         44 AsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgVal 63
              |||||||||||||||||||||:::||||||   ||||||||||||:::||||||||||||
Db        189 AACGTGACGGTTCGACAAGGGGACAGCGCCATCCTCAGGTGCACAGTAGACAACAGAGTG 248

Qy         64 ThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCys 83
              |||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db        249 ACACGAGTGGCCTGGCTAAATCGTAGTACCATCTTGTACACTGGCAATGACAAGTGGTCG 308

Qy         84 LeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGln 103
              :::|||||||||||||||||||||:::||||||::::::|||||||||||||||||||||
Db        309 ATAGACCCCCGTGTGGTGCTTCTGGCCAACACAAAGAGTCAGTACAGCATTGAGATCCAA 368

Qy        104 AsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisPro 123
              |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AATGTGGACATTTATGATGAGGGACCCTACACCTGCTCTGTGCAGACAGACAATCACCCC 428

Qy        124 LysThrSerArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSer 143
```

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              |||||||||||||||||||||||||||||||||   |||:::||||||:::|||||||||
Db        429 AAAACCTCTCGTGTACATCTCATTGTGCAAGTTCCCCCTCGAATTGTTGATATTTCTTCA 488

Qy        144 AspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgPro 163
              :::|||::::::|||||||||:::|||:::||||||   |||||||||||||||||||||
Db        489 AATATTGCTGTTAATGAAGGCAGTAATGTCAGCCTGATTTGCATTGCAACCGGGAGACCT 548

Qy        164 GluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAsp 183
              ||||||   |||   ||||||::::::||||||||||||   ||||||||||||||||||
Db        549 GAACCCGTAGTGAACTGGAGATACTTGTCCCCTAAAGCACGGGGTTTTGTAAGTGAAGAT 608

Qy        184 GluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAla 203
              |||||||||||||||   ||||||||||||||||||||||||   |||||||||||||||
Db        609 GAGTACCTGGAAATCACAGGAATCACTAGGGAGCAGTCTGGAATATATGAATGCAGTGCG 668

Qy        204 SerAsnAspValAlaAlaProValValArgArgValLysValThrValAsnTyrProPro 223
              ||||||||||||:::||||||   |||||||||||||||:::||||||||||||||||||
Db        669 TCCAATGATGTCTCGGCACCAGATGTCCGAAGGGTTAAATTAACAGTTAATTACCCACCA 728

Qy        224 TyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCys 243
              ||||||   :::|||:::      |||   |||:::|||   :::|||   |||||||||
Db        729 TACATTCTGGATGCACAGAACATCGGGGCTCCCCTTGGCCATCGAGGTATTTTGCAGTGT 788

Qy        244 GluAlaSerAlaValProSerAla-GluPheGlnTrpTyrLysAspAspLysArgLeuIl 263
              ||||||||||||||||||:::||| :::|||   |||||||||:::||||||||||||
Db        789 GAAGCCTCTGCTGTACCTGCAGCCCGACTTCTTCTGGTACAAGGAAGACAAAAGGCTGAG 848

Qy        263 eGluGlyLysLys-GlyValLysValGlu 272
               :::      ::: |||||||||||||||
Db        849 TGATTCATGGAGGGGGGGTCAAAGTAGAG 877

RESULT 12
CF737474
LOCUS       CF737474                 759 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  UI-M-HD0-cks-o-09-0-UI.r1 NIH_BMAP_HD0 Mus musculus cDNA clone
            IMAGE:30614264 5', mRNA sequence.
ACCESSION   CF737474
VERSION     CF737474.1  GI:37633810
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 759)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1..759
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30614264"
                     /tissue_type="whole eye"
                     /dev_stage="embryo 12.5,13.5,14.5 dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_HD0"
                     /note="Organ: Eye; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I;. The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel.First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site .Double strand cDNA was
                     size selected according to mRNA size fraction ,ligated
                     with EcoR I adaptor , digested with NotI and then cloned
                     directionally into pYX-Asc vector . The library tag
                     sequence located between the Not I site and the polyA tail
                     is TTATTGAAGT. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH)."
ORIGIN

Alignment Scores:
Pred. No.:              9.25e-118      Length:        759
Score:                  1094.50        Matches:       216
Percent Similarity:     92.83%         Conservative:  4
Best Local Similarity:  91.14%         Mismatches:    14
Query Match:            60.60%         Indels:        4
DB:                     7              Gaps:          1

US-10-017-084A-523 (1-344) x CF737474 (1-759)

Qy         12 IleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe---------GlnGly 28
              :::   |||               ::::::         ||||||            |||
Db         45 CTGCCCTGGAAGTGCCTCGTGGTCGTGTCTCTCAGGCTGCTATTCCTTGTACCCACAGGA 104

Qy         29 ValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArg 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 GTGCCGGTGCGTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAACGTGACGGTCAGG 164

Qy         49 GlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrp 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 CAGGGGGAGAGCGCCACCCTCAGGTGCACAATTGACAACCGAGTCACCCGGGTGGCCTGG 224

Qy         69 LeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgVal 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 CTAAACCGCAGTACCATCCTCTATGCTGGAAATGACAAGTGGTGCCTAGATCCTCGTGTG 284

Qy         89 ValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyr 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GTCCTCCTGAGTAACACCCAGACCCAGTACAGCATTGAGATCCAGAATGTGGATGTGTAC 344

Qy        109 AspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgVal 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 GATGAGGGCCCTTATACCTGCTCGGTACAGACAGACAACCACCCTAAGACCTCCAGGGTC 404

Qy        129 HisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsn 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 CACCTCATTGTACAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAAT 464

Qy        149 GluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThr 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GAAGGGAACAACATCAGCCTCACTTGCATAGCCACAGGTAGACCGGAGCCTACAGTAACC 524

Qy        169 TrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIle 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 TGGAGACATATTTCTCCCAAGGCCGTTGGCTTTGTGAGTGAGGATGAGTACCTGGAGATC 584

Qy        189 GlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAla 208
              |||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db        585 CAGGGCATCACTCGGGAACAGTCAGGCGAGTACGAGTGCAGCGCCTCCAACGACGTGGCG 644

Qy        209 AlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAla 228
              |||||||||||||||||||||||||||||||||   ||||||||||||||||||   |||
Db        645 GCACCAGTGGTACGAAGAGTGAAGGTCACCGTGNACTATCCACCATACATCTCAAGAGCT 704

Qy        229 LysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAla 245
              |||||||||||||||||||||||||||   |||   |||||||||||||||
Db        705 AAGGGCACAGGTGTCCCCGTGGGGCAAGANGGACT-CTGCAGTGTGAAGCT 754

RESULT 13
AL533026
LOCUS       AL533026                1027 bp    mRNA    linear   EST 24-MAR-2004
```

```
DEFINITION  AL533026 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
            CS0DN005YD20 5-PRIME, mRNA sequence.
ACCESSION   AL533026
VERSION     AL533026.3  GI:45707932
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1027)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:31070858.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 6387.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DN005DB10QP1&c=6387.f.
FEATURES             Location/Qualifiers
     source          1..1027
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DN005YD20"
                     /tissue_type="ADULT BRAIN"
                     /dev_stage="adult"
                     /clone_lib="Homo sapiens ADULT BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN

Alignment Scores:
Pred. No.:              8.59e-114      Length:        1027
Score:                  1062.50        Matches:       211
Percent Similarity:     84.19%         Conservative:  2
Best Local Similarity:  83.40%         Mismatches:    0
Query Match:            58.83%         Indels:        40
DB:                     1              Gaps:          1

US-10-017-084A-523 (1-344) x AL533026 (1-1027)

Qy          132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
                ::::::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           98 ATTAAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC 157

Qy          152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          158 AATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACAC 217

Qy          172 IleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIle 191
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          218 ATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATC 277

Qy          192 ThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          278 ACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTG 337

Qy          212 ValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThr 231
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          338 GTACGGAGAGTAAAGGTCACCGTGAACTATCCACCATACATTTCAGAAGCCAAGGGTACA 397

Qy          232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          398 GGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCA 457

Qy          252 GluPheGlnTrpTyrLysAspAsp-Lys-------------------------------- 260
                |||||||||||||||||||||||| |||
Db          458 GAATTCCAGTGGTACAAGGATGACAAAAGAGCTGAAATCTCATTCACAGTTTGGTTATGA 517

Qy          260 ------------------------------------------------------------ 260

Db          518 TGGGAAAGCTTCCTCCCCATGGTGGACGAATGGTGTCAAAACGGCCAGTGGGATCAATCA 577

Qy          261 -------------------------ArgLeuIleGluGlyLysLysGlyValLysValGl 272
                                         |||||||||||||||||||||||||||||||||||
Db          578 GCCTGACTTGCTCGCAGAATCCTCCCGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGA 637

Qy          272 uAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAs 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          638 AAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA 697

Qy          292 nTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGl 312
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          698 CTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGG 757

Qy          312 yProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLe 332
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          758 TCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCT 817

Qy          332 uLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
                |||||||||||||||||||||||||||||||||||||
Db          818 GCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 854

RESULT 14
CR602526
LOCUS       CR602526                2512 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DN005YD20 of Adult brain of Homo sapiens
            (human).
ACCESSION   CR602526
VERSION     CR602526.1  GI:50483333
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2512)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2512)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1..2512
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DN005YD20"
                     /tissue_type="Adult brain"
                     /plasmid="pCMVSPORT_6"
ORIGIN

Alignment Scores:
Pred. No.:              3.34e-113      Length:        2512
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```
Score:                    1062.50       Matches:        211
Percent Similarity:       84.19%        Conservative:   2
Best Local Similarity:    83.40%        Mismatches:     0
Query Match:              58.83%        Indels:         40
DB:                       3             Gaps:           1

US-10-017-084A-523 (1-344) x CR602526 (1-2512)

Qy        132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
              ::::::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 ATTAAAGTATCTCCCAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAC 156

Qy        152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 AATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACAC 216

Qy        172 IleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIle 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 ATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATC 276

Qy        192 ThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211
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Db        277 ACCAGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTG 336

Qy        212 ValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThr 231
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Qy        232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251
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Db        397 GGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCA 456

Qy        252 GluPheGlnTrpTyrLysAspAsp-Lys-------------------------------- 260
              |||||||||||||||||||||||| |||
Db        457 GAATTCCAGTGGTACAAGGATGACAAAAGAGCTGAAATCTCATTCACAGTTTGGTTATGA 516

Qy        260 ------------------------------------------------------------ 260

Db        517 TGGGAAAGCTTCCTCCCCATGGTGGACGAATGGTGTCAAAACGGCCAGTGGGATCAATCA 576

Qy        261 -------------------------ArgLeuIleGluGlyLysLysGlyValLysValGl 272
                                       |||||||||||||||||||||||||||||||||||
Db        577 GCCTGACTTGCTCGCAGAATCCTCCCGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGA 636

Qy        272 uAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAs 292
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Db        637 AAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA 696

Qy        292 nTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGl 312
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Db        697 CTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGG 756

Qy        312 yProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrpLe 332
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Db        757 TCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCT 816

Qy        332 uLeuProLeuLeuValLeuHisLeuLeuLeuLysPhe 344
              |||||||||||||||||||||||||||||||||||||
Db        817 GCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT 853

RESULT 15
BU368328
LOCUS       BU368328                 740 bp    mRNA    linear   EST 28-NOV-2002
DEFINITION  603789424F1 CSEQCHN72 Gallus gallus cDNA clone ChEST750p6 5', mRNA
            sequence.
ACCESSION   BU368328
VERSION     BU368328.1  GI:25876329
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
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REFERENCE   1  (bases 1 to 740)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
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                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="Compton Line 15I"
                     /db_xref="taxon:9031"
                     /clone="ChEST750p6"
                     /sex="Female"
                     /tissue_type="cerebrum"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN72"
                     /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
                     EcoRI; Site_2: Not1; This normalized library was
                     constructed from 1 million independent clones. cDNA
                     synthesis was initiated using an oligo(dT) primer, using
                     methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
ORIGIN

Alignment Scores:
Pred. No.:                3.49e-112     Length:         740
Score:                    1047.00       Matches:        192
Percent Similarity:       91.85%        Conservative:   22
Best Local Similarity:    82.40%        Mismatches:     19
Query Match:              57.97%        Indels:         0
DB:                       5             Gaps:           0

US-10-017-084A-523 (1-344) x BU368328 (1-740)

Qy        101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
              :::|||   :::||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CAGATCCACGACGTGGACGTGTACGATGAAGGGCCCTACACCTGCTCCGTGCAGACAGAC 62

Qy        121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         63 AATCACCCCAAGACATCTCGCGTGCACCTCATTGTGCAAGTGTCGCCGAAAATTACCGAG 122

Qy        141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
              ||||||||||||||||||||||||||||||   |||:::|||||||||||||||||||||
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Qy        161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
              |||||||||:::||||||:::||||||||||||||||||||||||||||||||||||:::
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              ||||||||||||||||||||||||   ||||||||||||||||||||||||:::||||||
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Qy        201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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Db        303 TGCAGTGCCTCCAACGACGTGGCCGCGCCTGTCGTCCAGCGAGTCAAAGTCACCGTCAAC 362

Qy        221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
              ||||||||||||||||||:::||||||   |||||||||||||||||||||||||||
Db        363 TACCCACCGTACATCTCGGATGCGAAGAGCACCGGTGTGCCGGTGGGGCAGAAGGGCATC 422

Qy        241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
              |||   |||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db        423 CTGATGTGTGAAGCCTCCGCTGTGCCCTCCGCTGACTTCCAGTGGTACAAAGACGACAAG 482

Qy        261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
              ||||||   ||||||:::||||||:::||||||||||||:::   |||   |||:::|||
Db        483 CGGCTGGCTGAAGGACAGAAAGGGCTGAAGGTGGAAAACAAAGCCTTCTTCTCCCGACTG 542

Qy        281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
                 ||||||||||||||||||   |||||||||||||||||||||||||||||||||:::
Db        543 ACTTTCTTCAACGTCTCCGAGCAGGACTACGGCAACTACACCTGCGTGGCCTCCAACCAG 602

Qy        301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
              ||||||:::||||||||||||::::::|||:::|||||||||||||||   :::   :::
Db        603 CTAGGAAACACCAACGCCAGCATGATCCTTTATGGCCCCGGTGCAGTGCACGATGGCAAC 662

Qy        321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeu 333
              :::|||      ||||||      |||   |||||||||
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Search completed: June 16, 2005, 14:15:04
Job time : 4049 secs
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